cobas® eplex blood culture identification gram-positive (BCID-GP) panel

Package Insert

CE 2797 IVD UKCA

Rx Only

Designed For the Patient, Optimized For the Lab®

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INTENDED USE

The **cobas eplex** blood culture identification gram-positive (BCID-GP) panel is a qualitative nucleic acid multiplex *in vitro* diagnostic test intended for use on **cobas eplex** instrument for simultaneous qualitative detection and identification of multiple potentially pathogenic gram-positive bacterial organisms and select determinants associated with antimicrobial resistance in positive blood culture. In addition, the **cobas eplex** BCID-GP panel is capable of detecting a wide variety of gram-negative bacteria (Pan Gram-Negative assay) and several *Candida* species (Pan *Candida* assay). The **cobas eplex** BCID-GP panel is performed directly on blood culture samples identified as positive by a continuous monitoring blood culture system and which contain gram-positive organism.

The following bacterial organisms and genes associated with antibiotic resistance are identified using the **cobas eplex** BCID-GP panel: *Bacillus cereus* group, *Bacillus subtilis* group, *Corynebacterium*, *Cutibacterium acnes* (*Propionibacterium acnes*), *Enterococcus*, *Enterococcus faecalis*, *Enterococcus faecium*, *Lactobacillus*, *Listeria*, *Listeria monocytogenes*, *Micrococcus*, *Staphylococcus*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus lugdunensis*, *Streptococcus*, *Streptococcus agalactiae* (GBS), *Streptococcus anginosus* group, *Streptococcus pneumoniae*, *Streptococcus pyogenes* (GAS), *mecA*, *mecC*, *vanA* and *vanB*.

The **cobas eplex** BCID-GP panel contains assays for the detection of genetic determinants associated with resistance to methicillin (*mecA* and *mecC*) and vancomycin (*vanA* and *vanB*) to aid in the identification of potentially antimicrobial resistant organisms in positive blood culture samples. The antimicrobial resistance gene detected may or may not be associated with the agent responsible for disease.

The **cobas eplex** BCID-GP panel also contains targets designed to detect a broad range of organisms with a potentially misleading Gram stain result or organisms that may be missed by Gram staining altogether, for example in the case of co-infections. These include a broad Pan Gram-Negative assay as well as a Pan *Candida* assay, which is designed to detect four of the most prevalent *Candida* species: *Candida albicans*, *Candida glabrata*, *Candida krusei* and *Candida parapsilosis*.

The detection and identification of specific bacterial and fungal nucleic acids from individuals exhibiting signs and/or symptoms of bloodstream infection aids in the diagnosis of bloodstream infection when used in conjunction with other clinical information. The results from the **cobas eplex** BCID-GP panel are intended to be interpreted in conjunction with Gram stain results and should not be used as the sole basis for diagnosis, treatment, or other patient management decisions.

Negative results in the setting of a suspected bloodstream infection may be due to infection with pathogens that are not detected by this test. Positive results do not rule out co-infection with other organisms; the organism(s) detected by the **cobas eplex** BCID-GP panel may not be the definite cause of disease. Additional laboratory testing (e.g. sub-culturing of positive blood cultures for identification of organisms not detected by **cobas eplex** BCID-GP panel and for susceptibility testing, differentiation of mixed growth and association of antimicrobial resistance marker genes to a specific organism) and clinical presentation must be taken into consideration in the final diagnosis of blood stream infection.

SUMMARY AND EXPLANATION OF TEST

The **cobas eplex** BCID-GP panel is an automated qualitative nucleic acid multiplex *in vitro* diagnostic test for simultaneous detection and identification of multiple potentially pathogenic gram-positive bacterial organisms and select determinants associated with antimicrobial resistance in positive blood culture. The test also detects a wide variety of gram-negative bacteria and several pathogenic *Candida* species. The test is able to detect 20 gram-positive bacterial targets and 4 resistance genes. Multiple *Candida* species are detected as well as most relevant gram-negative organisms as summarized in **Table 1**. This test is performed on *The True Sample-to-Answer Solution*® **cobas eplex** instrument.

Gram-positive bacteria are a major cause of sepsis throughout the world. Many gram-positive organisms can cause severe sepsis, while others are considered opportunistic and are often deemed contaminants of blood products introduced into tests from the skin.[1]

Table 1: Targets Detected by the cobas eplex BCID-GP panel

Bacterial Targets	
Bacillus cereus group	*Micrococcus*
Bacillus subtilis group	*Staphylococcus*
Corynebacterium	*Staphylococcus aureus*
Cutibacterium acnes (*Propionibacterium acnes*)	*Staphylococcus epidermidis*
Enterococcus	*Staphylococcus lugdunensis*
Enterococcus faecalis	*Streptococcus*
Enterococcus faecium	*Streptococcus agalactiae*
Lactobacillus	*Streptococcus anginosus* group
Listeria	*Streptococcus pneumoniae*
Listeria monocytogenes	*Streptococcus pyogenes*
Antimicrobial Resistance Markers	
mecA (associated with resistance to methicillin)	*vanA* (associated with resistance to vancomycin)
mecC (associated with resistance to methicillin)	*vanB* (associated with resistance to vancomycin)
Pan Targets	
Pan Gram-Negative	Pan *Candida*

Local, state, and federal rules and regulations for notification of reportable diseases are continually updated and include a number of organisms that are important for surveillance and outbreak investigations.[2,3] Laboratories are responsible for following their state and/or local rules pertaining to reportable pathogens and should consult their local and/or state public health laboratories for isolate and/or clinical sample submission guidelines.

SUMMARY OF DETECTED ORGANISMS

Bacteria

***Bacillus cereus* group**
Bacillus cereus is a motile, aerobic to facultatively-anaerobic bacterium which has previously been considered a contaminant.[4] *Bacillus cereus* group consists of several species including *B. cereus, B. weihenstephanensis, B. thuringiensis* and *B. anthracis.*[5] These organisms have been implicated in pathologies ranging from progressive pneumonia to fulminant sepsis as well as infections of the central nervous system. Furthermore, *Bacillus cereus* is of growing concern in patients with hematologic malignancies, wound infections and intravascular devices.[6] *Bacillus cereus* has also been noted in intravenous drug users.[7]

***Bacillus subtilis* group**
Members of the *Bacillus subtilis* group are facultatively-aerobic, motile, commonly found in the soil[8] and consist of several species and subspecies including *B. subtilis*, *B. tequilensis*, *B. vallismortis*, *B. mojavensis*, *B. atrophaeus*, *B. amyloliquefaciens* (including *B. siamensis* and *B. velezensis*, *B. methylotrophicus*) and *B. licheniformis* (including *B. sonorensis*).[9, 10] *Bacillus* species are one of the most common sources of blood culture contamination which represent an estimated 3% of all blood culture tests run.[11] Despite being common contaminant, *Bacillus subtilis* group members have also been implicated in disease and have shown resistance to a range of antimicrobial agents leading to recurrent septicemia in some patients.[12]

Corynebacterium
Corynebacterium are catalase-positive, non-motile, gram-positive rods and are often a part of natural skin flora. These bacteria are typically considered contaminants of blood cultures unless found in multiple bottles but are increasingly recognized as opportunistic pathogens, especially in immunocompromised patients and catheter-related bloodstream infections.[13] Antibiotic resistance is common in *Corynebacterium*.[14]

***Cutibacterium acnes* (*Propionibacterium acnes*)**
Cutibacterium acnes is a non-sporulating, gram-positive, facultatively-anaerobic bacillus which is part of the natural flora of the human skin, conjunctiva, oral cavity and large intestine.[15] Although typically considered a blood culture contaminant, *Cutibacterium acnes* has been implicated in cases of endocarditis, endophthalmitis, intravascular infections, central nervous system infections and even arthritis.[16] In the cases of bloodstream infection, the mortality rate has been placed at approximately 5% despite its general susceptibility to a broad range of antibiotics.[16] *Cutibacterium acnes* is increasingly found in association with implanted devices including prosthetic joints, cerebrovascular shunts, breast implants and cardiovascular devices. This association with implanted devices may be due to the ability of the bacterium to form biofilms.[17]

Enterococcus
Enterococcus species are the third leading cause of hospital-acquired bacteremia, accounting for approximately 12% of all hospital infections.[18] *Enterococci* are inherently resistant to β-lactams, cephalosporins, glycopeptides, fluoroquinolones and aminoglycosides.[18,19] Furthermore, acquired resistance to other antibiotics including plasmid-mediated *vanA* and *vanB* gene complexes, which confer high and moderate-level vancomycin resistance, respectively, has increased in recent years.[18] Infections with vancomycin resistant strains of *Enterococcus* increase the risk of death from 45% to 75% as compared to susceptible strains.[20]

Enterococcus faecalis, Enterococcus faecium
Although several species of *Enterococcus* can cause infections, the two most common are *Enterococcus faecalis,* which accounts for 80-90% of human infections and *Enterococcus faecium,* which accounts for most of the remaining infections.[21,22] While both species can harbor vancomycin resistance, *Enterococcus faecium* is responsible for the majority of vancomycin-resistant enterococcal (VRE) infections, which have resulted in mortality rates as high as 75%.[22,23]

Lactobacillus
Lactobacilli are anaerobic or facultatively-anaerobic gram-positive rods. They are part of normal GI flora and are commonly considered blood culture contaminants although they have been reported as opportunistic organisms in immunocompromised patients.[24]

Listeria
Bacteria in the *Listeria* genus are facultatively-anaerobic, rod-shaped coccobacilli and are ubiquitous in the environment. Food-borne outbreaks of *Listeria* have occurred throughout the world and have been on the rise since 2008.[25] The *Listeria* genus contains at least 17 species. With the exception of *Listeria monocytogenes*, *Listeria* species are considered opportunistic and typically cause severe or even fatal infections only in immunocompromised persons.[26]

Listeria monocytogenes
Listeria monocytogenes is most typically a foodborne pathogen and is associated with infections especially in immunocompromised persons, the elderly and pregnant women.[26] In the case of pregnant women, the fetal mortality rate has been reported as high as 45% in some countries.[27] Listeriosis in persons with weakened immune systems may also lead to meningitis, brain infection, or severe bloodstream infection.[28]

Micrococcus
This highly diverse genera is made up of oxidase-positive, strictly aerobic cocci which typically occur in pairs, tetrads, or irregular clusters.[29] *Micrococcus* species are generally considered to be blood culture contaminants due to their ubiquity on human skin and in the environment,[30] they have proven to be opportunistic pathogens and implicated in recurrent bacteremia, septic shock, endocarditis, meningitis and other conditions in immunosuppressed patients.[31]

Staphylococcus
Staphylococci are members of the family *Micrococcaceae* and have an irregular grape-like clustering morphology. *Staphylococci* are divided into two major groups: coagulase-positive and coagulase-negative *Staphylococci* (CoNS).[32] In the past, coagulase-negative *Staphylococci* were typically believed to represent contamination when isolated from blood cultures. More recent studies have shown that CoNS can also be a source of true bacteremia, especially in patients with prosthetic devices and central venous catheters. Though only a low percentage of CoNS isolates are clinically significant, they are ranked as the third most common cause of bacteremia due to their high overall prevalence. Most organisms within the genera do not infect humans, however, *S. aureus* and *S. lugdunensis* have been implicated in a range of clinical infections including bacteremia, bone and joint infections and meningitis.[33]

Staphylococcus aureus
Staphylococcus aureus is a coagulase-positive bacteria frequently found in the human nose, respiratory tract and on the skin. *Staphylococcus aureus* infection can cause a diverse array of potentially fatal infections,[34] including bacteremia, pneumonia, endocarditis and osteomyelitis.[35]
When isolated from blood culture, *Staphylococcus aureus* is associated with a high morbidity and mortality rate.[36]

Approximately 10% of *Staphylococcus aureus* isolates in the United States are susceptible to penicillin, although many may be susceptible to oxacillin and methicillin.[37] Recent estimates point to methicillin-resistant *Staphylococcus aureus* (MRSA), which are resistant to both methicillin and oxacillin, as the cause of over 70,000 invasive infections and over 9,000 deaths in the United States each year alone.[37]

A major reason that *Staphylococcus aureus* can develop resistance to antibiotics so readily is its ability to harbor mobile genetic elements, which allow for transfer of resistance genes among *Staphylococcus aureus* strains. The two most common genes are *mecA* and *mecC,* which code for proteins that confer resistance to methicillin and oxacillin.

Staphylococcus epidermidis
Staphylococcus epidermidis has traditionally been considered an innocuous commensal organism of the human skin. It is now being seen as an important opportunistic pathogen and accounts for between 74% and 92% of all hospital-acquired CoNS infections.[38] *Staphylococcus epidermidis* is able to form biofilms on plastic devices, and isolates are often resistant to a multitude of antibiotics, further complicating effective treatment. Reports of mortality rates approaching 25% have been noted in retrospective studies.[39]

Staphylococcus lugdunensis
Staphylococcus lugdunensis is unique among CoNS due to its propensity for causing aggressive native valve infective endocarditis. *Staphylococcus lugdunensis* has also been implicated in bone and joint infections, soft tissue infections, bacteremia and meningitis.[40] This species is similar to *Staphylococcus aureus* in that infections can be severe and progress rapidly, however, most isolates of *Staphylococcus lugdunensis* remain susceptible to a wide variety of antimicrobial agents.[41,42] Approximately 3% of CoNS infections are caused by *Staphylococcus lugdunensis,* although cases are likely underreported due to a lack of speciation of CoNS in clinical labs. [43]

Streptococcus
Streptococcus are spherical or ovoid bacteria that group together in pairs or in chains. They are catalase-negative, non-spore-forming, facultative anaerobes.[44] Some species, like *Streptococcus pneumoniae* and *Streptococcus pyogenes* are well characterized pathogens, while others are considered opportunistic pathogens.[44]

***Streptococcus agalactiae* (GBS)**
Streptococcus agalactiae, also known as Group B *Streptococcus* (GBS), is a commensal beta-hemolytic bacteria present in the gastrointestinal and urogenital tracts of up to 30% of healthy adults.[45] Approximately one in ten children acquire GBS during the birthing process, although only 1% develop invasive disease.[455] While *Streptococcus agalactiae* does not typically cause disease, it is capable of causing a wide range of infections including pneumonia, bloodstream infections, urinary tract infections, and meningitis, in addition to stillbirth.[43] There are approximately 26,500 cases of severe GBS infections in the United States each year, with most represented as bloodstream infections, of which 5% prove fatal.[46]

***Streptococcus anginosus* group**
The *Streptococcus anginosus* group includes *S. anginosus*, *S. intermedius* and *S. constellatus,* all of which are typically considered commensal oral and gastrointestinal flora. When they do cause disease, they have a propensity toward dissemination and abscess formation.[47] Members of this group may be alpha, beta, or gamma hemolytic with the type of hemolysis varying even within each species. *Streptococcus anginosus* group species can cause invasive pyogenic infections, endocarditis, as well as localized infections of the gastrointestinal and urogenital tracts, the liver, lungs and brain.[48]

Streptococcus pneumoniae
Streptococcus pneumoniae is an alpha-hemolytic *Streptococcus* species which can cause a diverse set of infections including those of the ear, eye and sinuses. While more than 90 serotypes of *Streptococcus pneumoniae* exist, the 10 most common are responsible for over 60% of invasive disease worldwide. As a colonizer of the upper respiratory tract, *Streptococcus pneumoniae* is a common cause of pneumonia with between 25 and 30% of these cases progressing to pneumococcal bacteremia.[49]

***Streptococcus pyogenes* (GAS)**
Streptococcus pyogenes, also known as Group A *Streptococcus* (GAS), is a beta-hemolytic bacteria capable of causing a wide range of diseases which can be invasive or non-invasive in nature. These diseases include pharyngitis, impetigo, scarlet fever, bacteremia, toxic shock syndrome and others.[50] Invasive GAS infections are associated with an overall mortality rate of 10-13% according to the Centers for Disease Control.[51]

Antimicrobial Resistance Markers

mecA* / *mecC
Both *mecA* and *mecC* are genetic determinants associated with methicillin resistance, most commonly with Methicillin Resistant *Staphylococcus aureus* (MRSA). Methicillin resistant *Staphylococcus aureus* strains are resistant to all beta-lactams including cephalosporins and carbapenems.[52] Resistance in MRSA is caused by the production of a novel *mecA*-encoded penicillin-binding protein 2a (PBP2a) or its novel homologue encoded by *mecC*. Resistance in MRSA is achieved through the decreased binding affinity to beta-lactams which prevents effective treatment with methicillin. While both *mecA* and *mecC* are capable of conferring resistance to methicillin, they share only 70% sequence similarity,[53] which has resulted in many early PCR-based assays misclassifying *mecC* positive strains as methicillin-susceptible.

vanA* / *vanB
Both *vanA* and *vanB* are genetic determinants associated with vancomycin resistance found on mobile genetic elements called transposons. Transposons can either be found chromosomally integrated or on plasmids. Isolates containing the *vanA* marker are resistant to high levels of vancomycin as well as teicoplanin. In contrast, *vanB* isolates are typically moderately resistant to vancomycin and susceptible to teicoplanin. Mortality rates for vancomycin resistant *Enterococcus* species have been reported as high as 75% as compared to 45% for susceptible strains.[20]

Pan Targets

Gram staining is highly accurate; however some organisms are known to be gram-variable, meaning that the Gram stain may produce misleading results. Additionally, inaccurate Gram stains have been noted in the instance of polymicrobial infections.[54] The **cobas eplex** BCID-GP panel includes two pan targets designed to detect but not differentiate organisms that may be missed by Gram stain.

Pan Gram-Negative
The Pan Gram-Negative assay is designed to detect a broad range of gram-negative organisms including those with a potentially misleading Gram stain result. The Pan Gram-Negative assay may provide data to facilitate the correct testing algorithm. If a Pan Gram-Negative target is detected, supplementary testing to determine the identity of the gram-negative organism is recommended.

Pan *Candida*
The Pan *Candida* assay is designed to detect four of the most prevalent *Candida* species: *Candida albicans, Candida glabrata, Candida krusei* and *Candida parapsilosis*. Since some fungal organisms, like *Candida*, are known to grow slowly, they may go unnoticed on Gram stains, especially in the case of mixed infection. The Pan *Candida* target may provide data to facilitate the correct testing algorithm. If the Pan *Candida* assay is positive, supplementary testing to determine the identity of the *Candida* species is recommended.

PRINCIPLES OF TECHNOLOGY

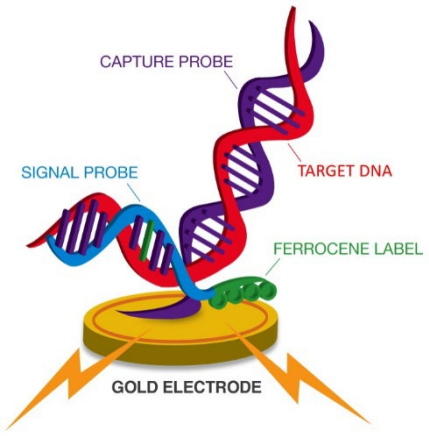
The True Sample-to-Answer Solution **cobas eplex** instrument automates all aspects of nucleic acid testing including extraction, amplification and detection, combining electrowetting and the eSensor® technology in a single-use cartridge. eSensor technology is based on the principles of competitive DNA hybridization and electrochemical detection, which is highly specific and is not based on fluorescent or optical detection.

Electrowetting, or digital microfluidics, uses electrical fields to directly manipulate discrete droplets on the surface of a hydrophobically coated printed circuit board (PCB). Sample and reagents are moved in a programmable fashion in the **cobas eplex** cartridge to complete all portions of the sample processing from nucleic acid extraction to detection.

A sample is loaded into the **cobas eplex** cartridge, and the cartridge is placed into the **cobas eplex** instrument. Nucleic acids are extracted and purified from the specimen via magnetic solid phase extraction. PCR is used to create double-stranded DNA, which is treated with exonuclease to create single-stranded DNA in preparation for eSensor technology detection.

The target DNA is mixed with ferrocene-labeled signal probes that are complementary to the specific targets on the panel. Target DNA hybridizes to its complementary signal probe and capture probes, which are bound to gold-plated electrodes, as shown below in **Figure 1**. The presence of each target is determined by voltammetry which generates specific electrical signals from the ferrocene-labeled signal probe.

Figure 1: Hybridization complex. Target-specific capture probes are bound to the gold electrodes in the eSensor microarray on the **cobas eplex** cartridge. The amplified target DNA hybridizes to the capture probe and to a complementary ferrocene-labeled signal probe. Electrochemical analysis determines the presence or absence of targets using voltammetry.



MATERIALS PROVIDED

Table 2: *The True Sample-to-Answer Solution*®
cobas eplex blood culture identification gram-positive panel Kit Contents

Product	Item number	Components (quantity)	Storage
cobas eplex blood culture identification gram-positive (BCID-GP) panel	GenMark: EA003012 Roche: 9556508001	**cobas eplex** BCID-GP panel Cartridge (12)	2–8 ˚C

COMPOSITION OF REAGENTS

Component	Concentration (w/v)
Salting Buffer	
Guanidine hydrochloride	≤ 45%
Sodium perchlorate	≤ 14%
Binding Buffer	
PEG 8000	≤ 20%
NaH_2PO_4	≤ 1.0%
EDTA	≤ 0.1%
NaCl	≤ 5.0%
NaN_3	≤ 0.2%
Cysteamine HCl	≤ 1.0%
MTG	≤ 1.0%
Lysis Buffer	
Tris-HCl	≤ 5.0%
Urea	25% - 50%
Guanidine hydrochloride	≤ 2.0%
Calcium Chloride	≤ 1.0%
SDS	≤ 5.0%
Tween-20	10% - 20% (v/v)
Oil Component	
Polydimethylsiloxane, Trimethylsiloxy Terminated, 5 cSt	≥ 95%

Component	Concentration (w/v)
Recon/Elution Buffer	
Sodium azide	≤ 0.2%
Tween-20	≤ 2.0% (v/v)
Wash Buffer	
PEG 8000	≤ 20%
NaH_2PO_4	≤ 1.0%
EDTA	≤ 0.1%
NaCl	≤ 5.0%
NaN_3	≤ 0.2%
Cysteamine HCl	≤ 1.0%
MTG	≤ 1.0%
Tween-20	≤ 2.0% (v/v)
PCR Reaction	
Tris-HCl	≤ 5.0%
KCl	≤ 5.0%
Trehalose	10% - 50%
Bovine Serum Albumin	≤ .05%
dNTPs	Trace
$MgCl_2$	≤ 0.1%
Oligonucleotides	Trace

Upon receipt, reagents should be stored at 2–8 °C. SDSs are available on request from your local Roche representative or can be accessed via eLabDoc.

REAGENT STORAGE, STABILITY AND HANDLING

- Store the **cobas eplex** BCID-GP panel kit at 2–8 ˚C.
- Do not use **cobas eplex** BCID-GP panel kit beyond the expiration date.
- Do not open a cartridge pouch until you are ready to perform testing.

MATERIALS NOT PROVIDED

Equipment

- **cobas eplex** instrument and software
- Pipettes capable of delivering 50µL
- Printer (optional) - See **cobas eplex** Operator Manual for compatibility guidelines

Consumables

- Pipette tips, aerosol resistant, RNase/DNase-free
- Disposable, powder free gloves
- 10% bleach for appropriate surfaces
- 70% ethanol or isopropyl alcohol (or equivalent) for appropriate surfaces
- 1.5mL RNase/DNase-free microcentrifuge tube or equivalent (optional)

WARNINGS AND PRECAUTIONS

General

- For *in vitro* diagnostic use only, by laboratory professionals.
- A trained healthcare professional should carefully interpret the results from the **cobas eplex** BCID-GP panel in conjunction with a patient's signs and symptoms and results from other diagnostic tests.
- Positive results do not rule out co-infection with other viruses, bacteria, or fungi. The agent(s) detected may not be the definitive cause of disease. The use of additional laboratory testing (*e.g.*, bacterial, fungal and viral culture, immunofluorescence and radiography) and clinical presentation must be taken into consideration in the final diagnosis of a bloodstream infection.
- Do not reuse **cobas eplex** BCID-GP panel kit components.
- Do not use reagents beyond the expiration date printed on the labeling.
- Follow the procedure as described in this package insert. Read all instructions before starting the test.
- Inform your local competent authority and the manufacturer about any serious incidents which may occur when using this assay.

Safety

- Handle all specimens and waste materials as if they were capable of transmitting infectious agents in accordance with Universal Precautions. Observe safety guidelines such as those outlined in CDC/NIH *Biosafety in Microbiological and Biomedical Laboratories,* CLSI Document M29 *Protection of Laboratory Workers from Occupationally Acquired Infections*, or other appropriate guidelines.
- Follow routine laboratory safety procedures for handling of reagents (*e.g.*, do not pipette by mouth, wear appropriate protective clothing and eye protection).
- Follow your institution's safety procedures for handling biological samples.
- Dispose materials used in this test, including reagents, specimens and used vials, in accordance with all federal, state and local regulations.
- Do not stick fingers or other objects inside the **cobas eplex** instrument bays.
- Wash hands thoroughly with soap and water after handling reagents. Launder contaminated clothing prior to re-use.
- Do not puncture or pierce reagent blisters on the **cobas eplex** cartridge. Reagents may cause irritation to skin, eyes and respiratory tract. Harmful if swallowed or inhaled. Contains oxidizing liquids.
- The **cobas eplex** BCID-GP panel cartridge contains chemicals that are classified as hazardous. Review the Safety Data Sheet (SDS) before use and in cases of exposure, refer to the SDS for more information. Safety Data Sheets (SDS) are available on request from your local Roche representative or can be accessed via eLabDoc.
- Contamination of the sample may occur if laboratory personnel processing the sample are colonized with any number of commensal organisms. To avoid this, specimens should be processed in biosafety cabinets utilizing proper personal protective equipment. If a biosafety cabinet is not used, a splash shield or face mask should be worn when processing samples.
- Change gloves frequently during testing to reduce the risk of contamination.
- Thoroughly decontaminate the lab and all equipment with 10% bleach followed by 70% ethanol or isopropyl alcohol (or equivalent).

Laboratory

- Contamination of the sample may occur if laboratory personnel processing the sample carry common pathogens and contaminants. To avoid this, specimens should be processed in biosafety cabinets. If a biosafety cabinet is not used, a splash shield or face mask should be used when processing samples.
- A biosafety cabinet that is used for bacterial or fungal culture should not be used for sample preparation.
- Samples and cartridges should be handled and/or tested one at a time. To mitigate the risk of sample-to-sample contamination, change gloves after dispensing sample into the cartridge.
- Thoroughly decontaminate the lab and all equipment with 10% bleach followed by 70% ethanol or isopropyl alcohol (or equivalent) prior to processing a specimen.
- Contamination of the sample may occur if the sample is loaded in an area where PCR amplicons are generated. Avoid loading sample in areas that are potentially contaminated with PCR amplicon.

SPECIMEN COLLECTION, HANDLING AND STORAGE

- Blood culture bottles should be handled according to manufacturer's recommended procedure.
- Clinical specimens can remain in the incubator for up to 12 hours beyond bottle positivity.
- Clinical specimens can be stored at room temperature for up to 7 days.
- Clinical specimens can be stored at 4˚C for up to 1 month.
- Clinical specimens can be stored at -20˚C to -80˚C for up to 18 months.
- Clinical specimens can be subjected to up to two freeze/thaw cycles.

PROCEDURE

Procedural Notes

- The detection of bacterial or fungal nucleic acid is dependent upon proper specimen collection, handling, transportation, storage and preparation. Failure to observe proper procedures in any one of these steps can lead to incorrect results. There is a risk of both false positive and false negative results due to improperly collected, transported, or handled specimens.
- Not Detected results may occur due to the presence of inhibitors, technical error, sample mix-up, or an infection caused by an organism not detected by the panel
- Samples should be positive blood culture as confirmed by Gram stain.
- Samples, consumables and lab areas should be protected from aerosol or direct contamination with amplicon. Decontaminate laboratory areas and affected equipment with 10% bleach followed by 70% ethanol or isopropyl alcohol (or equivalent).
- Samples should be loaded to **cobas eplex** BCID-GP panel cartridge in an amplicon-free, clean environment.
- Samples should be processed in biosafety cabinets. If a biosafety cabinet is not used, a splash shield or face mask should be worn when processing samples.
- Change gloves frequently during testing to reduce the risk of contamination.
- Once a cartridge is removed from foil pouch, it should be used within 2 hours. Do not open the test cartridge pouch until the sample is ready to be tested.
- All frozen samples should be thawed completely and mixed well before testing.
- The blood culture bottle should be inverted several times to mix.
- Allow approximately 10 seconds for the resin to settle.
- The septum of the positive blood culture bottle should be wiped with 70% ethanol or isopropyl alcohol (or equivalent) prior to withdrawing the sample.
- Use sterile materials for transfer and loading of each sample. Ensure that no part of the transfer device touches the inside of any transfer container that may be used. A shallow vessel such as a 1.5mL microcentrifuge tube is recommended for transfer.
- Once the sample is loaded onto the **cobas eplex** BCID-GP panel cartridge, the sample should be processed within 2 hours.
- Do not insert a wet cartridge into the **cobas eplex** instrument. If liquid is present on outside of test cartridge, use a low lint lab wipe (e.g. Kimwipes™) to remove liquid prior to inserting into **cobas eplex** bay.
- Dispose materials used in this test, including reagents, specimens and used vials, in accordance with all regulations.
- Do not re-use cartridges.

Detailed Procedure

1. Decontaminate the area used for setting up the **cobas eplex** BCID-GP panel with 10% bleach followed by 70% ethanol or isopropyl alcohol (or equivalent).
2. Remove one **cobas eplex** BCID-GP panel cartridge pouch from kit packaging.
3. Open **cobas eplex** BCID-GP panel cartridge pouch.
4. Write the accession ID or place a barcode label with accession ID on the **cobas eplex** BCID-GP panel cartridge.
5. Invert the blood culture bottle several times to mix.
6. Allow approximately 10 seconds for the resin to settle.
7. Wipe the septum of the positive blood culture bottle with 70% ethanol or isopropyl alcohol (or equivalent) prior to withdrawing the sample.
8. Using a loading device capable of accurately delivering 50µL, aspirate 50µL of blood culture sample and load into the sample loading port of the **cobas eplex** BCID-GP panel cartridge.
   NOTE: a 1.5mL microcentrifuge tube is recommended for transfer of sample from the blood culture bottle prior to loading **cobas eplex** cartridge.
9. Close the sample loading port immediately by sliding the cap over the port and firmly pushing down on the cap to securely seal the sample delivery port.
   NOTE: Bubbles can be present when closing the cap.
10. Scan the **cobas eplex** BCID-GP panel cartridge using the barcode reader provided with the **cobas eplex** instrument.
    NOTE: If an accession ID barcode label is not used, manually enter accession ID with the on-screen keyboard.
    NOTE: The barcode scanner will read both the accession ID barcode (if placed on the cartridge by the operator) and the 2D barcode printed on the cartridge label; however, the barcode scanner will only beep once to indicate that both barcodes have been read.
11. Insert the **cobas eplex** BCID-GP panel cartridge into any available bay, indicated by a flashing, white LED light. The test will begin automatically when the cartridge has been inserted into the bay and the pre-run check is completed, as indicated by a blue LED light.

QUALITY CONTROL

Internal Controls

Each cartridge includes internal controls that monitor performance of each step of the testing process, including extraction, amplification and detection of targets.

Each amplification reaction on the cartridge has an internal control and in each reaction either the internal control or a target must generate signal above the defined threshold for a valid test result. Internal control results are interpreted by the **cobas eplex** software and displayed on the **cobas eplex** BCID-GP panel Reports as Internal Control with a result of PASS, FAIL, N/A or INVALID. **Table 3** includes details on the interpretation of Internal Control results.

Table 3: Internal Control Results

Internal Control Result	Explanation	Action
PASS	Signal above threshold has been detected from each amplification reaction. The test was completed and internal controls were successful, indicating valid results were generated.	All results are displayed on the **cobas eplex** BCID-GP panel Detection Report. Test is valid, report results.
FAIL	Signal above threshold has not been detected from at least one amplification reaction. The test was completed but internal controls were not detected, indicating that results may not be valid.	No results are displayed on the **cobas eplex** BCID-GP panel Detection Report. Test is not valid, repeat the test using a new cartridge.
N/A	The internal control in every amplification reaction does not generate signal above the threshold, but a target in every amplification reaction does generate signal above the threshold. The test was completed and internal controls were not successful, however detection of signal above the threshold for a target in every amplification reaction indicates valid results were generated.	All results are displayed on the **cobas eplex** BCID-GP panel Detection Report. Test is valid, report results.
INVALID	An error has occurred during processing that prevents analysis of signal data. The test has not successfully completed and results for this test are not valid. This may be due to an instrument or software error.	No results are displayed on the **cobas eplex** BCID-GP panel Detection Report. Test is not valid, repeat the test using a new cartridge.

External Controls

Positive and negative external controls should be tested as part of good laboratory practice, in accordance with the appropriate accrediting organization as applicable and following the user's laboratory standard quality control procedures. Blood culture medium can be used as the negative control. Previously characterized positive samples or blood culture medium spiked with well characterized organisms can be used as the external positive control. External controls should be run in accordance with laboratory protocols and accrediting organizations, as applicable.

RESULTS

Table 4: Interpretation of Results on the cobas eplex BCID-GP panel Detection Report

Target Result	Explanation	Action
Detected	The test was completed successfully and the target has generated signal above its defined threshold and the Internal Control was reported as PASS.	All results are displayed on the **cobas eplex** BCID-GP panel Detection Report. Test is valid, report results.
Not Detected	The test was completed successfully and the target did not generate signal above its defined threshold and the Internal Control was reported as PASS.	All results are displayed on the **cobas eplex** BCID-GP panel Detection Report. Test is valid, report results.
N/A	The test was completed successfully and an associated organism for the antibiotic resistance gene target was not detected (see **Table 9** for resistance marker organism associations).	All results are displayed on the **cobas eplex** BCID-GP panel Detection Report. Test is valid, report results.
Invalid	The test has not successfully completed and results for this test are not valid. This may be due to an instrument or software error.	No results are displayed on the **cobas eplex** BCID-GP panel Detection Report. Test is not valid, repeat test.

Genus and Group Assay Result Interpretation

While many results on the **cobas eplex** BCID-GP panel are based on a single assay, the **cobas eplex** BCID-GP panel uses multiple assays for the *Enterococcus*, *Listeria*, *Staphylococcus* and *Streptococcus* results.

The **cobas eplex** BCID-GP panel *Enterococcus* result is based on three assays: the species-specific *Enterococcus faecalis* and *Enterococcus faecium* assays and a broad *Enterococcus* assay. The broad *Enterococcus* assay will detect *Enterococcus faecalis* and *Enterococcus faecium*, however, its primary purpose is to detect non-*faecalis/faecium Enterococcus* species. If all three assays are negative, the *Enterococcus* result will be Not Detected. If any of the three assays is positive, the *Enterococcus* result will be 'Detected'. If only the *Enterococcus* assay is positive, an unspeciated *Enterococcus* species has been detected. See **Table 5** for detailed *Enterococcus* target call logic.

Table 5: *Enterococcus* Target Results from cobas eplex BCID-GP panel Detection Report

***Enterococcus* Result**	***Enterococcus* Assay**	***Enterococcus faecalis* Assay**	***Enterococcus faecium* Assay**	**Description**
Not Detected	Negative	Negative	Negative	No *Enterococcus* species Detected
Detected	Positive	Positive	Negative	*Enterococcus faecalis* Detected
Detected	Positive	Negative	Positive	*Enterococcus faecium* Detected
Detected	Positive	Positive	Positive	*Enterococcus faecalis* Detected *Enterococcus faecium* Detected
Detected	Positive	Negative	Negative	Unspeciated *Enterococcus* Detected

The **cobas eplex** BCID-GP panel *Listeria* result is based on two assays: the species-specific *Listeria monocytogenes* assay and a broad *Listeria* assay. The broad *Listeria* assay will detect multiple *Listeria* species including *Listeria monocytogenes*, however, its primary purpose is to detect non-*monocytogenes* *Listeria* species. If either assay is positive, the *Listeria* result will be 'Detected'. If only the *Listeria* assay is positive, an unspeciated *Listeria* species has been detected. See **Table 6** for detailed *Listeria* target call logic.

Table 6: *Listeria* Target Results from cobas eplex BCID-GP panel Detection Report

***Listeria* Result**	***Listeria* Assay**	***Listeria monocytogenes* Assay**	**Description**
Not Detected	Negative	Negative	No *Listeria* species Detected
Detected	Positive	Positive	*Listeria monocytogenes* Detected
Detected	Positive	Negative	Unspeciated *Listeria* Detected

The **cobas eplex** BCID-GP panel *Staphylococcus* result is based on four assays: the species-specific *Staphylococcus aureus, Staphylococcus epidermidis* and *Staphylococcus lugdunensis* assays and a broad *Staphylococcus* assay. The broad *Staphylococcus* assay will detect each of the species targeted by the species-specific assays, but its primary purpose is to detect other *Staphylococcus* species. If all four assays are negative, the *Staphylococcus* result will be 'Not Detected'. If any of the four assays is positive, the *Staphylococcus* result will be 'Detected'. If only the *Staphylococcus* assay is positive, an unspeciated *Staphylococcus* has been detected. See **Table 7** for detailed *Staphylococcus* target call logic**.**

Table 7: *Staphylococcus* Target Results from cobas eplex BCID-GP panel Detection Report

***Staphylococcus* Result**	***Staphylococcus* Assay**	***Staphylococcus aureus* Assay**	***Staphylococcus epidermidis* Assay**	***Staphylococcus lugdunensis* Assay**	**Description**
Not Detected	Negative	Negative	Negative	Negative	No *Staphylococcus* species Detected
Detected	Positive	Positive	Negative	Negative	*Staphylococcus aureus* Detected
Detected	Positive	Negative	Positive	Negative	*Staphylococcus epidermidis* Detected
Detected	Positive	Negative	Negative	Positive	*Staphylococcus lugdunensis* Detected
Detected	Positive	Positive	Positive	Negative	*Staphylococcus aureus* Detected *Staphylococcus epidermidis* Detected
Detected	Positive	Positive	Negative	Positive	*Staphylococcus aureus* Detected *Staphylococcus lugdunensis* Detected
Detected	Positive	Negative	Positive	Positive	*Staphylococcus epidermidis* Detected *Staphylococcus lugdunensis* Detected
Detected	Positive	Positive	Positive	Positive	*Staphylococcus aureus* Detected *Staphylococcus epidermidis* Detected *Staphylococcus lugdunensis* Detected
Detected	Positive	Negative	Negative	Negative	Unspeciated *Staphylococcus* Detected

The **cobas eplex** BCID-GP panel *Streptococcus* result is based on five assays: the species-specific *Streptococcus agalactiae, Streptococcus anginosus* group, *Streptococcus pneumoniae* and *Streptococcus pyogenes* assays and a broad *Streptococcus* assay. The broad *Streptococcus* assay will detect each of the species targeted by the species-specific assays, but its primary purpose is to detect other *Streptococcus* species. If all five assays are negative, the *Streptococcus* result will be 'Not Detected'. If any of the five assays is positive, the *Streptococcus* result will be 'Detected'. If only the *Streptococcus* assay is positive, an unspeciated *Streptococcus* species has been detected. See **Table 8** for detailed *Streptococcus* target call logic.

Table 8: *Streptococcus* Target Results from cobas eplex BCID-GP panel Detection Report

***Streptococcus* Result**	***Streptococcus* Assay**	***Streptococcus agalactiae* Assay**	***Streptococcus anginosus* group Assay**	***Streptococcus pneumoniae* Assay**	***Streptococcus pyogenes* Assay**	**Description**
Not Detected	Negative	Negative	Negative	Negative	Negative	No *Streptococcus* species Detected
Detected	Positive	Positive	Negative	Negative	Negative	*Streptococcus agalactiae* Detected
Detected	Positive	Negative	Positive	Negative	Negative	*Streptococcus anginosus* group Detected
Detected	Positive	Negative	Negative	Positive	Negative	*Streptococcus pneumonia* Detected
Detected	Positive	Negative	Negative	Negative	Positive	*Streptococcus pyogenes* Detected
Detected	Positive	Positive	Positive	Negative	Negative	*Streptococcus agalactiae* Detected *Streptococcus anginosus* group Detected
Detected	Positive	Positive	Negative	Positive	Negative	*Streptococcus agalactiae* Detected *Streptococcus pneumoniae* Detected
Detected	Positive	Positive	Negative	Negative	Positive	*Streptococcus agalactiae* Detected *Streptococcus pyogenes* Detected
Detected	Positive	Negative	Positive	Positive	Negative	*Streptococcus anginosus* group Detected *Streptococcus pneumoniae* Detected
Detected	Positive	Negative	Positive	Negative	Positive	*Streptococcus anginosus* group Detected *Streptococcus pyogenes* Detected
Detected	Positive	Negative	Negative	Positive	Positive	*Streptococcus pneumoniae* Detected *Streptococcus pyogenes* Detected
Detected	Positive	Positive	Positive	Positive	Negative	*Streptococcus agalactiae* Detected *Streptococcus anginosus* group Detected *Streptococcus pneumoniae* Detected
Detected	Positive	Positive	Positive	Negative	Positive	*Streptococcus agalactiae* Detected *Streptococcus anginosus* group Detected *Streptococcus pyogenes* Detected
Detected	Positive	Positive	Negative	Positive	Positive	*Streptococcus agalactiae* Detected *Streptococcus pneumoniae* Detected *Streptococcus pyogenes* Detected
Detected	Positive	Negative	Positive	Positive	Positive	*Streptococcus anginosus* group Detected *Streptococcus pneumoniae* Detected *Streptococcus pyogenes* Detected
Detected	Positive	Positive	Positive	Positive	Positive	*Streptococcus agalactiae* Detected *Streptococcus anginosus* Detected *Streptococcus pneumoniae* Detected *Streptococcus pyogenes* Detected
Detected	Positive	Negative	Negative	Negative	Negative	Unspeciated *Streptococcus* Detected

Resistance Marker Assay Result Interpretation

Test results for resistance genes are only reported when an associated organism assay is positive in the same sample. See **Table 9** for organisms specifically associated with the four resistance markers on the **cobas eplex** BCID-GP panel.

Table 9: Resistance Marker Organism Associations

Resistance Gene Result	Associated Targets
mecA and/or *mecC*	Any *Staphylococcus* assay (*Staphylococcus*, *S. aureus*, *S. epidermidis*, *S. lugdunensis*)
vanA and/or *vanB*	Any *Enterococcus* assay (*Enterococcus*, *E. faecalis*, *E. faecium*)

Pan Assay Results

The **cobas eplex** BCID-GP panel Pan Gram-Negative result is based on a broad assay that covers most gram-negative organisms which include but are not limited to *Acinetobacter, Bacteroides, Enterobacteriaceae, Neisseria, Pseudomonas, Serratia* and *Stenotrophomonas maltophilia*, as shown in **Table 10**.

Table 10: Pan Gram-Negative Target Results from cobas eplex BCID-GP panel Detection Report

Pan Gram-Negative Result	Description
Not Detected	No gram-negative organism detected.
Detected	One or more gram-negative organisms detected: including but not limited to *Acinetobacter, Bacteroides*, *Enterobacteriaceae, Neisseria, Pseudomonas, Serratia, Stenotrophomonas maltophilia.* Additional testing for identification is recommended.

The **cobas eplex** BCID-GP panel Pan *Candida* result indicates the presence of one or more of the following *Candida* species targets: *Candida albicans, Candida glabrata, Candida krusei, or Candida parapsilosis* as shown in **Table 11**.

Table 11: Pan *Candida* Target Results from cobas eplex BCID-GP panel Detection Report

Pan *Candida* Result	Description
Not Detected	No specified *Candida* species detected.
Detected	One or more of the following *Candida* organisms has been detected: *Candida albicans, Candida glabrata, Candida krusei and* /or *Candida parapsilosis*. Additional testing for identification is recommended.

TEST REPORTS

Several different reports are available on the **cobas eplex** system. Results are provided in a printable format and may be viewed electronically or exported for additional analysis. Reports can be customized with account specific information such as the address, logo and institutional specific footers on each report. For more information on **cobas eplex** Reports, refer to the **cobas eplex** Operator Manual.

Detection Report

The **cobas eplex** BCID-GP panel Detection Report includes the results for each individual sample run on the **cobas eplex** system. The Summary section indicates the overall test result and lists all detected targets in that sample. The Results section includes a list of all targets on the panel with an individual result for each target. Results are reported as Detected, Not Detected, N/A, or Invalid (displayed as a red **x**); results for the Internal Control are reported as PASS, FAIL, INVALID, or N/A.

External Control Report

The **cobas eplex** BCID-GP panel External Control Report is generated for an external control that has been pre-defined in the **cobas eplex** BCID-GP panel software. For more information on defining external controls on the **cobas eplex** system, refer to the **cobas eplex** Operator Manual.

The Summary section indicates the overall result (PASS or FAIL status) and lists all detected targets for that external control. The Results section includes a list of all panel targets with the result, expected result and PASS/FAIL status for each. Results are reported as Detected, Not Detected, or Invalid (displayed as a red **x**). A target is reported as PASS if the actual result matches the expected result (as defined for that control); a target is reported as FAIL if the actual result does not match the expected result. If the actual result for each target matches the expected result (all targets reported as PASS), the overall result for the external control is reported as PASS in the Summary section. If the actual result for any target does not match the expected result, the overall result for the external control is reported as FAIL in the Summary section.

Summary Report

The Summary Report allows the operator to use searchable criteria to create customized reports, using specified targets, dates, range of dates, sample, external control, test bay, or operator. For more information on creating Summary Reports, refer to the **cobas eplex** Operator Manual.

LIMITATIONS OF THE PROCEDURE

- For prescription use only.
- This test is a qualitative test and does not provide a quantitative value.
- This product should not be used with blood culture media that contains charcoal.
- False results were observed for some targets using the BacT Alert FN Plus bottle type (see the **Sample Matrix Equivalency (Bottle Evaluation)** section of the package insert for additional details) and with a specific lot of BD BACTEC™ Plus Anaerobic bottles.
- Bacterial and fungal nucleic acids may be present in blood culture, independent of bacterial or fungal viability. Detection of an assay target does not guarantee that the corresponding bacteria or fungi are infectious or are the causative agents for clinical symptoms.
- There is a risk of false negative results due to the presence of sequence variants in the bacterial or fungal targets of the test.
- For some strains within the *Corynebacterium*, *Streptococcus* and Pan *Candida* results, 100% detection was not observed at concentrations expected at bottle positivity. See the **Analytical Reactivity (Inclusivity)** section for additional details.
- A result of “No Targets Detected” on the **cobas eplex** BCID-GP panel does not preclude the possibility of bacterial or fungal infection. A specimen with a result of No Targets Detected may contain an organism not targeted by the **cobas eplex** BCID-GP panel.

- Antimicrobial resistance can occur via multiple mechanisms. A Not Detected result for the BCID-GP antimicrobial resistance gene assays does not indicate antimicrobial susceptibility. Subculturing and standard susceptibility testing of isolates is required to determine antimicrobial susceptibility.
- In mixed cultures, the **cobas eplex** BCID-GP panel may not identify all organisms in the specimen, depending upon the concentration of each target present.
- The results of the **cobas eplex** BCID-GP panel should not be used as the sole basis for diagnosis, treatment or other patient management decisions.
- *Bacillus badius* was shown to cross-react with the *Bacillus subtilis* group assay.
- *Burkholderia cepacia* was shown to cross-react with the *Corynebacterium* assay at levels ≥1x10^7 CFU/mL.
- An unspeciated *Rhodococcus* strain (ATCC 49988) was shown to cross-react with the *Micrococcus* assay at levels ≥1x10^7 CFU/mL.
- *Streptococcus pneumoniae* may cross react with *Streptococcus mitis* group species due to potential gene transfer from *S. pneumoniae.*
- The genus level and group assays included as a part of the BCID-GP panel are designed to detect a broad range of species but will not necessarily detect all species within a genus or group. For species detected by these assays please refer to the analytical and *in silico* inclusivity sections of this package insert.
- For genus level assays it is possible that an unspeciated target may be masked in the case of a co-infection. For example, in the event that an unspeciated *Staphylococcus* species is present in the same sample as a *Staphylococcus epidermidis*, there is no ability to determine that the unspeciated *Staphylococcus* species is present.

EXPECTED VALUES

A prospective, multicenter clinical study was conducted to evaluate the clinical performance of the **cobas eplex** BCID-GP panel in positive blood culture samples. A total of 711 samples were prospectively collected at 7 clinical sites in 2 phases from patients of all ages and genders. In the first phase from June 2014 through July 2016, 399 samples were prospectively collected and frozen; from January through February 2018, 312 samples were prospectively collected and tested fresh (never frozen). The expected values of individual analytes based on the **cobas eplex** BCID-GP panel results in prospective samples are summarized by age group and by site in **Table 12** and **Table 13** below.

Table 12: Expected Value by Age Group (Prospective Samples)

Target	All Ages (N=711)	Age <1 (N=27)	Age 1-17 (N=42)	Age 18-44 (N=121)	Age 45-64 (N=2500)	Age 65-84 (N=217)	Age 85+ (N=54)
Bacillus cereus group	5 (0.7)	0 (0.0)	0 (0.0)	3 (2.5)	2 (0.8)	0 (0.0)	0 (0.0)
Bacillus subtilis group	2 (0.3)	0 (0.0)	0 (0.0)	1 (0.8)	0 (0.0)	0 (0.0)	1 (1.9)
Corynebacterium	14 (2.0)	1 (3.7)	0 (0.0)	4 (3.3)	5 (2.0)	4 (1.8)	0 (0.0)
Cutibacterium acnes (P. acnes)	8 (1.1)	0 (0.0)	0 (0.0)	3 (2.5)	2 (0.8)	3 (1.4)	0 (0.0)
Enterococcus	62 (8.7)	0 (0.0)	6 (14.3)	8 (6.6)	20 (8.0)	24 (11.1)	4 (7.4)
Enterococcus faecalis	50 (7.0)	0 (0.0)	6 (14.3)	6 (5.0)	15 (6.0)	20 (9.2)	3 (5.6)
Enterococcus faecium	12 (1.7)	0 (0.0)	0 (0.0)	1 (0.8)	6 (2.4)	5 (2.3)	0 (0.0)
Lactobacillus	5 (0.7)	0 (0.0)	0 (0.0)	2 (1.7)	1 (0.4)	1 (0.5)	1 (1.9)
Listeria	1 (0.1)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (0.5)	0 (0.0)
Listeria monocytogenes	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
Micrococcus	19 (2.7)	0 (0.0)	3 (7.1)	2 (1.7)	8 (3.2)	5 (2.3)	1 (1.9)
Staphylococcus	452 (63.6)	23 (85.2)	23 (54.8)	78 (64.5)	154 (61.6)	139 (64.1)	35 (64.8)
Staphylococcus aureus	162 (22.8)	8 (29.6)	4 (9.5)	37 (30.6)	69 (27.6)	38 (17.5)	6 (11.1)
Staphylococcus epidermidis	182 (25.6)	10 (37.0)	11 (26.2)	26 (21.5)	54 (21.6)	62 (28.6)	19 (35.2)
Staphylococcus lugdunensis	5 (0.7)	1 (3.7)	0 (0.0)	0 (0.0)	3 (1.2)	0 (0.0)	1 (1.9)
Streptococcus	110 (15.5)	5 (18.5)	9 (21.4)	16 (13.2)	40 (16.0)	31 (14.3)	9 (16.7)
Streptococcus agalactiae	12 (1.7)	1 (3.7)	0 (0.0)	1 (0.8)	5 (2.0)	5 (2.3)	0 (0.0)
Streptococcus anginosus group	10 (1.4)	0 (0.0)	0 (0.0)	2 (1.7)	3 (1.2)	3 (1.4)	2 (3.7)
Streptococcus pneumoniae	28 (3.9)	2 (7.4)	2 (4.8)	3 (2.5)	12 (4.8)	8 (3.7)	1 (1.9)
Streptococcus pyogenes	8 (1.1)	0 (0.0)	0 (0.0)	1 (0.8)	5 (2.0)	2 (0.9)	0 (0.0)
Pan *Candida*	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
Pan Gram-Negative	25 (3.5)	0 (0.0)	4 (9.5)	4 (3.3)	10 (4.0)	6 (2.8)	1 (1.9)
mecA (Staphylococcus)	261 (36.7)	14 (51.9)	10 (23.8)	41 (33.9)	83 (33.2)	94 (43.3)	19 (35.2)
mecA (S. aureus)	86 (12.1)	4 (14.8)	1 (2.4)	17 (14.0)	35 (14.0)	26 (12.0)	3 (5.6)
mecA (S. epidermidis)	137 (19.3)	8 (29.6)	9 (21.4)	19 (15.7)	38 (15.2)	48 (22.1)	15 (27.8)
mecA (S. lugdunensis)	1 (0.1)	0 (0.0)	0 (0.0)	0 (0.0)	1 (0.4)	0 (0.0)	0 (0.0)
mecA (CoNS excluding *S. epidermidis / S. lugdunensis)*	40 (5.6)	2 (7.4)	0 (0.0)	6 (5.0)	10 (4.0)	20 (9.2)	2 (3.7)
mecC (Staphylococcus)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
vanA (Enterococcus)	9 (1.3)	0 (0.0)	0 (0.0)	0 (0.0)	6 (2.4)	3 (1.4)	0 (0.0)
vanA (E. faecalis)	1 (0.1)	0 (0.0)	0 (0.0)	0 (0.0)	1 (0.4)	0 (0.0)	0 (0.0)
vanA (E. faecium)	8 (1.1)	0 (0.0)	0 (0.0)	0 (0.0)	5 (2.0)	3 (1.4)	0 (0.0)
vanB (Enterococcus)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)

Table 13: Expected Value by Collection Site (Prospective Samples)

Target	All Sites (N=711)	Site 1 (N=161)	Site 2 (N=58)	Site 3 (N=164)	Site 4 (N=145)	Site 5 (N=77)	Site 6 (N=33)	Site 7 (N=73)
Bacillus cereus group	5 (0.7)	3 (1.9)	1 (1.7)	1 (0.6)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
Bacillus subtilis group	2 (0.3)	0 (0.0)	1 (1.7)	0 (0.0)	0 (0.0)	1 (1.3)	0 (0.0)	0 (0.0)
Corynebacterium	14 (2.0)	2 (1.2)	2 (3.4)	0 (0.0)	6 (4.1)	2 (2.6)	0 (0.0)	2 (2.7)
Cutibacterium acnes (P. acnes)	8 (1.1)	1 (0.6)	0 (0.0)	1 (0.6)	2 (1.4)	0 (0.0)	0 (0.0)	4 (5.5)
Enterococcus	62 (8.7)	20 (12.4)	7 (12.1)	15 (9.1)	9 (6.2)	10 (13.0)	1 (3.0)	0 (0.0)
Enterococcus faecalis	50 (7.0)	14 (8.7)	6 (10.3)	13 (7.9)	8 (5.5)	8 (10.4)	1 (3.0)	0 (0.0)
Enterococcus faecium	12 (1.7)	6 (3.7)	1 (1.7)	1 (0.6)	2 (1.4)	2 (2.6)	0 (0.0)	0 (0.0)
Lactobacillus	5 (0.7)	1 (0.6)	1 (1.7)	2 (1.2)	0 (0.0)	1 (1.3)	0 (0.0)	0 (0.0)
Listeria	1 (0.1)	0 (0.0)	0 (0.0)	0 (0.0)	1 (0.7)	0 (0.0)	0 (0.0)	0 (0.0)
Listeria monocytogenes	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
Micrococcus	19 (2.7)	2 (1.2)	2 (3.4)	5 (3.0)	6 (4.1)	0 (0.0)	0 (0.0)	4 (5.5)
Staphylococcus	452 (63.6)	106 (65.8)	27 (46.6)	109 (66.5)	98 (67.6)	52 (67.5)	24 (72.7)	36 (49.3)
Staphylococcus aureus	162 (22.8)	36 (22.4)	7 (12.1)	56 (34.1)	27 (18.6)	18 (23.4)	6 (18.2)	12 (16.4)
Staphylococcus epidermidis	182 (25.6)	41 (25.5)	14 (24.1)	34 (20.7)	44 (30.3)	23 (29.9)	13 (39.4)	13 (17.8)
Staphylococcus lugdunensis	5 (0.7)	0 (0.0)	0 (0.0)	2 (1.2)	2 (1.4)	0 (0.0)	0 (0.0)	1 (1.4)
Streptococcus	110 (15.5)	18 (11.2)	9 (15.5)	28 (17.1)	20 (13.8)	11 (14.3)	5 (15.2)	19 (26.0)
Streptococcus agalactiae	12 (1.7)	2 (1.2)	0 (0.0)	2 (1.2)	2 (1.4)	2 (2.6)	2 (6.1)	2 (2.7)
Streptococcus anginosus group	10 (1.4)	2 (1.2)	0 (0.0)	6 (3.7)	0 (0.0)	2 (2.6)	0 (0.0)	0 (0.0)
Streptococcus pneumoniae	28 (3.9)	3 (1.9)	5 (8.6)	5 (3.0)	4 (2.8)	1 (1.3)	0 (0.0)	10 (13.7)
Streptococcus pyogenes	8 (1.1)	1 (0.6)	0 (0.0)	3 (1.8)	1 (0.7)	1 (1.3)	0 (0.0)	2 (2.7)
Pan *Candida*	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
Pan Gram-Negative	25 (3.5)	9 (5.6)	4 (6.9)	3 (1.8)	2 (1.4)	5 (6.5)	1 (3.0)	1 (1.4)
mecA (Staphylococcus)	261 (36.7)	69 (42.9)	17 (29.3)	68 (41.5)	55 (37.9)	25 (32.5)	13 (39.4)	14 (19.2)
mecA (S. aureus)	86 (12.1)	19 (11.8)	5 (8.6)	28 (17.1)	19 (13.1)	7 (9.1)	3 (9.1)	5 (6.8)
mecA (S. epidermidis)	137 (19.3)	36 (22.4)	10 (17.2)	31 (18.9)	29 (20.0)	17 (22.1)	8 (24.2)	6 (8.2)
mecA (S. lugdunensis)	1 (0.1)	0 (0.0)	0 (0.0)	1 (0.6)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
mecA (CoNS excluding *S. epidermidis / S. lugdunensis)*	40 (5.6)	15 (9.3)	2 (3.4)	9 (5.5)	7 (4.8)	2 (2.6)	2 (6.1)	3 (4.1)
mecC (Staphylococcus)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
vanA (Enterococcus)	9 (1.3)	6 (3.7)	0 (0.0)	1 (0.6)	1 (0.7)	1 (1.3)	0 (0.0)	0 (0.0)
vanA (E. faecalis)	1 (0.1)	1 (0.6)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
vanA (E. faecium)	8 (1.1)	5 (3.1)	0 (0.0)	1 (0.6)	1 (0.7)	1 (1.3)	0 (0.0)	0 (0.0)
vanB (Enterococcus)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)

PERFORMANCE CHARACTERISTICS

CLINICAL PERFORMANCE

Samples with final, valid **cobas eplex** BCID-GP panel test results and a valid comparator result were evaluable and included in summaries and analyses of demographics, expected values (positivity rate), and performance characteristics. Evaluable samples included 312 prospective fresh and 399 prospective frozen samples as well as 586 retrospective samples and 565 contrived samples.

Comparator Method

The performance of the **cobas eplex** BCID-GP panel was compared to standard laboratory procedures for identification of blood culture isolates, including traditional and automated identification methods, MALDI-TOF IVD, and microbiological and biochemical techniques. Identification for samples with *Corynebacterium*, *Staphylococcus epidermidis*, *Staphylococcus hominis*, or *Candida parapsilosis* identified by standard laboratory procedures was confirmed using analytically validated PCR assays followed by bi-directional sequencing or 16S sequencing. For antibiotic resistance genes, the **cobas eplex** BCID-GP panel was compared to analytically validated qPCR amplification assays followed by bi-directional sequencing in samples with an associated organism identified by culture (i.e., *Staphylococcus*, *Enterococcus*).

The comparator method(s) results were used to determine the Detected / Not Detected status for each target organism on the **cobas eplex** BCID-GP panel. The comparator methods for each target are summarized in **Table 14**.

Table 14: Comparator Method(s) by cobas eplex BCID-GP panel Target

Target	Comparator Method
Bacillus cereus group	Standard laboratory procedures for organism ID.
Bacillus subtilis group	
Cutibacterium acnes (Propionibacterium acnes)	
Enterococcus	
Enterococcus faecalis	
Enterococcus faecium	
Lactobacillus	
Listeria	
Listeria monocytogenes	
Micrococcus	
Staphylococcus	
Staphylococcus aureus	
Staphylococcus lugdunensis	
Streptococcus	
Streptococcus agalactiae	
Streptococcus anginosus group	
Streptococcus pneumoniae	
Streptococcus pyogenes	

Target	Comparator Method
Pan Gram-Negative	
Corynebacterium	Standard laboratory procedures for organism ID. PCR/sequencing and 16S sequencing to confirm (or identify Coryneform) or exclude *Corynebacterium* species not included in this panel target*.
Staphylococcus epidermidis	Standard laboratory procedures for organism ID. PCR/sequencing to confirm *S. epidermidis, S. hominis.*
Pan *Candida*	Standard laboratory procedures for organism ID. PCR/sequencing to confirm *C. parapsilosis* or identify *C. metapsilosis, C. orthopsilosis.*
mecA	qPCR/sequencing in samples with *Staphylococcus* identified by comparator method.
mecC	
vanA	qPCR/sequencing in samples with *Enterococcus* identified by comparator method.
vanB	

*The *Corynebacterium* assay is not designed to detect the following *Corynebacterium* species: *C. amycolatum, C. argentoratense, C. bovis, C. durum, C. glucuronolyticum, C. macginleyi, C. propinquum*, *C. riegelii,* and *C. sundsvallense*

Demographics of Clinical Samples

Clinical performance was evaluated in positive blood culture samples prospectively and retrospectively collected. Prospective samples were collected at 7 clinical sites in 2 phases. From June 2014 through July 2016, 400 samples were prospectively collected and frozen; from January through February 2018, 319 samples were prospectively collected and tested fresh (never frozen) for a total of 719 samples across the 2 phases. 8 of these samples were withdrawn; 5 due to the sample coming from a patient already enrolled; 1 was collected outside of the required timeframe; 1 was not viable upon subculture and 1 was from an autopsy. Samples with final, valid **cobas eplex** BCID-GP panel results and a valid comparator result were evaluable. Of the 711 prospectively-collected samples eligible for testing, all 711 were evaluable. Demographic information for prospectively-collected samples is described in **Table 15.** Subjects enrolled in this study were from a diverse demographic distribution and represent the intended patient population.

To supplement the number of positives for low prevalence targets in the prospective collection, 586 samples were collected retrospectively, and all 586 were evaluable. Demographic information for retrospectively-collected samples is described in **Table 16**.

Table 15: Demographic Data for Clinical Samples by Collection Site (Prospective Collection)

	All Sites N = 711	Site 1 N = 161	Site 2 N = 58	Site 3 N = 164	Site 4 N = 145	Site 5 N = 77	Site 6 N = 33	Site 7 N = 73
Sex								
Male	377 (53.0)	93 (57.8)	28 (48.3)	91 (55.5)	66 (45.5)	42 (54.5)	17 (51.5)	40 (54.8)
Female	334 (47.0)	68 (42.2)	30 (51.7)	73 (44.5)	79 (54.5)	35 (45.5)	16 (48.5)	33 (45.2)
Age								
<1 yr	27 (3.8)	3 (1.9)	0 (0.0)	8 (4.9)	10 (6.9)	4 (5.2)	2 (6.1)	0 (0.0)
1-17 yrs	42 (5.9)	8 (5.0)	2 (3.4)	11 (6.7)	10 (6.9)	7 (9.1)	2 (6.1)	2 (2.7)
18-44 yrs	121 (17)	32 (19.9)	9 (15.5)	24 (14.6)	24 (16.6)	13 (16.9)	4 (12.1)	15 (20.5)
45-64 yrs	250 (35.2)	66 (41.0)	18 (31.0)	67 (40.9)	36 (24.8)	25 (32.5)	11 (33.3)	27 (37.0)
65-84 yrs	217 (30.5)	44 (27.3)	20 (34.5)	41 (25.0)	51 (35.2)	23 (29.9)	13 (39.4)	25 (34.2)
85+ yrs	54 (7.6)	8 (5.0)	9 (15.5)	13 (7.9)	14 (9.7)	5 (6.5)	1 (3.0)	4 (5.5)

Table 16: Demographic Data for Clinical Samples by Collection Site (Retrospective Collection)

	All Sites N = 586	Site 1 N = 80	Site 2 N = 98	Site 3 N = 51	Site 4 N = 43	Site 5 N = 3	Site 6 N = 61	Site 7 N = 85	Site 8 N = 25	Site 9 N = 46	Site 10 N = 94
Sex											
Male	317 (54.1)	39 (48.8)	59 (60.2)	24 (47.1)	20 (46.5)	1 (33.3)	36 (59.0)	45 (52.9)	17 (68.0)	28 (60.9)	48 (51.1)
Female	269 (45.9)	41 (51.3)	39 (39.8)	27 (52.9)	23 (53.5)	2 (66.7)	25 (41.0)	40 (47.1)	8 (32.0)	18 (39.1)	46 (48.9)
Age											
<1 yr	11 (1.9)	1 (1.3)	2 (2)	0 (0)	3 (7)	0 (0)	1 (1.6)	0 (0)	0 (0)	1 (2.2)	3 (3.2)
1-17 yrs	17 (2.9)	6 (7.5)	1 (1)	0 (0)	4 (9.3)	0 (0)	0 (0)	0 (0)	1 (4)	1 (2.2)	4 (4.3)
18-44 yrs	104 (17.7)	14 (17.5)	13 (13.3)	5 (9.8)	9 (20.9)	0 (0)	15 (24.6)	11 (12.9)	7 (28)	5 (10.9)	25 (26.6)
45-64 yrs	193 (32.9)	25 (31.3)	33 (33.7)	17 (33.3)	15 (34.9)	1 (33.3)	21 (34.4)	30 (35.3)	10 (40)	12 (26.1)	29 (30.9)
65-84 yrs	209 (35.7)	26 (32.5)	42 (42.9)	22 (43.1)	9 (20.9)	0 (0)	20 (32.8)	35 (41.2)	7 (28)	18 (39.1)	30 (31.9)
85+ yrs	50 (8.5)	8 (10)	7 (7.1)	7 (13.7)	3 (7)	2 (66.7)	4 (6.6)	7 (8.2)	0 (0)	9 (19.6)	3 (3.2)
Unknown	2 (0.3)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	2 (2.4)	0 (0)	0 (0)	0 (0)

Clinical Performance

Sensitivity or positive percent agreement (PPA) was calculated by dividing the number of true positive (TP) results by the sum of TP and false negative (FN) results, while specificity or negative percent agreement (NPA) was calculated by dividing the number of true negative (TN) results by the sum of TN and false positive (FP) results. A TP result being defined as a sample where the detected **cobas eplex** BCID-GP panel result matched the detected comparator method result, while a TN result was one where a negative **cobas eplex** BCID-GP panel result matched a negative comparator method result. The two-sided 95% confidence interval was also calculated.

A total of 711 prospectively-collected samples (312 tested fresh and 399 tested after previously frozen) and 586 retrospectively collected samples from blood culture bottles flagged positive in a continuously monitoring blood culture system and removed from the system within 8 hours of positivity were evaluated for the **cobas eplex** BCID-GP panel targets. Specimens evaluated were determined to contain gram-positive or gram-variable organisms based on Gram stain. A total of 565 contrived samples were prepared by spiking an isolate into a blood culture bottle with human whole blood and growing until flagged positive by a continuously monitoring blood culture system. Contrived samples were removed from the system within 8 hours of positivity and stored frozen until the time of testing. PPA and NPA results are summarized by target in **Tables 17-41** below, and the strains used to contrive samples are summarized in **Table 42**.

Table 17: Clinical Performance for *Bacillus cereus* group

Target	Sample Type	Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
Bacillus cereus group	Prospective (Fresh)	2/2	100 (34.2-100)	310/310	100 (98.8-100)
	Prospective (Frozen)	3/3	100 (43.9-100)	396/396	100 (99.0-100)
	Prospective (All)	**5/5**	**100 (56.6-100)**	**706/706**	**100 (99.5-100)**
	Retrospective	6/7	85.7 (48.7-97.4)	579/579	100 (99.3-100)
	Prospective/Retrospective	**11/12**	**91.7 (64.6-98.5)**	**1285/1285**	**100 (99.7-100)**
	Contrived	**46/46**	**100 (92.3-100)**	**519/519**	**100 (99.3-100)**
	Overall	**57/58**	**98.3 (90.9-99.7)**	**1804/1804**	**100 (99.8-100)**

CI= Confidence Interval

Table 18: Clinical Performance for *Bacillus subtilis* group

Target	Sample Type	Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
Bacillus subtilis group	Prospective (Fresh)	2/2	100 (34.2-100)	309/309	100 (98.8-100)
	Prospective (Frozen)	0/0	---	399/399	100 (99.0-100)
	Prospective (All)	**2/2**	**100 (34.2-100)**	**708/708**	**100 (99.5-100)**
	Retrospective	0/0	---	586/586	100 (99.3-100)
	Prospective/Retrospective	**2/2**	**100 (34.2-100)**	**1294/1294**	**100 (99.7-100)**
	Contrived	50/50	100 (92.9-100)	515/515	100 (99.3-100)
	Overall	**52/52**	**100 (93.1-100)**	**1809/1809**	**100 (99.8-100)**

Table 19: Clinical Performance for *Corynebacterium*

Target	Sample Type	Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
Corynebacterium	Prospective (Fresh)	5/7	71.4 (35.9-91.8)	304/305	99.7 (98.2-99.9)
	Prospective (Frozen)	8/12	66.7 (39.1-86.2)	387/387	100 (99.0-100)
	Prospective (All)	**13/19**	**68.4 (46.0-84.6)**	**691/692**	**99.9 (99.2-100)**
	Retrospective	27/32	84.4 (68.2-93.1)	553/554	99.8 (99.0-100)
	Prospective/Retrospective	**40/51[A]**	**78.4 (65.4-87.5)**	**1244/1246[B]**	**99.8 (99.4-100)**
	Contrived	20/20	100 (83.9-100)	545/545	100 (99.3-100)
	Overall	**60/71**	**84.5 (74.3-91.1)**	**1789/1791**	**99.9 (99.6-100)**

A. *Corynebacterium* was not detected in 4 of the false negative samples using PCR/sequencing, but 16S sequencing instead detected *Staphylococcus pettenkoferi, Macrococcus caseolyticus, Lactobacillus fermentum,* and *Cutibacterium acnes*, which were not identified by standard laboratory procedures.

B. *Corynebacterium* was detected in 2/2 false positive samples using PCR/sequencing.

Table 20: Clinical Performance for *Cutibacterium acnes*

Target	Sample Type	Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
Cutibacterium acnes	Prospective (Fresh)	4/5	80.0 (37.6-96.4)	306/307	99.7 (98.2-99.9)
	Prospective (Frozen)	2/2	100 (34.2-100)	396/397	99.7 (98.6-100)
	Prospective (All)	**6/7**	**85.7 (48.7-97.4)**	**702/704**	**99.7 (99.0-99.9)**
	Retrospective	12/13	92.3 (66.7-98.6)	573/573	100 (99.3-100)
	Prospective/Retrospective	**18/20**	**90.0 (69.9-97.2)**	**1275/1277[A]**	**99.8 (99.4-100)**
	Contrived	25/26	96.2 (81.1-99.3)	539/539	100 (99.3-100)
	Overall	**43/46**	**93.5 (82.5-97.8)**	**1814/1816**	**99.9 (99.6-100)**

A. *Cutibacterium acnes* was detected in 1/2 false positive samples using PCR/sequencing.

Table 21: Clinical Performance for *Enterococcus*

Target	Sample Type	Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
Enterococcus	Prospective (Fresh)	25/25	100 (86.7-100)	287/287	100 (98.7-100)
	Prospective (Frozen)	36/36	100 (90.4-100)	362/363	99.7 (98.5-100)
	Prospective (All)	**61/61**	**100 (94.1-100)**	**649/650**	**99.8 (99.1-100)**
	Retrospective	139/147	94.6 (89.6-97.2)	439/439	100 (99.1-100)
	Prospective/Retrospective	**200/208[A]**	**96.2 (92.6-98.0)**	**1088/1089[B]**	**99.9 (99.5-100)**
	Contrived	126/126	100 (97.0-100)	439/439	100 (99.1-100)
	Overall	**326/334**	**97.6 (95.3-98.8)**	**1527/1528**	**99.9 (99.6-100)**

A. *Enterococcus* was not detected in 1 false negative sample, but PCR/sequencing instead detected *Lactococcus lactis*, which was not identified by standard laboratory procedures.

B. *Enterococcus* was detected in 1/1 false positive samples using PCR/sequencing.

Table 22: Clinical Performance for *Enterococcus faecalis*

Target	Sample Type	Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
Enterococcus faecalis	Prospective (Fresh)	21/21	100 (84.5-100)	291/291	100 (98.7-100)
	Prospective (Frozen)	28/28	100 (87.9-100)	370/370	100 (99.0-100)
	Prospective (All)	**49/49**	**100 (92.7-100)**	**661/661**	**100 (99.4-100)**
	Retrospective	82/90	91.1 (83.4-95.4)	496/496	100 (99.2-100)
	Prospective/Retrospective	**131/139[A]**	**94.2 (89.1-97.1)**	**1157/1157**	**100 (99.7-100)**
	Contrived	52/52	100 (93.1-100)	513/513	100 (99.3-100)
	Overall	**183/191**	**95.8 (92.0-97.9)**	**1670/1670**	**100 (99.8-100)**

A. *Enterococcus faecalis* was not detected in 4 false negative samples, but PCR/sequencing instead detected *Enterococcus faecium* (3) and *Lactococcus lactis* (1), which were not identified by standard laboratory procedures.

Table 23: Clinical Performance for *Enterococcus faecium*

Target	Sample Type	Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
Enterococcus faecium	Prospective (Fresh)	3/3	100 (43.9-100)	309/309	100 (98.8-100)
	Prospective (Frozen)	8/9	88.9 (56.5-98.0)	388/389	99.7 (98.6-100)
	Prospective (All)	**11/12**	**91.7 (64.6-98.5)**	**697/698**	**99.9 (99.2-100)**
	Retrospective	52/53	98.1 (90.1-99.7)	526/533	98.7 (97.3-99.4)
	Prospective/Retrospective	**63/65**	**96.9 (89.5-99.2)**	**1223/1231[A]**	**99.4 (98.7-99.7)**
	Contrived	60/60	100 (94.0-100)	505/505	100 (99.2-100)
	Overall	**123/125**	**98.4 (94.4-99.6)**	**1728/1736**	**99.5 (99.1-99.8)**

A. *Enterococcus faecium* was detected in 5/8 false positive samples using PCR/sequencing.

Table 24: Clinical Performance for *Lactobacillus*

Target	Sample Type	Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
Lactobacillus	Prospective (Fresh)	2/2	100 (34.2-100)	309/310	99.7 (98.2-99.9)
	Prospective (Frozen)	2/2	100 (34.2-100)	397/397	100 (99.0-100)
	Prospective (All)	**4/4**	**100 (51.0-100)**	**706/707**	**99.9 (99.2-100)**
	Retrospective	9/9	100 (70.1-100)	576/577	99.8 (99.0-100)
	Prospective/Retrospective	**13/13**	**100 (77.2-100)**	**1282/1284[A]**	**99.8 (99.4-100)**
	Contrived	32/33	97.0 (84.7-99.5)	532/532	100 (99.3-100)
	Overall	**45/46**	**97.8 (88.7-99.6)**	**1814/1816**	**99.9 (99.6-100)**

A. *Lactobacillus casei* was detected in 1/2 false positive samples using PCR/sequencing.

Table 25: Clinical Performance for *Listeria*

Target	Sample Type	Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
Listeria	Prospective (Fresh)	0/0	---	312/312	100 (98.8-100)
	Prospective (Frozen)	0/0	---	398/399	99.7 (98.6-100)
	Prospective (All)	**0/0**	**---**	**710/711**	**99.9 (99.2-100)**
	Retrospective	2/2	100 (34.2-100)	584/584	100 (99.3-100)
	Prospective/Retrospective	**2/2**	**100 (34.2-100)**	**1294/1295[A]**	**99.9 (99.6-100)**
	Contrived	74/75	98.7 (92.8-99.8)	490/490	100 (99.2-100)
	Overall	**76/77**	**98.7 (93.0-99.8)**	**1784/1785**	**99.9 (99.7-100)**

A. *Listeria* was not detected in the false positive sample using PCR/sequencing.

Table 26: Clinical Performance for *Listeria monocytogenes*

Target	Sample Type	Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
Listeria monocytogenes	Prospective (Fresh)	0/0	---	312/312	100 (98.8-100)
	Prospective (Frozen)	0/0	---	399/399	100 (99.0-100)
	Prospective (All)	**0/0**	**---**	**711/711**	**100 (99.5-100)**
	Retrospective	2/2	100 (34.2-100)	584/584	100 (99.3-100)
	Prospective/Retrospective	**2/2**	**100 (34.2-100)**	**1295/1295**	**100 (99.7-100)**
	Contrived	46/46	100 (92.3-100)	519/519	100 (99.3-100)
	Overall	**48/48**	**100 (92.6-100)**	**1814/1814**	**100 (99.8-100)**

Table 27: Clinical Performance for *Micrococcus*

Target	Sample Type	Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
Micrococcus	Prospective (Fresh)	9/10	90.0 (59.6-98.2)	302/302	100 (98.7-100)
	Prospective (Frozen)	10/11	90.9 (62.3-98.4)	388/388	100 (99.0-100)
	Prospective (All)	**19/21**	**90.5 (71.1-97.3)**	**690/690**	**100 (99.4-100)**
	Retrospective	20/23	87.0 (67.9-95.5)	562/563	99.8 (99.0-100)
	Prospective/Retrospective	**39/44[A]**	**88.6 (76.0-95.0)**	**1252/1253[B]**	**99.9 (99.5-100)**
	Contrived	27/27	100 (87.5-100)	538/538	100 (99.3-100)
	Overall	**66/71**	**93.0 (84.6-97.0)**	**1790/1791**	**99.9 (99.7-100)**

A. *Micrococcus* was not detected in 3 false negative samples, but PCR/sequencing instead detected *Brevibacterium ravenspurgense*, *Nesterenkonia halotolerans*, and *Staphylococcus pettenkoferi*, which were not identified by standard laboratory procedures.

B. *Micrococcus* was not detected in the false positive sample using PCR/sequencing.

Table 28: Clinical Performance for *Staphylococcus*

Target	Sample Type	Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
Staphylococcus	Prospective (Fresh)	178/182	97.8 (94.5-99.1)	127/130	97.7 (93.4-99.2)
	Prospective (Frozen)	269/274	98.2 (95.8-99.2)	123/125	98.4 (94.4-99.6)
	Prospective (All)	**447/456**	**98.0 (96.3-99.0)**	**250/255**	**98.0 (95.5-99.2)**
	Retrospective	185/191	96.9 (93.3-98.6)	390/395	98.7 (97.1-99.5)
	Prospective/Retrospective	**632/647[A]**	**97.7 (96.2-98.6)**	**640/650[B]**	**98.5 (97.2-99.2)**
	Contrived	105/105	100 (96.5-100)	460/460	100 (99.2-100)
	Overall	**737/752**	**98.0 (96.7-98.8)**	**1100/1110**	**99.1 (98.3-99.5)**

A. *Staphylococcus* was not detected in 3 false negative samples, but PCR/sequencing instead detected *Escherichia coli*, *Klebsiella pneumoniae*, and *Streptococcus salivarius*, which were not identified by standard laboratory procedures.
B. *Staphylococcus* was detected in 9/10 false positive samples using PCR/sequencing.

Table 29: Clinical Performance for *Staphylococcus aureus*

Target	Sample Type	Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
Staphylococcus aureus	Prospective (Fresh)	62/65	95.4 (87.3-98.4)	244/245	99.6 (97.7-99.9)
	Prospective (Frozen)	98/101	97.0 (91.6-99.0)	222/223	99.6 (97.5-99.9)
	Prospective (All)	**160/166**	**96.4 (92.3-98.3)**	**466/468**	**99.6 (98.5-99.9)**
	Retrospective	122/125	97.6 (93.2-99.2)	454/458	99.1 (97.8-99.7)
	Prospective/Retrospective	**282/291[A]**	**96.9 (94.2-98.4)**	**920/926[B]**	**99.4 (98.6-99.7)**
	Contrived	59/59	100 (93.9-100)	506/506	100 (99.2-100)
	Overall	**341/350**	**97.4 (95.2-98.6)**	**1426/1432**	**99.6 (99.1-99.8)**

A. *Staphylococcus aureus* was not detected in 3 false negative samples, but PCR/sequencing instead detected *Klebsiella pneumoniae, Staphylococcus simulans,* and *Streptococcus agalactiae*, which were not identified by standard laboratory procedures.
B. *Staphylococcus aureus* was detected in 5/6 false positive samples using PCR/sequencing.

Table 30: Clinical Performance for *Staphylococcus epidermidis*

Target	Sample Type	Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
Staphylococcus epidermidis	Prospective (Fresh)	59/63	93.7 (84.8-97.5)	223/229	97.4 (94.4-98.8)
	Prospective (Frozen)	56/58	96.6 (88.3-99.0)	258/265	97.4 (94.6-98.7)
	Prospective (All)	**115/121**	**95.0 (89.6-97.7)**	**481/494**	**97.4 (95.6-98.5)**
	Retrospective	33/38	86.8 (72.7-94.2)	539/545	98.9 (97.6-99.5)
	Prospective/Retrospective	**148/159[A]**	**93.1 (88.0-96.1)**	**1020/1039[B]**	**98.2 (97.2-98.8)**
	Contrived	1/1	100 (20.7-100)	564/564	100 (99.3-100)
	Overall	**149/160**	**93.1 (88.1-96.1)**	**1584/1603**	**98.8 (98.2-99.2)**

A. *Staphylococcus epidermidis* was not detected in 7 false negative samples, but PCR/sequencing instead detected *Staphylococcus aureus* (4), *Staphylococcus capitis* (1), *Staphylococcus pettenkoferi* (1), and *Escherichia coli* (1), which were not identified by standard laboratory procedures.
B. *Staphylococcus epidermidis* was detected in 3/19 false positive samples using PCR/sequencing.

Table 31: Clinical Performance for *Staphylococcus lugdunensis*

Target	Sample Type	Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
Staphylococcus lugdunensis	Prospective (Fresh)	1/1	100 (20.7-100)	290/291	99.7 (98.1-99.9)
	Prospective (Frozen)	1/1	100 (20.7-100)	321/322	99.7 (98.3-99.9)
	Prospective (All)	**2/2**	**100 (34.2-100)**	**611/613**	**99.7 (98.8-99.9)**
	Retrospective	4/4	100 (51.0-100)	579/579	100 (99.3-100)
	Prospective/Retrospective	**6/6**	**100 (61.0-100)**	**1190/1192[A]**	**99.8 (99.4-100)**
	Contrived	45/45	100 (92.1-100)	519/520	99.8 (98.9-100)
	Overall	**51/51**	**100 (93.0-100)**	**1709/1712**	**99.8 (99.5-99.9)**

A. *Staphylococcus lugdunensis* was detected in 2/2 false positive samples using PCR/sequencing.

Table 32: Clinical Performance for *Streptococcus*

Target	Sample Type	Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
Streptococcus	Prospective (Fresh)	54/55	98.2 (90.4-99.7)	253/257	98.4 (96.1-99.4)
	Prospective (Frozen)	49/55	89.1 (78.2-94.9)	341/344	99.1 (97.5-99.7)
	Prospective (All)	**103/110**	**93.6 (87.4-96.9)**	**594/601**	**98.8 (97.6-99.4)**
	Retrospective	171/173	98.8 (95.9-99.7)	411/413	99.5 (98.3-99.9)
	Prospective/Retrospective	**274/283**	**96.8 (94.1-98.3)**	**1005/1014[A]**	**99.1 (98.3-99.5)**
	Contrived	57/57	100 (93.7-100)	508/508	100 (99.2-100)
	Overall	**331/340**	**97.4 (95.0-98.6)**	**1513/1522**	**99.4 (98.9-99.7)**

A. *Streptococcus* was detected in 8/9 false positive samples using PCR/sequencing.

Table 33: Clinical Performance for *Streptococcus agalactiae*

Target	Sample Type	Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
Streptococcus agalactiae	Prospective (Fresh)	5/6	83.3 (43.6-97.0)	298/300	99.3 (97.6-99.8)
	Prospective (Frozen)	5/5	100 (56.6-100)	374/374	100 (99.0-100)
	Prospective (All)	**10/11**	**90.9 (62.3-98.4)**	**672/674**	**99.7 (98.9-99.9)**
	Retrospective	36/37	97.3 (86.2-99.5)	548/548	100 (99.3-100)
	Prospective/Retrospective	**46/48 [A]**	**95.8 (86.0-98.8)**	**1220/1222[B]**	**99.8 (99.4-100)**
	Contrived	8/8	100 (67.6-100)	557/557	100 (99.3-100)
	Overall	**54/56**	**96.4 (87.9-99.0)**	**1777/1779**	**99.9 (99.6-100)**

A. *Streptococcus agalactiae* was not detected in 1 false negative sample, but PCR/sequencing instead detected *Streptococcus mitis*, which was not identified by standard laboratory procedures.

B. *Streptococcus agalactiae* was detected in 1/2 false positive samples using PCR/sequencing.

Table 34: Clinical Performance for *Streptococcus anginosus* group

Target	Sample Type	Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
Streptococcus anginosus group	Prospective (Fresh)	3/3	100 (43.9-100)	303/303	100 (98.7-100)
	Prospective (Frozen)	1/2	50.0 (9.5-90.5)	375/377	99.5 (98.1-99.9)
	Prospective (All)	**4/5**	**80.0 (37.6-96.4)**	**678/680**	**99.7 (98.9-99.9)**
	Retrospective	38/40	95.0 (83.5-98.6)	544/545	99.8 (99.0-100)
	Prospective/Retrospective	**42/45[A]**	**93.3 (82.1-97.7)**	**1222/1225[B]**	**99.8 (99.3-99.9)**
	Contrived	23/23	100 (85.7-100)	542/542	100 (99.3-100)
	Overall	**65/68**	**95.6 (87.8-98.5)**	**1764/1767**	**99.8 (99.5-99.9)**

A. *Streptococcus anginosus* group was not detected in 3 false negative samples, but PCR/sequencing instead detected *Granulicatella adiacens*, *Streptococcus dysgalactiae*, and *Streptococcus lutetiensis*, which were not identified by standard laboratory procedures.
B. *Streptococcus intermedius* was detected in 1/3 false positive samples using PCR/sequencing.

Table 35: Clinical Performance for *Streptococcus pneumoniae*

Target	Sample Type	Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
Streptococcus pneumoniae	Prospective (Fresh)	19/19	100 (83.2-100)	286/287	99.7 (98.1-99.9)
	Prospective (Frozen)	8/9	88.9 (56.5-98.0)	370/370	100 (99.0-100)
	Prospective (All)	**27/28**	**96.4 (82.3-99.4)**	**656/657**	**99.8 (99.1-100)**
	Retrospective	39/41	95.1 (83.9-98.7)	542/543	99.8 (99.0-100)
	Prospective/Retrospective	**66/69[A]**	**95.7 (88.0-98.5)**	**1198/1200[B]**	**99.8 (99.4-100)**
	Contrived	0/0	---	565/565	100 (99.3-100)
	Overall	**66/69**	**95.7 (88.0-98.5)**	**1763/1765**	**99.9 (99.6-100)**

A. *Streptococcus pneumoniae* was not detected in 3 false negative samples, but PCR/sequencing instead detected *Streptococcus mitis* (2) and *Streptococcus anginosus* (1), which were not detected by standard laboratory procedures.
B. *Streptococcus pneumoniae* was detected in 1/2 false positive samples using PCR/sequencing.

Table 36: Clinical Performance for *Streptococcus pyogenes*

Target	Sample Type	Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
Streptococcus pyogenes	Prospective (Fresh)	4/4	100 (51.0-100)	302/302	100 (98.7-100)
	Prospective (Frozen)	4/4	100 (51.0-100)	375/375	100 (99.0-100)
	Prospective (All)	**8/8**	**100 (67.6-100)**	**677/677**	**100 (99.4-100)**
	Retrospective	19/20	95.0 (76.4-99.1)	564/564	100 (99.3-100)
	Prospective/Retrospective	**27/28**	**96.4 (82.3-99.4)**	**1241/1241**	**100 (99.7-100)**
	Contrived	26/26	100 (87.1-100)	539/539	100 (99.3-100)
	Overall	**53/54**	**98.1 (90.2-99.7)**	**1780/1780**	**100 (99.8-100)**

Table 37: Clinical Performance for *mecA*

Target	Sample Type	Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
mecA *Staphylococcus*	Prospective (Fresh)	86/89	96.6 (90.6-98.8)	85/93	91.4 (83.9-95.6)
	Prospective (Frozen)	164/171	95.9 (91.8-98.0)	101/103	98.1 (93.2-99.5)
	Prospective (All)	**250/260**	**96.2 (93.1-97.9)**	**186/196**	**94.9 (90.9-97.2)**
	Retrospective	151/153	98.7 (95.4-99.6)	37/38	97.4 (86.5-99.5)
	Prospective/Retrospective	**401/413[A]**	**97.1 (95.0-98.3)**	**223/234[B]**	**95.3 (91.8-97.4)**
	Contrived	11/11	100 (74.1-100)	94/94	100 (96.1-100)
	Overall	**412/424**	**97.2 (95.1-98.4)**	**317/328**	**96.6 (94.1-98.1)**
mecA *Staphylococcus aureus*	Prospective (Fresh)	27/28	96.4 (82.3-99.4)	34/37	91.9 (78.7-97.2)
	Prospective (Frozen)	56/58	96.6 (88.3-99.0)	43/43	100 (91.8-100)
	Prospective (All)	**83/86**	**96.5 (90.2-98.8)**	**77/80**	**96.3 (89.5-98.7)**
	Retrospective	107/108	99.1 (94.9-99.8)	16/17	94.1 (73.0-99.0)
	Prospective/Retrospective	190/194	**97.9 (94.8-99.2)**	93/97	**95.9 (89.9-98.4)**
	Contrived	10/10	100 (72.2-100)	49/49	100 (92.7-100)
	Overall	**200/204**	**98.0 (95.1-99.2)**	**142/146**	**97.3 (93.2-98.9)**
mecA *Staphylococcus epidermidis*	Prospective (Fresh)	36/36	100 (90.4-100)	24/27	88.9 (71.9-96.1)
	Prospective (Frozen)	41/43	95.3 (84.5-98.7)	15/15	100 (79.6-100)
	Prospective (All)	**77/79**	**97.5 (91.2-99.3)**	**39/42**	**92.9 (81.0-97.5)**
	Retrospective	30/30	100 (88.6-100)	7/8	87.5 (52.9-97.8)
	Prospective/Retrospective	**107/109**	**98.2 (93.6-99.5)**	**46/50**	**92.0 (81.2-96.8)**
	Contrived	1/1	100 (20.7-100)	0/0	---
	Overall	**108/110**	**98.2 (93.6-99.5)**	**46/50**	**92.0 (81.2-96.8)**
mecA *Staphylococcus lugdunensis*	Prospective (Fresh)	0/0	---	1/1	100 (20.7-100)
	Prospective (Frozen)	0/0	---	1/1	100 (20.7-100)
	Prospective (All)	**0/0**	**---**	**2/2**	**100 (34.2-100)**
	Retrospective	1/1	100 (20.7-100)	3/3	100 (43.9-100)
	Prospective/Retrospective	**1/1**	**100 (20.7-100)**	**5/5**	**100 (56.6-100)**
	Contrived	0/0	---	45/45	100 (92.1-100)
	Overall	**1/1**	**100 (20.7-100)**	**50/50**	**100 (92.9-100)**

A. Additional testing of the 12 false negative *mecA* samples indicated 2 may have been contaminated during the original extraction process for the comparator method testing and misidentified as having *mecA* present. Specifically, results for the 2 samples were negative for *mecA* from qPCR testing of 2 repeat extractions from the original sample.

B. *mecA* was detected in 4 of the 7 false positive samples that were tested with an FDA-cleared multiplex assay.

Table 38: Clinical Performance for *mecC*

Target	Sample Type	Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
mecC *Staphylococcus*	Prospective (Fresh)	0/0	---	182/182	100 (97.9-100)
	Prospective (Frozen)	0/0	---	274/274	100 (98.6-100)
	Prospective (All)	**0/0**	**---**	**456/456**	**100 (99.2-100)**
	Retrospective	0/0	---	191/191	100 (98.0-100)
	Prospective/Retrospective	**0/0**	**---**	**647/647**	**100 (99.4-100)**
	Contrived	49/49	100 (92.7-100)	56/56	100 (93.6-100)
	Overall	**49/49**	**100 (92.7-100)**	**703/703**	**100 (99.5-100)**
mecC *Staphylococcus aureus*	Prospective (Fresh)	0/0	---	65/65	100 (94.4-100)
	Prospective (Frozen)	0/0	---	101/101	100 (96.3-100)
	Prospective (All)	**0/0**	**---**	**166/166**	**100 (97.7-100)**
	Retrospective	0/0	---	125/125	100 (97.0-100)
	Prospective/Retrospective	**0/0**	**---**	**291/291**	**100 (98.7-100)**
	Contrived	49/49	100 (92.7-100)	10/10	100 (72.2-100)
	Overall	**49/49**	**100 (92.7-100)**	**301/301**	**100 (98.7-100)**
mecC *Staphylococcus epidermidis*	Prospective (Fresh)	0/0	---	63/63	100 (94.3-100)
	Prospective (Frozen)	0/0	---	58/58	100 (93.8-100)
	Prospective (All)	**0/0**	**---**	**121/121**	**100 (96.9-100)**
	Retrospective	0/0	---	38/38	100 (90.8-100)
	Prospective/Retrospective	**0/0**	**---**	**159/159**	**100 (97.6-100)**
	Contrived	0/0	---	1/1	100 (20.7-100)
	Overall	**0/0**	**---**	**160/160**	**100 (97.7-100)**
mecC *Staphylococcus lugdunensis*	Prospective (Fresh)	0/0	---	1/1	100 (20.7-100)
	Prospective (Frozen)	0/0	---	1/1	100 (20.7-100)
	Prospective (All)	**0/0**	**---**	**2/2**	**100 (34.2-100)**
	Retrospective	0/0	---	4/4	100 (51.0-100)
	Prospective/Retrospective	**0/0**	**---**	**6/6**	**100 (61.0-100)**
	Contrived	0/0	---	45/45	100 (92.1-100)
	Overall	**0/0**	**---**	**51/51**	**100 (93.0-100)**

Table 39: Clinical Performance for *vanA*

Target	Sample Type	Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
vanA *Enterococcus*	Prospective (Fresh)	0/0	---	24/25	96.0 (80.5-99.3)
	Prospective (Frozen)	8/8	100 (67.6-100)	28/28	100 (87.9-100)
	Prospective (All)	**8/8**	**100 (67.6-100)**	**52/53**	**98.1 (90.1-99.7)**
	Retrospective	53/57	93.0 (83.3-97.2)	89/90	98.9 (94.0-99.8)
	Prospective/Retrospective	**61/65[A]**	**93.8 (85.2-97.6)**	**141/143[B]**	**98.6 (95.0-99.6)**
	Contrived	60/60	100 (94.0-100)	66/66	100 (94.5-100)
	Overall	**121/125**	**96.8 (92.1-98.7)**	**207/209**	**99.0 (96.6-99.7)**
vanA *Enterococcus faecalis*	Prospective (Fresh)	0/0	---	21/21	100 (84.5-100)
	Prospective (Frozen)	1/1	100 (20.7-100)	27/27	100 (87.5-100)
	Prospective (All)	**1/1**	**100 (20.7-100)**	**48/48**	**100 (92.6-100)**
	Retrospective	11/14	78.6 (52.4-92.4)	76/76	100 (95.2-100)
	Prospective/Retrospective	**12/15**	**80.0 (54.8-93.0)**	**124/124**	**100 (97.0-100)**
	Contrived	10/10	100 (72.2-100)	42/42	100 (91.6-100)
	Overall	**22/25**	**88.0 (70.0-95.8)**	**166/166**	**100 (97.7-100)**
vanA *Enterococcus faecium*	Prospective (Fresh)	0/0	---	2/3	66.7 (20.8-93.9)
	Prospective (Frozen)	7/7	100 (64.6-100)	2/2	100 (34.2-100)
	Prospective (All)	**7/7**	**100 (64.6-100)**	**4/5**	**80.0 (37.6-96.4)**
	Retrospective	44/44	100 (92.0-100)	8/9	88.9 (56.5-98.0)
	Prospective/Retrospective	**51/51**	**100 (93.0-100)**	**12/14**	**85.7 (60.1-96.0)**
	Contrived	50/50	100 (92.9-100)	10/10	100 (72.2-100)
	Overall	**101/101**	**100 (96.3-100)**	**22/24**	**91.7 (74.2-97.7)**

A. In 2/4 false negative samples, *vanA* signal was above the threshold for detection; however, an associated organism was not detected by the BCID-GP panel and the *vanA* target was reported as 'N/A'. Additional testing of the remaining 2 false negative *vanA* samples indicated they may have been contaminated during the original extraction process for the comparator method testing and misidentified as having *vanA* present. Specifically, results for the 2 samples were negative for *vanA* from qPCR testing of 2 repeat extractions from the original sample (1 of these samples also did not have *vanA* detected when tested with an FDA-cleared multiplex assay).

B. *vanA* was detected in the 1 false positive sample that was tested using an FDA-cleared multiplex assay.

Table 40: Clinical Performance for *vanB*

Target	Sample Type	Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
vanB *Enterococcus*	Prospective (Fresh)	0/0	---	25/25	100 (86.7-100)
	Prospective (Frozen)	0/0	---	36/36	100 (90.4-100)
	Prospective (All)	**0/0**	**---**	**61/61**	**100 (94.1-100)**
	Retrospective	1/1	100 (20.7-100)	146/146	100 (97.4-100)
	Prospective/Retrospective	**1/1**	**100 (20.7-100)**	**207/207**	**100 (98.2-100)**
	Contrived	52/52	100 (93.1-100)	74/74	100 (95.1-100)
	Overall	**53/53**	**100 (93.2-100)**	**281/281**	**100 (98.7-100)**

Target	Sample Type	Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
vanB Enterococcus faecalis	Prospective (Fresh)	0/0	---	21/21	100 (84.5-100)
	Prospective (Frozen)	0/0	---	28/28	100 (87.9-100)
	Prospective (All)	**0/0**	**---**	**49/49**	**100 (92.7-100)**
	Retrospective	1/1	100 (20.7-100)	89/89	100 (95.9-100)
	Prospective/Retrospective	**1/1**	**100 (20.7-100)**	**138/138**	**100 (97.3-100)**
	Contrived	42/42	100 (91.6-100)	10/10	100 (72.2-100)
	Overall	**43/43**	**100 (91.8-100)**	**148/148**	**100 (97.5-100)**
vanB Enterococcus faecium	Prospective (Fresh)	0/0	---	3/3	100 (43.9-100)
	Prospective (Frozen)	0/0	---	9/9	100 (70.1-100)
	Prospective (All)	**0/0**	**---**	**12/12**	**100 (75.8-100)**
	Retrospective	0/0	---	53/53	100 (93.2-100)
	Prospective/Retrospective	**0/0**	**---**	**65/65**	**100 (94.4-100)**
	Contrived	10/10	100 (72.2-100)	50/50	100 (92.9-100)
	Overall	**10/10**	**100 (72.2-100)**	**115/115**	**100 (96.8-100)**

Pan Targets

In addition to the evaluable prospective and retrospective samples that contain gram-positive organisms, the clinical performance of the Pan *Candida* and Pan Gram-Negative targets was evaluated by testing an additional 480 non-intended use retrospective samples with gram-negative or fungal organisms; these are denoted as Retrospective (Non-Intended Use) samples. Results from those samples are summarized in **Table 41** below.

Table 41: Clinical Performance for Pan Targets

Target	Sample Type	Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
Pan *Candida*	Prospective (Fresh)	0/0	---	312/312	100 (98.8-100)
	Prospective (Frozen)	0/0	---	399/399	100 (99.0-100)
	Prospective (All)	0/0	---	711/711	100 (99.5-100)
	Retrospective	7/9[A]	77.8 (45.3-93.7)	576/577	99.8 (99.0-100)
	Retrospective (Non-Intended Use)	90/96[B]	93.8 (87.0-97.1)	383/384[C]	99.7 (98.5-100)
	Contrived	0/0	---	565/565	100 (99.3-100)
Pan Gram-Negative	Prospective (Fresh)	10/11	90.9 (62.3-98.4)	299/301	99.3 (97.6-99.8)
	Prospective (Frozen)	12/12	100 (75.8-100)	386/387	99.7 (98.6-100)
	Prospective (All)	22/23	95.7 (79.0-99.2)	685/688[D]	99.6 (98.7-99.9)
	Retrospective	36/43[E]	83.7 (70.0-91.9)	540/543[F]	99.4 (98.4-99.8)
	Retrospective (Non-Intended Use)	364/375	97.1 (94.8-98.4)	104/105	99.0 (94.8-99.8)
	Contrived	0/0	---	565/565	100 (99.3-100)

A. 2 of 2 (100%) false negative results occurred in samples in mixed infections with bacterial organisms where the BCID-GP panel results were correct for the other infections in these samples.

B. 2 of 6 (33%) false negative results occurred in samples in mixed infections with bacterial organisms where the BCID-GP panel results were correct for the other infections in these samples.
C. *Candida glabrata* was detected in 1/1 false positive samples using PCR/sequencing.
D. A gram-negative organism, *Klebsiella pneumoniae*, was detected in 1/3 false positive samples using PCR/sequencing.
E. 7 of 7 (100%) false negative results occurred in samples in mixed infections with bacterial organisms where the BCID-GP panel correctly detected a gram-positive organism.
F. A gram-negative organism, *Escherichia coli*, was detected in 1/3 false positive samples using PCR/sequencing.

Table 42: Contrived Sample Summary

Target	Organism	Strain	Independent Contrived Samples Tested
Bacillus cereus group	*Bacillus cereus*	ATCC 10876	11
		ATCC 21769	10
		ATCC 31430	9
		ATCC 53522	10
	Bacillus thuringiensis	ATCC 33679	1
		ATCC 10792	2
		ATCC 55173	3
	Bacillus cereus group total		46
Bacillus subtilis group	*Bacillus amyloliquefaciens*	ATCC 23350	3
		ATCC 23845	4
		ATCC 53495	3
	Bacillus atrophaeus	ATCC 51189	4
		ATCC 6455	3
		ATCC 6537	4
	Bacillus licheniformis	ATCC 21039	3
		ATCC 21667	3
		ATCC 53926	4
	Bacillus subtilis	ATCC 15040	5
		ATCC 15561	8
		ATCC 55614	6
	Bacillus subtilis group total		50
Corynebacterium	*Corynebacterium coyleae*	ATCC *700219*	7
	Corynebacterium falsenii	ATCC BAA-596	9
	Corynebacterium striatum	ATCC BAA-1293	4
	Corynebacterium total		20
Enterococcus	*Enterococcus faecalis, vanA*	JMI 876745	10
	Enterococcus faecalis, vanB	ATCC 51299	11
		ATCC 51575	11
		ATCC 700802	10
		ATCC BAA-2365	10
	Enterococcus faecium, vanA	ATCC 51559	4
		ATCC 700221	3
		ATCC BAA-2316	5
		ATCC BAA-2317	3
		ATCC BAA-2318	5
		ATCC BAA-2319	5
		ATCC BAA-2320	3
		LMC 002867	3
		LMC 003921	4
		LMC 032261	4
		LMC 055971	3

Target	Organism	Strain	Independent Contrived Samples Tested
		LMC 103676	5
		LMC 104266	3
	Enterococcus faecium, vanB	ATCC 51858	10
	Enterococcus flavescens	ATCC 49996	3
	Enterococcus gallinarum	ATCC 49610	1
		ATCC 700425	3
	Enterococcus hirae	ATCC 10541	1
	Enterococcus malodoratus	ATCC 43197	3
	Enterococcus raffinosus	ATCC 49464	2
	Enterococcus saccharolyticus	ATCC 43076	1
	Enterococcus total		126
Lactobacillus	*Lactobacillus casei*	ATCC 25598	2
		ATCC 334	6
		ATCC 39392	4
	Lactobacillus paracasei	148-260 *	3
		ATCC 27092	2
		ATCC BAA-52	6
	Lactobacillus rhamnosus	ATCC 39595	3
		ATCC 53103	5
		ATCC 55915	2
	Lactobacillus total		33
Listeria	*Listeria innocua*	ATCC 33090	4
		NCTC 11288	5
	Listeria ivanovii	ATCC 19119	2
		ATCC 700402	4
		ATCC BAA-139	4
Listeria	*Listeria monocytogenes*	ATCC 13932	5
		ATCC 19111	3
		ATCC 19112	4
		ATCC 19114	5
		ATCC 19116	5
		ATCC 19117	5
		ATCC 19118	5
		ATCC 7644	5
		ATCC BAA-751	5
		NCTC 10890	4
	Listeria seeligeri	ATCC 35967	5
	Listeria welshimeri	ATCC 35897	5
	Listeria total		75
Micrococcus	*Micrococcus luteus*	ATCC 10240	3
		ATCC 19212	3
		ATCC 400	3
		ATCC 4698	3
		ATCC 49732	3
		ATCC 53598	4
	Micrococcus lylae	ATCC 27566	4
	Micrococcus yunnanensis	ATCC 7468	4
	Micrococcus total		27

Target	Organism	Strain	Independent Contrived Samples Tested
Cutibacterium acnes	*Cutibacterium acnes*	ATCC 11827	8
		ATCC 11828	6
		ATCC 33179	4
		ATCC 6919	8
	Cutibacterium acnes total		26
Staphylococcus	*Staphylococcus aureus, mecA*	ATCC 33591	3
		ATCC BAA-44	5
		NCTC 12493	2
	Staphylococcus aureus, mecC	ATCC BAA-2312	23
		ATCC BAA-2313	26
	Staphylococcus epidermidis, mecA	ATCC 35984	1
	Staphylococcus lugdunensis	ATCC 49576	9
		NRS 878	9
		NRS 879	9
		NRS 880	9
		NRS 881	9
	Staphylococcus total		105
Streptococcus	*Streptococcus agalactiae*	ATCC 12403	2
		ATCC 12973	2
		ATCC 13813	2
		ATCC 27956	2
	Streptococcus anginosus	ATCC 700231	5
		ATCC 9895	3
		NCTC 10713	5
	Streptococcus constellatus	ATCC 27513	4
		ATCC 27823	2
	Streptococcus intermedius	ATCC 27335	4
	Streptococcus pyogenes	ATCC 12344	5
		ATCC 12384	4
		ATCC 14289	4
		ATCC 19615	4
Streptococcus		ATCC 49399	5
		NCIMB 13285	4
	Streptococcus total		57

*Derived from clinical specimen

Genus and Group Assay Species Stratification

The **cobas eplex** BCID-GP panel reports genus or group level results for *Bacillus cereus* group, *Bacillus subtilis* group, *Corynebacterium*, *Enterococcus*, *Lactobacillus*, *Listeria*, *Micrococcus*, *Staphylococcus*, *Streptococcus*, *Streptococcus anginosus* group, Pan Gram-Negative and Pan *Candida* targets. Sensitivity/PPA of these genus and group level targets for species as determined by comparator methods for all evaluable samples tested are summarized in **Table 43** and for the Pan targets for non-intended use samples in **Table 44**.

Table 43: Species Detected in Genus and Group Assays by Comparator Methods

Target Species detected by Comparator Method	Sensitivity/PPA (Prospective)		Sensitivity/PPA (Retrospective)		Sensitivity/PPA (Contrived)		Sensitivity/PPA (Combined)	
	TP/ TP+FN	% (95% CI)	TP/ TP+FN	% (95% CI)	TP/ TP+FN	% (95% CI)	TP/ TP+FN	% (95% CI)
***Bacillus cereus* group**	**5/5**	**100 (56.6-100)**	**6/7**	**85.7 (48.7-97.4)**	**46/46**	**100 (92.3-100)**	**57/58**	**98.3 (90.9-99.7)**
Bacillus cereus	3/3	100 (43.9-100)	6/7	85.7 (48.7-97.4)	40/40	100 (91.2-100)	49/50	98.0 (89.5-99.6)
Bacillus thuringiensis	2/2	100 (34.2-100)	-	-	6/6	100 (61.0-100)	8/8	100 (67.6-100)
***Bacillus subtilis* group**	**2/2**	**100 (34.2-100)**	**-**	**-**	**50/50**	**100 (92.9-100)**	**52/52**	**100 (93.1-100)**
Bacillus amyloliquefaciens	1/1	100 (20.7-100)	-	-	10/10	100 (72.2-100)	11/11	100 (74.1-100)
Bacillus atrophaeus	-	-	-	-	11/11	100 (74.1-100)	11/11	100 (74.1-100)
Bacillus licheniformis	-	-	-	-	10/10	100 (72.2-100)	10/10	100 (72.2-100)
Bacillus subtilis	1/1	100 (20.7-100)	-	-	19/19	100 (83.2-100)	20/20	100 (83.9-100)
Corynebacterium	**13/19**	**68.4 (46.0-84.6)**	**27/32**	**84.4 (68.2-93.1)**	**20/20**	**100 (83.9-100)**	**60/71**	**84.5 (74.3-91.1)**
Corynebacterium	4/9	44.4 (18.9-73.3)	5/7	71.4 (35.9-91.8)	-	-	9/16	56.3 (33.2-76.9)
Corynebacterium afermentans	0/1	0.0 (0.0-79.3)	3/3	100 (43.9-100)	-	-	3/4	75.0 (30.1-95.4)
*Corynebacterium amycolatum**	1/1	100 (20.7-100)	-	-	-	-	1/1	100 (20.7-100)
Corynebacterium aurimucosum	1/1	100 (20.7-100)	1/1	100 (20.7-100)	-	-	2/2	100 (34.2-100)
Corynebacterium casei	1/1	100 (20.7-100)	-	-	-	-	1/1	100 (20.7-100)
Corynebacterium coyleae	1/1	100 (20.7-100)	2/2	100 (34.2-100)	7/7	100 (64.6-100)	10/10	100 (72.2-100)
Corynebacterium falsenii	-	-	-	-	9/9	100 (70.1-100)	9/9	100 (70.1-100)
Corynebacterium imitans	2/2	100 (34.2-100)	2/2	100 (34.2-100)	-	-	4/4	100 (51.0-100)
Corynebacterium jeikeium	-	-	4/5	80.0 (37.6-96.4)	-	-	4/5	80.0 (37.6-96.4)
Corynebacterium kroppenstedtii	-	-	1/1	100 (20.7-100)	-	-	1/1	100 (20.7-100)
Corynebacterium matruchotii	-	-	1/1	100 (20.7-100)	-	-	1/1	100 (20.7-100)
Corynebacterium mucifaciens	1/1	100 (20.7-100)	2/2	100 (34.2-100)	-	-	3/3	100 (43.9-100)
Corynebacterium pseudotuberculosis	-	-	0/1	0.0 (0.0-79.3)	-	-	0/1	0.0 (0.0-79.3)
Corynebacterium striatum	1/1	100 (20.7-100)	6/6	100 (61.0-100)	4/4	100 (51.0-100)	11/11	100 (74.1-100)
Corynebacterium tuberculostearicum	1/1	100 (20.7-100)	-	-	-	-	1/1	100 (20.7-100)
Corynebacterium urealyticum	-	-	0/1	0.0 (0.0-79.3)	-	-	0/1	0.0 (0.0-79.3)

Target Species detected by Comparator Method	Sensitivity/PPA (Prospective)		Sensitivity/PPA (Retrospective)		Sensitivity/PPA (Contrived)		Sensitivity/PPA (Combined)	
	TP/ TP+FN	% (95% CI)	TP/ TP+FN	% (95% CI)	TP/ TP+FN	% (95% CI)	TP/ TP+FN	% (95% CI)
Enterococcus	**61/61**	**100 (94.1-100)**	**139/147**	**94.6 (89.6-97.2)**	**126/126**	**100 (97.0-100)**	**326/334**	**97.6 (95.3-98.8)**
Enterococcus	1/1	100 (20.7-100)	-	-	-	-	1/1	100 (20.7-100)
Enterococcus avium	1/1	100 (20.7-100)	2/3	66.7 (20.8-93.9)	-	-	3/4	75.0 (30.1-95.4)
Enterococcus casseliflavus	-	-	0/1	0.0 (0.0-79.3)	-	-	0/1	0.0 (0.0-79.3)
Enterococcus casseliflavus / gallinarum	-	-	1/1	100 (20.7-100)	-	-	1/1	100 (20.7-100)
Enterococcus faecalis	49/49	100 (92.7-100)	85/90	94.4 (87.6-97.6)	52/52	100 (93.1-100)	186/191	97.4 (94.0-98.9)
Enterococcus faecium	12/12	100 (75.8-100)	52/53	98.1 (90.1-99.7)	60/60	100 (94.0-100)	124/125	99.2 (95.6-99.9)
Enterococcus flavescens	-	-	-	-	3/3	100 (43.9-100)	3/3	100 (43.9-100)
Enterococcus gallinarum	-	-	2/2	100 (34.2-100)	4/4	100 (51.0-100)	6/6	100 (61.0-100)
Enterococcus hirae	-	-	-	-	1/1	100 (20.7-100)	1/1	100 (20.7-100)
Enterococcus malodoratus	-	-	-	-	3/3	100 (43.9-100)	3/3	100 (43.9-100)
Enterococcus raffinosus	-	-	-	-	2/2	100 (34.2-100)	2/2	100 (34.2-100)
Enterococcus saccharolyticus	-	-	-	-	1/1	100 (20.7-100)	1/1	100 (20.7-100)
Lactobacillus	**4/4**	**100 (51.0-100)**	**9/9**	**100 (70.1-100)**	**32/33**	**97.0 (84.7-99.5)**	**45/46**	**97.8 (88.7-99.6)**
Lactobacillus casei	-	-	1/1	100 (20.7-100)	12/12	100 (75.8-100)	13/13	100 (77.2-100)
Lactobacillus paracasei	1/1	100 (20.7-100)	-	-	11/11	100 (74.1-100)	12/12	100 (75.8-100)
Lactobacillus rhamnosus	2/2	100 (34.2-100)	8/8	100 (67.6-100)	9/10	90.0 (59.6-98.2)	19/20	95.0 (76.4-99.1)
Lactobacillus zeae	1/1	100 (20.7-100)	-	-	-	-	1/1	100 (20.7-100)
Listeria	**-**	**-**	**2/2**	**100 (34.2-100)**	**74/75**	**98.7 (92.8-99.8)**	**76/77**	**98.7 (93.0-99.8)**
Listeria innocua	-	-	-	-	9/9	100 (70.1-100)	9/9	100 (70.1-100)
Listeria ivanovii	-	-	-	-	9/10	90.0 (59.6-98.2)	9/10	90.0 (59.6-98.2)
Listeria monocytogenes	-	-	2/2	100 (34.2-100)	46/46	100 (92.3-100)	48/48	100 (92.6-100)
Listeria seeligeri	-	-	-	-	5/5	100 (56.6-100)	5/5	100 (56.6-100)
Listeria welshimeri	-	-	-	-	5/5	100 (56.6-100)	5/5	100 (56.6-100)
Micrococcus	**19/21**	**90.5 (71.1-97.3)**	**20/23**	**87.0 (67.9-95.5)**	**27/27**	**100 (87.5-100)**	**66/71**	**93.0 (84.6-97.0)**
Micrococcus	8/9	88.9 (56.5-98.0)	10/13	76.9 (49.7-91.8)	-	-	18/22	81.8 (61.5-92.7)
Micrococcus luteus	9/9	100 (70.1-100)	8/8	100 (67.6-100)	19/19	100 (83.2-100)	36/36	100 (90.4-100)
Micrococcus luteus/lylae	2/3	66.7 (20.8-93.9)	2/2	100 (34.2-100)	-	-	4/5	80.0 (37.6-96.4)
Micrococcus lylae	-	-	-	-	4/4	100 (51.0-100)	4/4	100 (51.0-100)
Micrococcus yunnanensis	-	-	-	-	4/4	100 (51.0-100)	4/4	100 (51.0-100)
Staphylococcus	**447/456**	**98.0 (96.3-99.0)**	**185/191**	**96.9 (93.3-98.6)**	**105/105**	**100 (96.5-100)**	**737/752**	**98.0 (96.7-98.8)**
Coagulase-negative *staphylococci (CoNS)*	18/18	100 (82.4-100)	-	-	-	-	18/18	100 (82.4-100)
CoNS (Not *S. epidermidis, S. lugdunensis*)	2/2	100 (34.2-100)	-	-	-	-	2/2	100 (34.2-100)
Staphylococcus	74/78	94.9 (87.5-98.0)	1/3	33.3 (6.1-79.2)	-	-	75/81	92.6 (84.8-96.6)
Staphylococcus aureus	158/160	98.8 (95.6-99.7)	121/123	98.4 (94.3-99.6)	59/59	100 (93.9-100)	338/342	98.8 (97.0-99.5)
Staphylococcus aureus subsp. *aureus*	6/6	100 (61.0-100)	2/2	100 (34.2-100)	-	-	8/8	100 (67.6-100)
Staphylococcus auricularis	2/2	100 (34.2-100)	2/2	100 (34.2-100)	-	-	4/4	100 (51.0-100)
Staphylococcus capitis	14/14	100 (78.5-100)	7/7	100 (64.6-100)	-	-	21/21	100 (84.5-100)
Staphylococcus carnosus subsp. *carnosus*	-	-	0/1	0.0 (0.0-79.3)	-	-	0/1	0.0 (0.0-79.3)
Staphylococcus cohnii	1/2	50.0 (9.5-90.5)	-	-	-	-	1/2	50.0 (9.5-90.5)

Target Species detected by Comparator Method	Sensitivity/PPA (Prospective)		Sensitivity/PPA (Retrospective)		Sensitivity/PPA (Contrived)		Sensitivity/PPA (Combined)	
	TP/ TP+FN	% (95% CI)	TP/ TP+FN	% (95% CI)	TP/ TP+FN	% (95% CI)	TP/ TP+FN	% (95% CI)
Staphylococcus epidermidis	117/121	96.7 (91.8-98.7)	37/38	97.4 (86.5-99.5)	1/1	100 (20.7-100)	155/160	96.9 (92.9-98.7)
Staphylococcus haemolyticus	6/6	100 (61.0-100)	2/2	100 (34.2-100)	-	-	8/8	100 (67.6-100)
Staphylococcus hominis	24/24	100 (86.2-100)	13/13	100 (77.2-100)	-	-	37/37	100 (90.6-100)
Staphylococcus hominis subsp. *hominis*	22/22	100 (85.1-100)	5/5	100 (56.6-100)	-	-	27/27	100 (87.5-100)
Staphylococcus hominis subsp. *novobiosepticus*	1/1	100 (20.7-100)	-	-	-	-	1/1	100 (20.7-100)
Staphylococcus lugdunensis	2/2	100 (34.2-100)	4/4	100 (51.0-100)	45/45	100 (92.1-100)	51/51	100 (93.0-100)
Staphylococcus pettenkoferi	2/2	100 (34.2-100)	-	-	-	-	2/2	100 (34.2-100)
Staphylococcus saccharolyticus	1/1	100 (20.7-100)	-	-	-	-	1/1	100 (20.7-100)
Staphylococcus saprophyticus	1/1	100 (20.7-100)	1/1	100 (20.7-100)	-	-	2/2	100 (34.2-100)
Staphylococcus schleiferi	-	-	1/1	100 (20.7-100)	-	-	1/1	100 (20.7-100)
Staphylococcus simulans	3/3	100 (43.9-100)	-	-	-	-	3/3	100 (43.9-100)
Staphylococcus warneri	4/4	100 (51.0-100)	-	-	-	-	4/4	100 (51.0-100)
Streptococcus	**103/110**	**93.6 (87.4-96.9)**	**171/173**	**98.8 (95.9-99.7)**	**57/57**	**100 (93.7-100)**	**331/340**	**97.4 (95.0-98.6)**
Alpha Hemolytic *Streptococcus*	1/1	100 (20.7-100)	-	-	-	-	1/1	100 (20.7-100)
Gamma Hemolytic *Streptococcus*	1/1	100 (20.7-100)	-	-	-	-	1/1	100 (20.7-100)
Streptococcus	5/7	71.4 (35.9-91.8)	-	-	-	-	5/7	71.4 (35.9-91.8)
Streptococcus (Group G)	1/1	100 (20.7-100)	-	-	-	-	1/1	100 (20.7-100)
Streptococcus agalactiae	10/11	90.9 (62.3-98.4)	37/37	100 (90.6-100)	8/8	100 (67.6-100)	55/56	98.2 (90.6-99.7)
Streptococcus anginosus	1/1	100 (20.7-100)	13/13	100 (77.2-100)	13/13	100 (77.2-100)	27/27	100 (87.5-100)
Streptococcus anginosus group	4/4	100 (51.0-100)	22/22	100 (85.1-100)	-	-	26/26	100 (87.1-100)
Streptococcus bovis	-	-	2/2	100 (34.2-100)	-	-	2/2	100 (34.2-100)
Streptococcus bovis group	1/1	100 (20.7-100)	-	-	-	-	1/1	100 (20.7-100)
Streptococcus constellatus	-	-	-	-	6/6	100 (61.0-100)	6/6	100 (61.0-100)
Streptococcus constellatus subsp. *constellatus*	-	-	2/2	100 (34.2-100)	-	-	2/2	100 (34.2-100)
Streptococcus constellatus subsp. *pharyngis*	-	-	1/1	100 (20.7-100)	-	-	1/1	100 (20.7-100)
Streptococcus dysgalactiae	-	-	2/2	100 (34.2-100)	-	-	2/2	100 (34.2-100)
Streptococcus dysgalactiae (Group G)	4/4	100 (51.0-100)	1/1	100 (20.7-100)	-	-	5/5	100 (56.6-100)
Streptococcus gallolyticus	1/1	100 (20.7-100)	-	-	-	-	1/1	100 (20.7-100)
Streptococcus gordonii	1/1	100 (20.7-100)	-	-	-	-	1/1	100 (20.7-100)
Streptococcus infantarius	-	-	1/1	100 (20.7-100)	-	-	1/1	100 (20.7-100)
Streptococcus intermedius	-	-	2/2	100 (34.2-100)	4/4	100 (51.0-100)	6/6	100 (61.0-100)
Streptococcus mitis	9/10	90.0 (59.6-98.2)	14/15	93.3 (70.2-98.8)	-	-	23/25	92.0 (75.0-97.8)
Streptococcus mitis group	10/10	100 (72.2-100)	-	-	-	-	10/10	100 (72.2-100)
Streptococcus mutans	-	-	1/1	100 (20.7-100)	-	-	1/1	100 (20.7-100)
Streptococcus oralis	-	-	3/3	100 (43.9-100)	-	-	3/3	100 (43.9-100)
Streptococcus parasanguinis	2/2	100 (34.2-100)	4/4	100 (51.0-100)	-	-	6/6	100 (61.0-100)
Streptococcus pneumoniae	28/28	100 (87.9-100)	41/41	100 (91.4-100)	-	-	69/69	100 (94.7-100)
Streptococcus pyogenes	8/8	100 (67.6-100)	19/20	95.0 (76.4-99.1)	26/26	100 (87.1-100)	53/54	98.1 (90.2-99.7)
Streptococcus salivarius	4/4	100 (51.0-100)	5/5	100 (56.6-100)	-	-	9/9	100 (70.1-100)
Streptococcus vestibularis	-	-	1/1	100 (20.7-100)	-	-	1/1	100 (20.7-100)

Target Species detected by Comparator Method	Sensitivity/PPA (Prospective)		Sensitivity/PPA (Retrospective)		Sensitivity/PPA (Contrived)		Sensitivity/PPA (Combined)	
	TP/ TP+FN	% (95% CI)	TP/ TP+FN	% (95% CI)	TP/ TP+FN	% (95% CI)	TP/ TP+FN	% (95% CI)
Streptococcus viridans group	14/17	82.4 (59.0-93.8)	2/2	100 (34.2-100)	-	-	16/19	84.2 (62.4-94.5)
***Streptococcus anginosus* group**	**4/5**	**80.0 (37.6-96.4)**	**38/40**	**95.0 (83.5-98.6)**	**23/23**	**100 (85.7-100)**	**65/68**	**95.6 (87.8-98.5)**
Streptococcus anginosus	0/1	0.0 (0.0-79.3)	12/13	92.3 (66.7-98.6)	13/13	100 (77.2-100)	25/27	92.6 (76.6-97.9)
Streptococcus anginosus group	4/4	100 (51.0-100)	21/22	95.5 (78.2-99.2)	-	-	25/26	96.2 (81.1-99.3)
Streptococcus constellatus	-	-	-	-	6/6	100 (61.0-100)	6/6	100 (61.0-100)
Streptococcus constellatus subsp. *constellatus*	-	-	2/2	100 (34.2-100)	-	-	2/2	100 (34.2-100)
Streptococcus constellatus subsp. *pharynges*	-	-	1/1	100 (20.7-100)	-	-	1/1	100 (20.7-100)
Streptococcus intermedius	-	-	2/2	100 (34.2-100)	4/4	100 (51.0-100)	6/6	100 (61.0-100)
Pan *Candida*	**-**	**-**	**7/9**	**77.8 (45.3-93.7)**	**-**	**-**	**7/9**	**77.8 (45.3-93.7)**
Candida albicans	-	-	4/4	100 (51.0-100)	-	-	4/4	100 (51.0-100)
Candida glabrata	-	-	1/2	50 (9.5-90.5)	-	-	1/2	50 (9.5-90.5)
Candida krusei	-	-	1/1	100 (20.7-100)	-	-	1/1	100 (20.7-100)
Candida parapsilosis	-	-	1/2	50 (9.5-90.5)	-	-	1/2	50 (9.5-90.5)
Pan Gram-Negative	**22/23**	**95.7 (79.0-99.2)**	**36/43**	**83.7 (70.0-91.9)**	**-**	**-**	**58/66**	**87.9 (77.9-93.7)**
Acinetobacter baumannii	3/3	100 (43.9-100)	2/4	50.0 (15.0-85.0)	-	-	5/7	71.4 (35.9-91.8)
Acinetobacter lwoffii	1/1	100 (20.7-100)	-	-	-	-	1/1	100 (20.7-100)
Aeromonas caviae	-	-	1/1	100 (20.7-100)	-	-	1/1	100 (20.7-100)
Bacteroides fragilis	2/2	100 (34.2-100)	-	-	-	-	2/2	100 (34.2-100)
Campylobacter gracilis	0/1	0.0 (0.0-79.3)	-	-	-	-	0/1	0.0 (0.0-79.3)
Citrobacter braakii	-	-	1/1	100 (20.7-100)	-	-	1/1	100 (20.7-100)
Citrobacter freundii	1/1	100 (20.7-100)	-	-	-	-	1/1	100 (20.7-100)
Citrobacter koseri	1/1	100 (20.7-100)	-	-	-	-	1/1	100 (20.7-100)
Enterobacter aerogenes	-	-	1/1	100 (20.7-100)	-	-	1/1	100 (20.7-100)
Enterobacter cloacae	-	-	4/4	100 (51.0-100)	-	-	4/4	100 (51.0-100)
Escherichia coli	4/4	100 (51.0-100)	14/14	100 (78.5-100)	-	-	18/18	100 (82.4-100)
Klebsiella oxytoca	1/1	100 (20.7-100)	3/3	100 (43.9-100)	-	-	4/4	100 (51.0-100)
Klebsiella pneumoniae	4/4	100 (51.0-100)	4/5	80.0 (37.6-96.4)	-	-	8/9	88.9 (56.5-98.0)
Moraxella (Branhamella) catarrhalis	-	-	1/1	100 (20.7-100)	-	-	1/1	100 (20.7-100)
Moraxella catarrhalis	-	-	1/1	100 (20.7-100)	-	-	1/1	100 (20.7-100)
Morganella morganii	-	-	2/2	100 (34.2-100)	-	-	2/2	100 (34.2-100)
Proteus mirabilis	5/5	100 (56.6-100)	4/5	80.0 (37.6-96.4)	-	-	9/10	90.0 (59.6-98.2)
Proteus vulgaris	-	-	1/1	100 (20.7-100)	-	-	1/1	100 (20.7-100)
Providencia stuartii	1/1	100 (20.7-100)	0/1	0.0 (0.0-79.3)	-	-	1/2	50.0 (9.5-90.5)
Pseudomonas	-	-	1/1	100 (20.7-100)	-	-	1/1	100 (20.7-100)
Pseudomonas aeruginosa	1/1	100 (20.7-100)	1/2	50.0 (9.5-90.5)	-	-	2/3	66.7 (20.8-93.9)
Serratia marcescens	2/2	100 (34.2-100)	-	-	-	-	2/2	100 (34.2-100)
Stenotrophomonas maltophilia	1/1	100 (20.7-100)	1/1	100 (20.7-100)	-	-	2/2	100 (34.2-100)
Veillonella species	-	-	0/1	0.0 (0.0-79.3)	-	-	0/1	0.0 (0.0-79.3)
Non-fermenting gram-negative bacilli	1/1	100 (20.7-100)	-	-	-	-	1/1	100 (20.7-100)

*Organism reported by the clinical site as *Corynebacterium*. Sequencing identified *C. amycolatum*. Due to a high amount of sequence similarities, there is a possibility that *C. jeikeium* was the species detected.

Table 44: Species Detected in Pan Assays by Comparator Methods for Samples in Retrospective (Non-Intended Use) Samples with Gram-Negative or Fungal Organisms

Target Species Detected by Comparator Method	Retrospective (Non-Intended Use) Samples	
	Sensitivity/PPA	
	TP/TP+FN	% (95% CI)
Pan *Candida*	90/96	93.8 (87.0-97.1)
Candida albicans	41/45	91.1 (79.3-96.5)
Candida glabrata	33/35	94.3 (81.4-98.4)
Candida krusei	3/3	100 (43.9-100)
Candida parapsilosis	16/16	100 (80.6-100)
Pan Gram-Negative	364/375	97.1 (94.8-98.4)
Achromobacter xylosoxidans ssp *xylosoxidans*	0/1	0.0 (0.0-79.3)
Acinetobacter baumannii	16/16	100 (80.6-100)
Acinetobacter baumannii complex (baum-calcoac-13TU)	1/1	100 (20.7-100)
Acinetobacter lwoffii	1/1	100 (20.7-100)
Acinetobacter nosocomialis	1/1	100 (20.7-100)
Acinetobacter radioresistens	1/1	100 (20.7-100)
Bacteroides fragilis	18/20	90.0 (69.9-97.2)
Bacteroides ovatus	1/1	100 (20.7-100)
Bacteroides thetaiotaomicron	0/4	0.0 (0.0-49.0)
Burkholderia cepacia complex	1/1	100 (20.7-100)
Citrobacter	2/2	100 (34.2-100)
Citrobacter amalonaticus	1/1	100 (20.7-100)
Citrobacter braakii	2/2	100 (34.2-100)
Citrobacter freundii	13/13	100 (77.2-100)
Citrobacter koseri	3/3	100 (43.9-100)
Citrobacter youngae	1/1	100 (20.7-100)
Delftia acidovorans	0/1	0.0 (0.0-79.3)
Enterobacter aerogenes	6/6	100 (61.0-100)
Enterobacter cloacae	14/14	100 (78.5-100)
Enterobacter gergoviae	1/1	100 (20.7-100)
Escherichia coli	112/112	100 (96.7-100)
Fusobacterium	3/3	100 (43.9-100)
Fusobacterium necrophorum	1/1	100 (20.7-100)
Fusobacterium nucleatum	5/5	100 (56.6-100)
Haemophilus influenzae	11/11	100 (74.1-100)
Klebsiella oxytoca	10/10	100 (72.2-100)
Klebsiella pneumoniae	46/47	97.9 (88.9-99.6)
Leclercia adecarboxylata	2/2	100 (34.2-100)
Moraxella sp.	1/1	100 (20.7-100)
Morganella morganii	8/8	100 (67.6-100)
Ochrobactrum anthropi	0/1	0.0 (0.0-79.3)
Proteus mirabilis	16/16	100 (80.6-100)
Providencia stuartii	2/2	100 (34.2-100)

Target Species Detected by Comparator Method	Retrospective (Non-Intended Use) Samples	
	Sensitivity/PPA	
	TP/TP+FN	% (95% CI)
Pseudomonas aeruginosa	25/25	100 (86.7-100)
Pseudomonas putida	1/1	100 (20.7-100)
Salmonella	15/15	100 (79.6-100)
Salmonella choleraesuis subsp. *arizonae*	1/1	100 (20.7-100)
Salmonella enterica subsp *enterica* serovar Typhimurium	1/1	100 (20.7-100)
Salmonella typhi	2/2	100 (34.2-100)
Serratia plymuthica	1/1	100 (20.7-100)
Serratia marcescens	36/36	100 (90.4-100)
Stenotrophomonas maltophilia	9/9	100 (70.1-100)
Wolinella species	0/1	0.0 (0.0-79.3)

Resistance Gene Assay Species Stratification

mecA/mecC

Test results for resistance genes are only reported when an associated organism assay is positive in the same sample. (See **Table 9** for organisms specifically associated with the four resistance markers on the **cobas eplex** BCID-GP panel).

The PPA and NPA of the BCID-GP panel *mecA* target stratified by the *Staphylococcus* species identified by comparator methods for prospective, retrospective and contrived samples are shown in **Table 45**.

Table 45: Clinical Performance of *mecA* Target by *Staphylococcus* Species Detected by Comparator Methods

Species detected by Comparator Method		Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
Coagulase-negative *staphylococci* (CoNS)	Prospective	12/12	100 (75.8-100)	6/6	100 (61.0-100)
	Retrospective	-	-	-	-
	Contrived	-	-	-	-
	Combined	12/12	100 (75.8-100)	6/6	100 (61.0-100)
CoNS (not *S. epidermidis* / *S. lugdunensis*)	Prospective	1/1	100 (20.7-100)	0/1	0.0 (0.0-79.3)
	Retrospective	-	-	-	-
	Contrived	-	-	-	-
	Combined	1/1	100 (20.7-100)	0/1	0.0 (0.0-79.3)
Staphylococcus	Prospective	49/52	94.2 (84.4-98.0)	24/26	92.3 (75.9-97.9)
	Retrospective	1/2	50.0 (9.5-90.5)	1/1	100 (20.7-100)
	Contrived	-	-	-	-
	Combined	50/54	92.6 (82.4-97.1)	25/27	92.6 (76.6-97.9)
Staphylococcus aureus	Prospective	80/83	96.4 (89.9-98.8)	74/77	96.1 (89.2-98.7)
	Retrospective	105/106	99.1 (94.8-99.8)	16/17	94.1 (73.0-99.0)
	Contrived	10/10	100 (72.2-100)	49/49	100 (92.7-100)
	Combined	195/199	98.0 (94.9-99.2)	139/143	97.2 (93.0-98.9)
Staphylococcus aureus subsp. *aureus*	Prospective	3/3	100 (43.9-100)	3/3	100 (43.9-100)
	Retrospective	2/2	100 (34.2-100)	0/0	-
	Contrived	-	-	-	-
	Combined	5/5	100 (56.6-100)	3/3	100 (43.9-100)
Staphylococcus auricularis	Prospective	1/1	100 (20.7-100)	1/1	100 (20.7-100)
	Retrospective	0/0	-	2/2	100 (34.2-100)
	Contrived	-	-	-	-
	Combined	1/1	100 (20.7-100)	3/3	100 (43.9-100)
Staphylococcus capitis	Prospective	4/5	80.0 (37.6-96.4)	5/5	100 (56.6-100)
	Retrospective	4/4	100 (51.0-100)	7/7	100 (64.6-100)
	Contrived	-	-	-	-
	Combined	8/9	88.9 (56.5-98.0)	12/12	100 (75.8-100)

Species detected by Comparator Method		Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
Staphylococcus carnosus subsp. *carnosus*	Prospective	-	-	-	-
	Retrospective	0/0	-	1/1	100 (20.7-100)
	Contrived	-	-	-	-
	Combined	0/0	-	1/1	100 (20.7-100)
Staphylococcus cohnii	Prospective	0/1	0.0 (0.0-79.3)	1/1	100 (20.7-100)
	Retrospective	-	-	-	-
	Contrived	-	-	-	-
	Combined	0/1	0.0 (0.0-79.3)	1/1	100 (20.7-100)
Staphylococcus epidermidis	Prospective	77/79	97.5 (91.2-99.3)	39/42	92.9 (81.0-97.5)
	Retrospective	30/30	100 (88.6-100)	7/8	87.5 (52.9-97.8)
	Contrived	1/1	100 (20.7-100)	0/0	-
	Combined	108/110	98.2 (93.6-99.5)	46/50	92.0 (81.2-96.8)
Staphylococcus haemolyticus	Prospective	4/4	100 (51.0-100)	2/2	100 (34.2-100)
	Retrospective	2/2	100 (34.2-100)	0/0	-
	Contrived	-	-	-	-
	Combined	6/6	100 (61.0-100)	2/2	100 (34.2-100)
Staphylococcus hominis	Prospective	12/13	92.3 (66.7-98.6)	10/11	90.9 (62.3-98.4)
	Retrospective	12/12	100 (75.8-100)	1/1	100 (20.7-100)
	Contrived	-	-	-	-
	Combined	24/25	96.0 (80.5-99.3)	11/12	91.7 (64.6-98.5)
Staphylococcus hominis subsp. *hominis*	Prospective	10/11	90.9 (62.3-98.4)	11/11	100 (74.1-100)
	Retrospective	2/2	100 (34.2-100)	3/3	100 (43.9-100)
	Contrived	-	-	-	-
	Combined	12/13	92.3 (66.7-98.6)	14/14	100 (78.5-100)
Staphylococcus hominis subsp. *novobiosepticus*	Prospective	1/1	100 (20.7-100)	0/0	-
	Retrospective	-	-	-	-
	Contrived	-	-	-	-
	Combined	1/1	100 (20.7-100)	0/0	-
Staphylococcus lugdunensis	Prospective	0/0	---	2/2	100 (34.2-100)
	Retrospective	1/1	100 (20.7-100)	3/3	100 (43.9-100)
	Contrived	0/0	---	45/45	100 (92.1-100)
	Combined	1/1	100 (20.7-100)	50/50	100 (92.9-100)
Staphylococcus pettenkoferi	Prospective	0/0	-	1/2	50.0 (9.5-90.5)
	Retrospective	-	-	-	-
	Contrived	-	-	-	-
	Combined	0/0	-	1/2	50.0 (9.5-90.5)
Staphylococcus saccharolyticus	Prospective	0/0	-	1/1	100 (20.7-100)
	Retrospective	-	-	-	-
	Contrived	-	-	-	-
	Combined	0/0	-	1/1	100 (20.7-100)

Species detected by Comparator Method		Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
Staphylococcus saprophyticus	Prospective	1/1	100 (20.7-100)	0/0	-
	Retrospective	0/0	-	1/1	100 (20.7-100)
	Contrived	-	-	-	-
	Combined	1/1	100 (20.7-100)	1/1	100 (20.7-100)
Staphylococcus schleiferi	Prospective	-	-	-	-
	Retrospective	0/0	-	1/1	100 (20.7-100)
	Contrived	-	-	-	-
	Combined	0/0	-	1/1	100 (20.7-100)
Staphylococcus simulans	Prospective	1/1	100 (20.7-100)	2/2	100 (34.2-100)
	Retrospective	-	-	-	-
	Contrived	-	-	-	-
	Combined	1/1	100 (20.7-100)	2/2	100 (34.2-100)
Staphylococcus warneri	Prospective	0/0	-	4/4	100 (51.0-100)
	Retrospective	-	-	-	-
	Contrived	-	-	-	-
	Combined	0/0	-	4/4	100 (51.0-100)

A comparison of specific *Staphylococcus* species and *mecA* identified by comparator methods versus the **cobas eplex** BCID-GP panel results are shown in **Table 46** and **Table 47** for prospective and retrospective samples.

Table 46: Distribution of *mecA* Results in *Staphylococcus aureus* Prospective/Retrospective Samples

	Comparator Method			
BCID-GP	**Org+/ARG+**	**Org+/ARG-**	**Org-**	**Total**
Org+/ARG+	190	2	2	194
Org+/ARG-	2	88	4	94
Org-	2	7	1000	1009
Total	**194**	**97**	**1006**	**1297**

% Agreement (95% CI) for Org+/ARG+: 190/194=97.9 (94.8-99.2)
% Agreement (95% CI) for Org+/ARG-: 88/97=90.7 (83.3-95.0)
% Agreement (95% CI) for Org-: 1000/1006=99.4 (98.7-99.7)

Table 47: Distribution of *mecA* Results in *Staphylococcus* Species (Excluding Known *S. aureus, S. epidermidis, S. lugdunensis*) Prospective/Retrospective Samples

	Comparator Method			
BCID-GP	**Org+/ARG+**	**Org+/ARG-**	**Org-**	**Total**
Org+/ARG+	33	1	4	38
Org+/ARG-	3	45	8	56
Org-	10*	4	1091	1105
Total	46	50	1103	1199

% Agreement (95% CI) for Org+/ARG+: 33/46=71.7 (57.5-82.7)
% Agreement (95% CI) for Org+/ARG-: 45/50=90.0 (78.6-95.7)
% Agreement (95% CI) for Org-: 1091/1103=98.9 (98.1-99.4)
*10 samples had a *Staphylococcus* species (not *S. aureus, S. epidermidis,* or *S. lugdunensis)* with *mecA* identified by comparator methods, whereas the **cobas eplex** BCID-GP panel detected *S. epidermidis* with *mecA*.

A table for *mecC* is not provided because *mecC* was only detected in a single species, *Staphylococcus aureus*. In the 49 contrived samples with *Staphylococcus aureus* containing *mecC*, the resulting PPA and NPA were both 100%.

vanA/vanB

The PPA and NPA of the BCID-GP panel *vanA* target stratified by the *Enterococcus* species identified by comparator methods for 208 clinical prospective/retrospective samples and 126 contrived samples are shown in **Table 48**.

A table for *vanB* is not provided because *vanB* was only detected in 1 clinical sample and 52 contrived samples comprised of two species, *E. faecalis* (*n*=43) and *E. faecium* (*n*=10), resulting in PPA and NPA of 100%.

Table 48: Clinical Performance of *vanA* Target by *Enterococcus* Species Detected by Comparator Methods

Species detected by Comparator Method		**Sensitivity/PPA**		**Specificity/NPA**	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
Enterococcus	Prospective	0/0	-	1/1	100 (20.7-100)
	Retrospective	-	-	-	-
	Contrived	-	-	-	-
	Combined	0/0	-	1/1	100 (20.7-100)
Enterococcus avium	Prospective	0/0		1/1	100 (20.7-100)
	Retrospective	0/1	0.0 (0.0-79.3)	2/2	100 (34.2-100)
	Contrived	-	-	-	-
	Combined	0/1	0.0 (0.0-79.3)	3/3	100 (43.9-100)
Enterococcus casseliflavus	Prospective	-	-	-	-
	Retrospective	0/0	---	1/1	100 (20.7-100)
	Contrived	-	-	-	-
	Combined	0/0	-	1/1	100 (20.7-100)

Species detected by Comparator Method		Sensitivity/PPA		Specificity/NPA	
		TP/TP+FN	% (95% CI)	TN/TN+FP	% (95% CI)
Enterococcus casseliflavus / E. gallinarum	Prospective	-	-	-	-
	Retrospective	0/0	---	1/1	100 (20.7-100)
	Contrived	-	-	-	-
	Combined	0/0	-	1/1	100 (20.7-100)
Enterococcus faecalis	Prospective	1/1	100 (20.7-100)	48/48	100 (92.6-100)
	Retrospective	11/14	78.6 (52.4-92.4)	76/76	100 (95.2-100)
	Contrived	10/10	100 (72.2-100)	42/42	100 (91.6-100)
	Combined	22/25	88.0 (70.0-95.8)	166/166	100 (97.7-100)
Enterococcus faecium	Prospective	7/7	100 (64.6-100)	4/5	80.0 (37.6-96.4)
	Retrospective	44/44	100 (92.0-100)	8/9	88.9 (56.5-98.0)
	Contrived	50/50	100 (92.9-100)	10/10	100 (72.2-100)
	Combined	101/101	100 (96.3-100)	22/24	91.7 (74.2-97.7)
Enterococcus flavescens	Prospective	-	-	-	-
	Retrospective	-	-	-	-
	Contrived	0/0	---	3/3	100 (43.9-100)
	Combined	0/0	-	3/3	100 (43.9-100)
Enterococcus gallinarum	Prospective	-	-	-	-
	Retrospective	0/0	-	2/2	100 (34.2-100)
	Contrived	0/0	---	4/4	100 (51.0-100)
	Combined	0/0	-	6/6	100 (61.0-100)
Enterococcus hirae	Prospective	-	-	-	-
	Retrospective	-	-	-	-
	Contrived	0/0	---	1/1	100 (20.7-100)
	Combined	0/0	-	1/1	100 (20.7-100)
Enterococcus malodoratus	Prospective	-	-	-	-
	Retrospective	-	-	-	-
	Contrived	0/0	---	3/3	100 (43.9-100)
	Combined	0/0	-	3/3	100 (43.9-100)
Enterococcus raffinosus	Prospective	-	-	-	-
	Retrospective	-	-	-	-
	Contrived	0/0	---	2/2	100 (34.2-100)
	Combined	0/0	-	2/2	100 (34.2-100)
Enterococcus saccharolyticus	Prospective	-	-	-	-
	Retrospective	-	-	-	-
	Contrived	0/0	---	1/1	100 (20.7-100)
	Combined	0/0	-	1/1	100 (20.7-100)

A comparison of *Enterococcus faecalis/Enterococcus faecium* and *vanA* identified by comparator methods versus the **cobas eplex** BCID-GP panel results is shown in **Table 49** and **Table 50** for prospective and retrospective samples.

Table 49: Distribution of *vanA* Results in *Enterococcus faecalis* Prospective/Retrospective Samples

	Comparator Method			
BCID-GP	**Org+/ARG+**	**Org+/ARG-**	**Org-**	**Total**
Org+/ARG+	10	0	0	10
Org+/ARG-	1[A]	120	1	122
Org-	4[B]	4	1157	1165
Total	15	124	1158	1297

% Agreement (95% CI) for Org+/ARG+: 10/15=66.7 (41.7-84.8)
% Agreement (95% CI) for Org+/ARG-: 120/124=96.8 (92.0-98.7)
% Agreement (95% CI) for Org-: 1157/1158=99.9 (99.5-100)

A. Additional testing indicated this sample may have been contaminated during the original extraction process for the comparator method and misidentified as having *vanA* present. Specifically, results were negative for *vanA* from qPCR testing of 2 repeat extractions from the original sample (this sample also did not have *vanA* detected when tested with an FDA-cleared multiplex assay).

B. 2 of the 4 samples had *E. faecium* (not *E.* faecalis) with *vanA* detected by the **cobas eplex** BCID-GP panel.
In the remaining 2 samples, *vanA* signal was above the threshold for detection; however an associated organism was not detected by the **cobas eplex** BCID-GP panel and the *vanA* target was reported as 'N/A'.

Table 50: Distribution of *vanA* Results in *Enterococcus faecium* Prospective/Retrospective Samples

	Comparator Method			
BCID-GP	**Org+/ARG+**	**Org+/ARG-**	**Org-**	**Total**
Org+/ARG+	51	2	3	56
Org+/ARG-	0	10	5	15
Org-	0	2	1224	1226
Total	51	14	1232	1297

% Agreement (95% CI) for Org+/ARG+: 51/51=100.0 (93.0-100)
% Agreement (95% CI) for Org+/ARG-: 10/14=71.4 (45.4-88.3)
% Agreement (95% CI) for Org-: 1224/1232=99.4 (98.7-99.7)

Co-detections in Clinical Samples

The **cobas eplex** BCID-GP panel identified a total of 103 bacterial co-detections in 1297 clinical samples (prospective/retrospective). Of the 711 prospective samples, 672 (94.5%) had single detections, 38 (5.3%) had double detections, and 1 (0.1%) had a triple detection. Of the 586 retrospective samples, 522 (89.1%) had single detections, 56 (9.6%) had double detections, and 8 (1.4%) had triple detections. Neither the prospective nor the retrospective arms of the clinical studies contained a sample with more than 3 organisms detected.

Tables 51-52 below summarize co-detections detected by the **cobas eplex** BCID-GP panel in prospective and retrospective samples.

Table 51: Co-Detections Identified by the cobas eplex BCID-GP panel (Prospective Samples)

Distinct Co-Detection Combinations Detected by the cobas eplex BCID-GP panel in Prospective Clinical Samples				Number of Samples (Number Discrepant)	Discrepant Organism(s) / Resistance Marker(s)[A,B]
Target 1	Target 2	Target 3	Resistance Marker		
C. acnes	*Staphylococcus*			1 (1)	*C. acnes (1)*
Corynebacterium	*S. epidermidis*		*mecA*	2 (0)	
E. faecalis	E. faecium			2 (1)	*E. faecium (1)*
E. faecalis	Pan GN			6 (0)	
E. faecalis	*S. epidermidis*		*mecA*	1 (0)	
E. faecalis	*Staphylococcus*			1 (0)	
E. faecalis	*Staphylococcus*		*mecA*	1 (0)	
E. faecium	Pan GN	*Staphylococcus*	*mecA, vanA*	1 (0)	
E. faecium	*S. epidermidis*		*mecA, vanA*	1 (0)	
Lactobacillus	*Streptococcus*			1 (1)	*Lactobacillus* (1)
Listeria	*Staphylococcus*			1 (1)	*Listeria* (1)
Pan GN	*S. anginosus* group			2 (0)	
Pan GN	*S. aureus*			1 (0)	
Pan GN	*S. epidermidis*		*mecA*	2 (2)	Pan GN (1), *S. epidermidis* (1)
Pan GN	*S. pneumoniae*			1 (1)	*S. pneumoniae* (1)
Pan GN	*Staphylococcus*			2 (0)	
Pan GN	*Staphylococcus*		*mecA*	1 (0)	
Pan GN	*Streptococcus*			1 (0)	
S. agalactiae	*S. aureus*			1 (0)	
S. anginosus group	*Staphylococcus*			2 (2)	*S. anginosus* gp (1), *Staphylococcus* (1)
S. aureus	*S. epidermidis*		*mecA*	2 (2)	*S. epidermidis* (2)
S. epidermidis	*S. lugdunensis*			1 (1)	*S. epidermidis* (1), *S. lugdunensis* (1)
S. epidermidis	*S. lugdunensis*		*mecA*	1 (1)	*S. lugdunensis* (1)
S. epidermidis	*Streptococcus*			2 (1)	*S. epidermidis* (1)
Staphylococcus	*Streptococcus*			1 (0)	
Staphylococcus	*Streptococcus*		*mecA*	1 (1)	*Streptococcus* (1)

A. A discrepant organism or resistance marker is defined as one that was detected by the BCID-GP panel but not by the comparator method(s).

B. 16/16 false positive organisms were investigated using PCR/sequencing; the discrepant organism was detected in 7/16, not detected in 2, and was indeterminate for the remaining 7:

i. *C. acnes* was not detected in the 1 *C. acnes* false positive sample.
ii. In 1/1 false positive *E. faecium* samples, *E. faecium* was detected.
iii. In 1/1 false positive *Lactobacillus* samples, *Lactobacillus* was detected.
iv. *Listeria* was not detected in the 1 *Listeria* false positive sample.
v. In the 1 false positive Pan Gram-Negative sample, PCR/sequencing was indeterminate.

vi. In the 1 false positive *S. anginosus* group sample, PCR/sequencing was indeterminate.
vii. In 2/5 false positive *S. epidermidis* samples, *S. epidermidis* was detected. PCR/sequencing was indeterminate in the remaining 3 samples.
viii. In 2/2 false positive *S. lugdunensis* samples, *S. lugdunensis* was detected.
ix. In the 1 false positive *S. pneumoniae* sample, PCR/sequencing was indeterminate.
x. In the 1 false positive *Staphylococcus* sample, PCR/sequencing was indeterminate.
xi. In 1/1 false positive *Streptococcus* samples, *Streptococcus* was detected.

Table 52: Co-Detections Identified by the cobas eplex BCID-GP panel (Retrospective Samples)

Distinct Co-Detection Combinations Detected by the cobas eplex BCID-GP panel in Retrospective Clinical Samples				Number of Samples (Number Discrepant)	Discrepant Organism(s) / Resistance Marker(s) [A,B]
Target 1	**Target 2**	**Target 3**	**Resistance Marker**		
Corynebacterium	*S. epidermidis*	*S. lugdunensis*	*mecA*	1 (1)	*Corynebacterium* (1)
Corynebacterium	*Staphylococcus*			1 (0)	
Corynebacterium	*Staphylococcus*		*mecA*	1 (0)	
E. faecalis	*E. faecium*			4 (3)	*E. faecium* (3)
E. faecalis	*E. faecium*		*vanA*	3 (1)	*E. faecium* (1)
E. faecalis	Pan *Candida*			1 (0)	
E. faecalis	Pan GN			6 (0)	
E. faecalis	Pan GN		*vanA*	2 (0)	
E. faecalis	Pan GN	*S. aureus*		1 (0)	
E. faecalis	*S. aureus*		*mecA*	1 (0)	
E. faecalis	*Staphylococcus*		*vanA*	1 (1)	*Staphylococcus* (1)
E. faecium	*Lactobacillus*	Pan GN	*vanA*	1 (1)	*Lactobacillus* (1)
E. faecium	Pan *Candida*		*vanA*	1 (1)	*E. faecium* (1)
E. faecium	Pan *Candida*	*S. epidermidis*	*mecA, vanA*	1 (1)	*S. epidermidis* (1)
E. faecium	Pan GN			3 (0)	
E. faecium	Pan GN		*vanA*	5 (0)	
E. faecium	Pan GN	*Staphylococcus*	*mecA, vanA*	1 (0)	
E. faecium	*S. aureus*		*mecA, vanA*	1 (0)	
E. faecium	*Streptococcus*		*vanA*	1 (1)	*Streptococcus* (1)
Enterococcus	*S. anginosus* group			1 (0)	
Lactobacillus	*S. anginosus* group			1 (0)	
Micrococcus	*S. pyogenes*			1 (1)	*Micrococcus* (1)
Pan *Candida*	*S. epidermidis*		*mecA*	2 (0)	
Pan *Candida*	*S. pneumoniae*			1 (0)	
Pan GN	*S. agalactiae*			2 (1)	Pan GN (1)
Pan GN	*S. anginosus group*			4 (0)	
Pan GN	*S. anginosus group*	*S. aureus*		1 (1)	Pan GN (1)

Distinct Co-Detection Combinations Detected by the cobas eplex BCID-GP panel in Retrospective Clinical Samples				Number of Samples (Number Discrepant)	Discrepant Organism(s) / Resistance Marker(s) [A,B]
Target 1	**Target 2**	**Target 3**	**Resistance Marker**		
Pan GN	*S. aureus*			1 (0)	
Pan GN	*S. aureus*	*S. epidermidis*	*mecA*	1 (1)	*S. epidermidis* (1)
Pan GN	*S. pneumoniae*			2 (0)	
Pan GN	*Streptococcus*			3 (0)	
S. agalactiae	*S. aureus*			2 (0)	
S. agalactiae	*S. aureus*		*mecA*	1 (0)	
S. agalactiae	*S. aureus*	*S. epidermidis*	*mecA*	1 (1)	*S. epidermidis* (1)
S. aureus	*S. epidermidis*		*mecA*	1 (0)	
S. aureus	*Streptococcus*		*mecA*	2 (1)	*Streptococcus* (1)
S. epidermidis	*Streptococcus*		*mecA*	1 (0)	

A. A discrepant organism or resistance marker is defined as one that was detected by the BCID-GP panel but not by the comparator method(s).

B. 16/16 false positive organisms were investigated using PCR/sequencing; the discrepant organism was detected in 6/16, not detected in 4, and was indeterminate for the remaining 6:

i. In 1/1 false positive *Corynebacterium* samples, *Corynebacterium* was detected.
ii. In 2/5 false positive *E. faecium* samples, *E. faecium* was detected. PCR/sequencing was indeterminate in the remaining 3 samples.
iii. *Lactobacillus* was not detected in the 1 *Lactobacillus* false positive sample.
iv. *Micrococcus* was not detected in the 1 *Micrococcus* false positive sample
v. In 1/2 false positive Pan Gram-Negative samples, a gram-negative organism was not detected. PCR/sequencing was indeterminate in the remaining sample.
vi. In 1/1 false positive *Staphylococcus* samples, *Staphylococcus* was detected.
vii. *S. epidermidis* was not detected in 1/3 *S. epidermidis* false positive samples, PCR/sequencing was indeterminate in the remaining 2 samples.
viii. In 2/2 false positive *Streptococcus* samples, *Streptococcus* was detected.

Tables 53-54 below summarize co-detections identified by comparator method in prospective and retrospective samples that differ from the co-detections represented in the previous tables that were identified by the **cobas eplex** BCID-GP panel. The following co-detections include an organism not targeted by the **cobas eplex** BCID-GP panel (i.e., off-panel organism denoted with an asterisk), an organism discrepant with the **cobas eplex** BCID-GP panel, and/or an organism with more detailed identification than provided by the **cobas eplex** BCID-GP panel (e.g., **cobas eplex** BCID-GP panel detected Pan Gram-Negative and comparator methods identified *E. coli*).

Table 53: Co-Detections Identified by the Comparator Method(s) (Prospective Samples)

Distinct Co-Detection Combinations Detected by the Comparator Methods in Prospective Clinical Samples					Number of Samples (Number Discrepant)	Discrepant Organism(s)/ Resistance Markers(s)*
Organism 1	**Organism 2**	**Organism 3**	**Organism 4**	**Resistance Marker**		
A. baumannii	*E. faecium*	*Staphylococcus*		*mecA, vanA*	1 (0)	
A. baumannii	*S. aureus*				1 (0)	
A. baumannii	*Staphylococcus*			*mecA*	1 (0)	
Acinetobacter lwoffii	*Staphylococcus hominis*			*mecA*	1 (0)	
*Aerococcus viridans**	*K. oxytoca*	*S. epidermidis*	*Staphylococcus cohnii*	*mecA*	1 (1)	*S. cohnii* (1), *S. epidermidis* (1), *mecA* (1)
*Aerococcus viridans**	*Staphylococcus hominis*				1 (0)	
B. fragilis	*Clostridium* species*				1 (0)	
B. fragilis	*S. anginosus* gp				1 (0)	
C. acnes	*S. epidermidis*				1 (1)	*S. epidermidis* (1)
C. acnes	*S. lugdunensis*				1 (1)	*C. acnes* (1)
Citrobacter freundii	*K. pneumoniae*	*Staphylococcus hominis*		*mecA*	1 (1)	*mecA* (1)
Citrobacter koseri	*E. faecalis*				1 (0)	
Corynebacterium	*S. epidermidis*	*Streptococcus*		*mecA*	1 (1)	*Streptococcus* (1)
Corynebacterium	*Streptococcus*				1 (1)	*Corynebacterium* (1)
E. coli	*E. faecalis*	*P. mirabilis*			1 (0)	
E. coli	*Lactococcus lactis**				1 (0)	
E. coli	*P. mirabilis*	*Providencia stuartii*	*S. anginosus* gp		1 (0)	
E. faecalis	*E. faecium*				1 (1)	*E. faecium* (1)
E. faecalis	*K. pneumoniae*				2 (0)	
E. faecalis	*P. mirabilis*				1 (0)	
E. faecalis	*S. aureus*			*mecA*	1 (1)	*S. aureus* (1), *mecA* (1)
E. faecalis	*S. marcescens*				1 (0)	
E. faecalis	*Staphylococcus* (CoNS)			*mecA*	1 (0)	
E. faecium	*S. epidermidis*	*Staphylococcus haemolyticus*		*mecA, vanA*	1 (0)	
K. pneumoniae	*Staphylococcus haemolyticus*	non-fermenting GN bacilli			1 (0)	
P. aeruginosa	*P. mirabilis*	*Streptococcus - viridans* group			1 (0)	
P. mirabilis	*Staphylococcus*			*mecA*	1 (1)	*Staphylococcus* (1), *mecA* (1)
Peptostreptococcus species*	*Staphylococcus*				1 (0)	
Rothia (stomatococcus) *mucilaginosus**	*S. epidermidis*				1 (0)	
*Rothia mucilaginosa**	*Streptococcus - viridans* group				1 (0)	
S. agalactiae	*S. aureus*	Staphylococcus		*mecA*	1 (1)	S. aureus (1), *Staphylococcus* (1), *mecA* (1)

Distinct Co-Detection Combinations Detected by the Comparator Methods in Prospective Clinical Samples					Number of Samples (Number Discrepant)	Discrepant Organism(s)/ Resistance Markers(s)*
Organism 1	**Organism 2**	**Organism 3**	**Organism 4**	**Resistance Marker**		
S. anginosus	*Streptococcus mitis*				1 (1)	*S. anginosus* (1)
S. epidermidis	*Staphylococcus capitis*			*mecA*	1 (0)	
S. epidermidis	*Staphylococcus hominis*				2 (0)	
S. epidermidis	*Staphylococcus hominis*			*mecA*	4 (1)	*S. epidermidis* (1)
S. epidermidis	*Staphylococcus hominis*	*Staphylococcus warneri*			1 (0)	
S. epidermidis	*Streptococcus - viridans* group				1 (1)	*S. epidermidis* (1)
S. epidermidis	*Streptococcus parasanguinis*				1 (0)	
S. maltophilia	*Streptococcus*				1 (1)	*Streptococcus* (1)
S. marcescens	*Streptococcus mitis* group	*Streptococcus salivarius*			1 (0)	
Staphylococcus cohnii	*Streptococcus - viridans* group				1 (1)	*S. viridans* group (1)
Staphylococcus hominis	*Staphylococcus pettenkoferi*				1 (0)	
Staphylococcus hominis	*Streptococcus mitis*			*mecA*	1 (1)	*mecA* (1)

* Indicates an off-panel organism not targeted by the BCID-GP panel.

A. A discrepant organism or resistance marker is defined as one that was detected by the comparator method(s) but not by the BCID-GP panel (excludes organisms not targeted by the BCID-GP panel).

B. 16 discrepant organisms were investigated using PCR/sequencing; 1 discrepant organism was not detected:

-In 1/1 false negative *S. anginosus* group sample, PCR/Sequencing instead detected *Streptococcus lutetiensis*.

Table 54: Co-Detections Identified by the Comparator Method(s) (Retrospective Samples)

Distinct Co-Detection Combinations Detected by the Comparator Methods in Retrospective Clinical Samples					Number of Samples (Number Discrepant)	Discrepant Organism(s)/ Resistance Markers(s)*
Organism 1	**Organism 2**	**Organism 3**	**Organism 4**	**Resistance Marker**		
A. baumannii	*E. faecalis*			*vanA*	2 (2)	*A. baumannii* (2)
A. baumannii	*E. faecalis*	*S. aureus*		*mecA*	1 (1)	*mecA* (1)
A. baumannii	*E. faecium*			*vanA*	1 (0)	
*Aerococcus sanguinicola**	*Corynebacterium*	*Staphylococcus saprophyticus*			1 (0)	
Aeromonas caviae	*E. coli*	*Enterococcus casseliflavus*	*K. oxytoca*		1 (1)	*E. casseliflavus* (1)
C. acnes	*Enterococcus avium*			*vanA*	1 (1)	*E. avium* (1), *vanA* (1)
C. albicans	*E. faecalis*			*vanA*	1 (1)	*E. faecalis* (1)
C. albicans	*E. faecium*	*Staphylococcus hominis*		*mecA, vanA*	1 (0)	
C. albicans	*S. epidermidis*			*mecA*	1 (0)	
C. glabrata	*Lactobacillus rhamnosus*				1 (1)	*C. glabrata* (1)
C. glabrata	*S. pneumoniae*				1 (0)	

Distinct Co-Detection Combinations Detected by the Comparator Methods in Retrospective Clinical Samples					Number of Samples (Number Discrepant)	Discrepant Organism(s)/ Resistance Markers(s)*
Organism 1	**Organism 2**	**Organism 3**	**Organism 4**	**Resistance Marker**		
C. krusei	*S. epidermidis*			*mecA*	1 (0)	
C. parapsilosis	*E. faecalis*				1 (0)	
C. parapsilosis	*E. faecalis*			*vanA*	1 (1)	*C. parapsilosis* (1)
Citrobacter braakii	*Streptococcus oralis*				1 (0)	
E. cloacae	*E. faecalis*				1 (0)	
E. cloacae	*E. faecium*			*vanA*	1 (0)	
E. cloacae	*E. faecium*	*Staphylococcus hominis*		*mecA, vanA*	1 (0)	
E. cloacae	*S. anginosus* gp				1 (0)	
E. coli	*E. faecalis*				3 (0)	
E. coli	*E. faecalis*	*K. pneumoniae*			1 (0)	
E. coli	*E. faecalis*	*P. mirabilis*			1 (0)	
E. coli	*E. faecium*				2 (0)	
E. coli	*K. oxytoca*	*Streptococcus infantarius*			1 (0)	
E. coli	*S. agalactiae*				1 (0)	
E. coli	*S. anginosus* gp				1 (0)	
E. coli	*S. aureus*			*mecA*	1 (0)	
E. coli	*S. pneumoniae*				1 (0)	
E. coli	*Streptococcus bovis*				1 (0)	
E. faecalis	*K. pneumoniae*			*vanA*	1 (1)	*E. faecalis* (1), *K. pneumoniae (1)*
E. faecalis	*M. morganii*			*vanA*	1 (0)	
E. faecalis	*M. morganii*	*Proteus vulgaris*		*vanA*	1 (1)	*E. faecalis* (1), *vanA* (1)
E. faecalis	*P. aeruginosa*	*S. aureus*		*mecA*	1 (1)	*E. faecalis* (1), P. *aeruginosa (1)*
E. faecalis	*P. mirabilis*				2 (2)	*E. faecalis* (1), *P. mirabilis (1)*
E. faecalis	*P. mirabilis*			*vanA*	1 (1)	*E. faecalis* (1), *vanA* (1)
E. faecalis	*Providencia stuartii*				1 (1)	*P. stuartii (1)*
E. faecalis	*S. maltophilia*			*vanA*	1 (0)	
E. faecium	*K. pneumoniae*				1 (0)	
E. faecium	*Moraxella (Branhamella) catarrhalis*	*Pediococcus pentosaceus**		*vanA*	1 (0)	
E. faecium	*P. aeruginosa*			*vanA*	1 (0)	
E. faecium	*P. mirabilis*			*vanA*	1 (0)	
E. faecium	*Pseudomonas*			*vanA*	1 (0)	
E. faecium	*S. epidermidis*	*Staphylococcus hominis*		*mecA*	1 (1)	*E. faecium* (1)
Enterobacter aerogenes	*S. anginosus* gp				1 (0)	
Enterococcus avium	*S. anginosus* gp				1 (0)	
K. oxytoca	*S. anginosus* gp				1 (0)	
K. pneumoniae	*S. aureus*				2 (1)	*S. aureus* (1)

Distinct Co-Detection Combinations Detected by the Comparator Methods in Retrospective Clinical Samples					Number of Samples (Number Discrepant)	Discrepant Organism(s)/ Resistance Markers(s)*
Organism 1	**Organism 2**	**Organism 3**	**Organism 4**	**Resistance Marker**		
L. monocytogenes	*Staphylococcus*			*mecA*	1 (1)	*Staphylococcus* (1), *mecA* (1)
Lactobacillus casei	*Veillonella species*				1 (1)	*Veillonella* species (1)
Lactobacillus rhamnosus	*Pediococcus acidilactici* *				1 (0)	
Lactobacillus rhamnosus	*S. anginosus* gp	*Staphylococcus*	*Streptococcus - viridans* group		1 (1)	*Staphylococcus* (1)
Micrococcus	*Pseudoclavibacter**				1 (0)	
Moraxella catarrhalis	*S. pneumoniae*				1 (0)	
S. agalactiae	*S. aureus*				1 (1)	*S. aureus* (1)
S. agalactiae	*S. aureus*	*Streptococcus - viridans* group			1 (0)	
S. aureus	*S. epidermidis*				1 (1)	*S. aureus* (1)
S. aureus	*S. pyogenes*			*mecA*	1 (1)	*S. pyogenes* (1)
S. aureus	*Staphylococcus capitis*				1 (0)	
S. aureus	*Streptococcus mitis*			*mecA*	1 (0)	
S. epidermidis	*Staphylococcus hominis*				1 (0)	
S. epidermidis	*Staphylococcus hominis*			*mecA*	3 (0)	
S. epidermidis	*Staphylococcus hominis*	*Streptococcus parasanguinis*		*mecA*	1 (0)	
Staphylococcus capitis	*Staphylococcus hominis*			*mecA*	1 (0)	

* Indicates an off-panel organism not targeted by the BCID-GP panel.

A. A discrepant organism or resistance marker is defined as one that was detected by the comparator method(s) but not by the BCID-GP panel (excludes organisms not targeted by the BCID-GP panel).

B. 24 discrepant organisms were investigated using PCR/sequencing; 2 discrepant organisms were not detected:

-In 2/6 false negative *E. faecalis* samples, PCR/Sequencing instead detected *Enterococcus faecium*.

Clinical Study cobas eplex instrument Performance

A total of 2354 samples (including prospective, retrospective, and contrived samples) were initially tested in the clinical evaluations. Of these, 24/2354 (1.0%) did not complete the run and the sample was retested. After repeat testing, all 2354 samples completed testing and 2246/2354 (95.4%, 95% CI: 94.5%-96.2%) generated valid results and 108/2354 (4.6%, 95% CI: 3.8%-5.5%) generated invalid results on the first completed attempt.

Upon repeat testing of the 108 samples with initially invalid results, 3/108 (2.8%) did not complete the run and the sample was retested. After repeat testing, all 108 samples completed testing and 106/108 (98.1%) generated valid results. Overall, after final testing, 2/2354 (0.1%, 95% CI: 0.0%-0.3%) had final, invalid results, resulting in a final validity rate of 2352/2354 (99.9%, 95% CI: 99.7%-100%).

ANALYTICAL PERFORMANCE CHARACTERISTICS

Limit of Detection (Analytical Sensitivity)

The limit of detection (LoD), or analytical sensitivity, was identified and verified for each assay on the BCID-GP panel using at least two quantified reference strains in simulated blood culture sample matrix, which is defined as a whole blood with EDTA added to a blood culture bottle in the same ratio as the manufacturer recommends and incubated for 8 hours. At least 20 replicates per target were tested for each condition. The limit of detection was defined as the lowest concentration of each target that is detected in ≥95% of tested replicates. The confirmed LoD for each **cobas eplex** BCID-GP panel organism is shown in **Table 55**.

Table 55: LoD Results Summary

Target	Organism	Strain	LoD Concentration (CFU/mL)
B. cereus group	*Bacillus cereus*	ATCC 21769	1×10^5
	Bacillus thuringiensis	ATCC 35646	1×10^5
B. subtilis group	*Bacillus subtilis*	ATCC 55614	1×10^6
	Bacillus atrophaeus	ATCC 51189	1×10^6
Corynebacterium	*Corynebacterium striatum*	ATCC 43735	1×10^6
	Corynebacterium jeikeium	ATCC 43217	1×10^7
Cutibacterium acnes (P. acnes)	*Cutibacterium acnes (P. acnes)*	ATCC 33179	1×10^7
	Cutibacterium acnes (P. acnes)	ATCC 6919	1×10^8
Enterococcus	*Enterococcus faecium*	ATCC BAA-2316	1×10^5
	Enterococcus faecium	ATCC BAA-2317	1×10^6
	Enterococcus raffinosus	ATCC 49464	1×10^6
Enterococcus faecium	*Enterococcus faecium*	ATCC BAA-2316	1×10^5
	Enterococcus faecium	ATCC BAA-2317	1×10^6
Enterococcus faecalis	*Enterococcus faecalis*	ATCC 51575	1×10^6
	Enterococcus faecalis	ATCC 700802	1×10^6
Lactobacillus	*Lactobacillus paracasei*	ATCC 25598	1×10^5
	Lactobacillus casei	ATCC 334	1×10^5
Listeria	*Listeria seeligeri*	ATCC 35967	1×10^5
	Listeria monocytogenes	ATCC 10890	1×10^5
	Listeria monocytogenes	ATCC 19111	1×10^6
Listeria monocytogenes	*Listeria monocytogenes*	ATCC 10890	1×10^5
	Listeria monocytogenes	ATCC 19111	1×10^5
Micrococcus	*Micrococcus luteus*	ATCC 19212	1×10^6
	Micrococcus luteus	ATCC 10240	1×10^7
Staphylococcus	*Staphylococcus aureus*	ATCC BAA-2313	1×10^4
	Staphylococcus aureus	ATCC BAA-2312	1×10^5
	Staphylococcus epidermidis	ATCC 35983	1×10^5
	Staphylococcus epidermidis	ATCC 35984	1×10^5
	Staphylococcus lugdunensis	NRS 879	1×10^5
	Staphylococcus lugdunensis	ATCC 49576	1×10^6
	Staphylococcus haemolyticus	NRS 62	1×10^7

Target	Organism	Strain	LoD Concentration (CFU/mL)
Staphylococcus aureus	*Staphylococcus aureus*	ATCC BAA-2313	1×10^5
	Staphylococcus aureus	ATCC BAA-2312	1×10^5
Staphylococcus epidermidis	*Staphylococcus epidermidis*	ATCC 35983	1×10^5
	Staphylococcus epidermidis	ATCC 35984	1×10^5
Staphylococcus lugdunensis	*Staphylococcus lugdunensis*	NRS 879	1×10^5
	Staphylococcus lugdunensis	ATCC 49576	1×10^5
Streptococcus	*Streptococcus pneumoniae*	ATCC BAA-475	1×10^5
	Streptococcus pneumoniae	ATCC 10357	1×10^5
	Streptococcus gordonii	ATCC 10558	1×10^6
	Streptococcus agalactiae	ATCC 12401	1×10^6
	Streptococcus agalactiae	ATCC 13813	1×10^7
Streptococcus agalactiae	*Streptococcus agalactiae*	ATCC 12401	1×10^5
	Streptococcus agalactiae	ATCC 13813	1×10^6
Streptococcus anginosus group	*Streptococcus intermedius*	ATCC 27335	1×10^4
	Streptococcus anginosus	ATCC 9895	1×10^6
Streptococcus pneumoniae	*Streptococcus pneumoniae*	ATCC BAA-475	1×10^5
	Streptococcus pneumoniae	ATCC 10357	1×10^5
Streptococcus pyogenes	*Streptococcus pyogenes*	ATCC 12384	1×10^5
	Streptococcus pyogenes	ATCC 49399	1×10^5
Pan Gram-Negative	*Stenotrophomonas maltophilia*	ATCC 13636	1×10^6
	Enterobacter cloacae	ATCC 13047	1×10^6
	Escherichia coli	ATCC 4157	1×10^6
	Klebsiella pneumoniae	ATCC BAA-1706	1×10^6
	Serratia marcescens	ATCC 8100	1×10^6
	Proteus mirabilis	ATCC 43071	1×10^6
	Acinetobacter baumannii	NCTC13302	1×10^7
	Neisseria meningitidis	ATCC 13113	1×10^7
Pan Gram-Negative	*Pseudomonas aeruginosa*	ATCC 15442	1×10^7
Pan *Candida*	*Candida albicans*	ATCC 24433	1×10^6
	Candida glabrata	ATCC 66032	1×10^6
mecA	*Staphylococcus epidermidis*	ATCC 35983	1×10^5
	Staphylococcus epidermidis	ATCC 35984	1×10^5
mecC	*Staphylococcus aureus*	ATCC BAA-2313	1×10^4
	Staphylococcus aureus	ATCC BAA-2312	1×10^4
vanA	*Enterococcus faecium*	ATCC BAA-2316	1×10^4
	Enterococcus faecium	ATCC BAA-2317	1×10^5
vanB	*Enterococcus faecalis*	ATCC 51575	1×10^5
	Enterococcus faecalis	ATCC 700802	1×10^5

Analytical Reactivity (Inclusivity)

A panel of 459 strains/isolates representing the genetic, temporal and geographic diversity of each target on the **cobas eplex** BCID-GP panel was evaluated to demonstrate analytical reactivity. Each bacterial strain was tested in triplicate at 1 x 10^8 CFU/mL or less and each fungal strain was tested at 1 x 10^6 CFU/mL. In the cases where the initial testing concentration did not result in a "Detected" result, the concentration was increased to the point where detection was observed (see footnotes for concentrations of these strains). Organisms detected are shown in **Table 56**. Additional strains were detected as a part of the Limit of Detection (Analytical Sensitivity) study and can be found in **Table 55**.

Table 56: Analytical Reactivity (Inclusivity)

Organism	Strain
Bacillus cereus	
Bacillus cereus	ATCC 21769
	ATCC 10876
	ATCC 31430
	ATCC 53522
Bacillus thuringiensis	ATCC 35646
	ATCC 33679
	ATCC 55173
	ATCC 10792
Bacillus subtilis	
Bacillus amyloliquefaciens	ATCC 23845
	ATCC 23842
	ATCC 23350
	ATCC 53495
Bacillus atrophaeus	ATCC 51189
	ATCC 6455
	ATCC 49337
	ATCC 7972
	ATCC 6537
Bacillus licheniformis	ATCC 53926
	ATCC 55768
	ATCC 21039
	ATCC 21667
Bacillus subtilis	ATCC 55614
	ATCC 15561
	ATCC 21008
Bacillus subtilis	ATCC 15040
Corynebacterium	
Corynebacterium afermentans subsp. *afermentans*	ATCC 51403[A]
Corynebacterium afermentans subsp. *lipophilum*	ATCC 51404
Corynebacterium confusum	ATCC 38268[A]
Corynebacterium coyleae	ATCC 700219
Corynebacterium diphtheriae	ATCC 13812
Corynebacterium falsenii	ATCC BAA-596[A]
Corynebacterium freneyi	ATCC 64424[B]
Corynebacterium imitans	ATCC 700354[B]
Corynebacterium jeikeium	ATCC 43217
	ATCC 43216
	ATCC 43734
	ATCC BAA-949
Corynebacterium minutissimum	ATCC 23348
Corynebacterium resistens	CCUG 50093T
Corynebacterium simulans	ATCC BAA-15

Organism	Strain
Staphylococcus lentus	ATCC 700403
Staphylococcus lugdunensis	NRS-879
	ATCC 49576
	NRS-878
	NRS-880
Staphylococcus muscae	ATCC 49910
Staphylococcus pasteuri	ATCC 51129
Staphylococcus pasteuri (*mecC+*)	ATCC 51128
Staphylococcus pettenkoferi	DSM-19554
Staphylococcus pseudintermedius	ATCC 49444
Staphylococcus saccharolyticus	ATCC 14953
Staphylococcus saprophyticus	ATCC 15305
	ATCC 35552
Staphylococcus schleiferi	ATCC 49545
	ATCC 43808
Staphylococcus sciuri	ATCC 29060
	ATCC 29061
	ATCC 29059
	ATCC 49575
	ATCC 29062
Staphylococcus simulans	ATCC 27848
	ATCC 27850
	ATCC 31432
	ATCC 27851
Staphylococcus species	ATCC 155
Staphylococcus species (mecA+)	ATCC 27626
Staphylococcus vitulinus	ATCC 51699
	ATCC 51161
Staphylococcus warneri	ATCC 27836
Staphylococcus xylosus	ATCC 49148
	ATCC 29971
Staphylococcus aureus	
Staphylococcus aureus	ATCC 25923
	ATCC 29247
	ATCC 6538P
	ATCC 29213
	NR-45889
	NR-45890
	NR-46074
	NR-45881
	NR-46411
	NR-46414
Staphylococcus aureus	NR-46418

Organism	Strain
Corynebacterium striatum	ATCC BAA-1293
	ATCC 43735
	ATCC 7094
Corynebacterium timonense	CCUG 64728[A]
Corynebacterium ulcerans	ATCC 51799
Corynebacterium urealyticum	ATCC 43044
	ATCC 43042
	ATCC 43043
Corynebacterium ureicelerivorans	CCUG 59144
Cutibacterium acnes	
Cutibacterium acnes	ATCC 11827
	ATCC 11828
	ATCC 33179
	ATCC 6919
Enterococcus	
Enterococcus avium	ATCC 14025
Enterococcus casseliflavus	ATCC 700668
	ATCC 25788
	ATCC 700327
Enterococcus cecorum	ATCC 43198
Enterococcus dispar	ATCC 51266
Enterococcus durans	ATCC 11576
Enterococcus faecalis	ATCC 51575
	ATCC 700802
	ATCC 10100
	ATCC 12399
	ATCC 14506
	ATCC 33186
	ATCC 49532
	ATCC 49533
	ATCC 7080
	ATCC 49474
	ATCC 49332
	ATCC 29200
Enterococcus faecalis	ATCC BAA-2128
	ATCC 51188
	ATCC 49149
	NCTC-775
	ATCC 19433
	ATCC 49452
Enterococcus faecalis (vanA+)	JMI 876745
Enterococcus faecalis (vanB+)	ATCC BAA-2365
	ATCC 51299
Enterococcus faecium	ATCC 19434
	ATCC 23828
	ATCC 27273
	ATCC BAA-2127
	ATCC 6057
	ATCC 49624
	ATCC 6569
Enterococcus faecium	ATCC BAA-472

Organism	Strain
	NR-46417
Staphylococcus aureus (mecA+)	NR-13524
	NR-13527
	NR-13525
	NR-13526
	NRS-123
	NR-46805
	NRS-662
	ATCC BAA-1707
	ATCC 43300
	NRS-383
	NCTC-12493
	NRS-676
	NRS-678
	NRS-648
	NRS-651
	NRS-643
	NRS-484
	NRS-385
	NRS-384
	ATCC BAA-40
	ATCC 700698
	NRS-382
	NRS-659
	NRS-657
	NRS-655
	NRS-654
	NRS-647
	ATCC BAA-42
	ATCC BAA-41
	NRS-483
	NRS-675
	NRS-645
	NRS-687
Staphylococcus aureus (mecA+)	NRS-667
	NRS-677
	NRS-683
	NRS-688
	NRS-22
	NRS-387
	NRS-70
	ATCC 33591
Staphylococcus aureus (mecC+)	ATCC BAA-2312
	ATCC BAA-2313
Staphylococcus epidermidis	
Staphylococcus epidermidis	ATCC 12228
	ATCC 49134
	NCIMB-8853
	ATCC 700583
	ATCC 14990
Staphylococcus epidermidis (mecA+)	ATCC 35983

Organism	Strain
	ATCC 9756
	ATCC 49224
	ATCC BAA-2846
	ATCC 19953
	ATCC 27270
	ATCC 35667
Enterococcus faecium (vanA+)	ATCC BAA-2316
	ATCC BAA-2317
	ATCC 700221
	ATCC BAA-2319
	ATCC BAA-2320
	LMC 003921
	LMC 103676
	LMC 089524
	LMC 104266
	LMC 032261
	LMC 110371
	LMC 002867
	LMC 055971
	ATCC 51559
	ATCC BAA-2318
Enterococcus faecium (vanB+)	ATCC 51858
Enterococcus gallinarum	ATCC 49573
	ATCC 49609
	ATCC 49610
	ATCC 700425
	ATCC 49608
Enterococcus hirae	ATCC 49479
	ATCC 10541
Enterococcus italicus	CCUG 47860
Enterococcus malodoratus	ATCC 43197
Enterococcus pseudoavium	CCUG 33310T
Enterococcus raffinosus	ATCC 49464
Enterococcus saccharolyticus	ATCC 43076
Enterococcus sanguinicola	DSM-21767
Enterococcus faecalis	
Enterococcus faecalis	ATCC 51575
	ATCC 700802
	ATCC 10100
	ATCC 12399
Enterococcus faecalis	ATCC 14506
	ATCC 33186
	ATCC 49532
	ATCC 49533
	ATCC 7080
	ATCC 49474
	ATCC 49332
Enterococcus faecalis	ATCC 29200

Organism	Strain
	ATCC 35984
	ATCC 29887
	ATCC 49461
	ATCC 700565
	ATCC 51625
Staphylococcus lugdunensis	
Staphylococcus lugdunensis	NRS-879
	ATCC 49576
	NRS-878
	NRS-880
Streptococcus	
Streptococcus agalactiae	ATCC 12401
	ATCC 13813
	ATCC 12386
	ATCC 12973
	ATCC 27956
	NCTC-8017
	ATCC 12403
Streptococcus anginosus	ATCC 9895
	ATCC 33397
	NCTC-10713
Streptococcus bovis	ATCC 33317
	ATCC 35034
Streptococcus constellatus	ATCC 27513
Streptococcus criceti	ATCC 19642[C]
Streptococcus dysgalactiae	ATCC 35666
	ATCC 43078
	ATCC 12394
Streptococcus equi	ATCC 43079
	ATCC 9528
Streptococcus equinus	ATCC 15351
	ATCC 9812
Streptococcus gallolyticus	ATCC 49475
	ATCC 9809
	ATCC 43144
Streptococcus gordonii	ATCC 10558
	ATCC 35557
Streptococcus infantarius	ATCC BAA-102
	ATCC BAA-103
Streptococcus infantis	ATCC BAA-2089
	ATCC 700779
Streptococcus intermedius	ATCC 27335
Streptococcus mitis	ATCC 15914
	ATCC 6249
Streptococcus mitis	ATCC 49456
	NCIMB-13770
Streptococcus oralis	ATCC 35037
Streptococcus oralis	ATCC 55229

Organism	Strain
	ATCC BAA-2128
	ATCC 51188
	ATCC 49149
	NCTC-775
	ATCC 19433
	ATCC 49452
Enterococcus faecalis (vanA+)	JMI 876745
Enterococcus faecalis (vanB+)	ATCC BAA-2365
	ATCC 51299
Enterococcus faecium	
Enterococcus faecium	ATCC 19434
	ATCC 23828
	ATCC 27273
	ATCC BAA-2127
	ATCC 6057
	ATCC 49624
	ATCC 6569
	ATCC BAA-472
	ATCC 9756
	ATCC 49224
	ATCC BAA-2846
	ATCC 19953
	ATCC 27270
	ATCC 35667
Enterococcus faecium (vanA+)	ATCC BAA-2316
	ATCC BAA-2317
Enterococcus faecium (vanA+)	ATCC 700221
	ATCC BAA-2319
	ATCC BAA-2320
	LMC 003921
	LMC 103676
	LMC 089524
	LMC 104266
	LMC 032261
	LMC 110371
	LMC 002867
	LMC 055971
Enterococcus faecium (vanA+)	ATCC 51559

Organism	Strain
Streptococcus parasanguinis	ATCC 15909
Streptococcus peroris	ATCC 700780
Streptococcus pneumoniae	ATCC BAA-475
	ATCC 10357
	ATCC 49619
	ATCC 49136
	ATCC BAA-659
	ATCC 6315
	ATCC BAA-1667
	ATCC 700674
	ATCC 6321
	ATCC 700673
	ATCC 51916
	ATCC 8338
	ATCC 6301
	ATCC 8335
	NCIMB-13286
	ATCC BAA-1656
Streptococcus pyogenes	ATCC 12384
	ATCC 49399
	ATCC 12344
	ATCC 19615
	NCIMB-13285
	ATCC 14289
Streptococcus salivarius	ATCC 13419[C]
	ATCC 7073
Streptococcus salivarius	ATCC 25975
	ATCC 31067[C]
Streptococcus sanguinis	ATCC 10556
Streptococcus thoraltensis	ATCC 700865
Streptococcus agalactiae	
Streptococcus agalactiae	ATCC 12401
	ATCC 13813
	ATCC 12386
	ATCC 12973
	ATCC 27956
	NCTC-8017
	ATCC 12403

Organism	Strain
	ATCC BAA-2318
Enterococcus faecium (vanB+)	ATCC 51858
Lactobacillus	
Lactobacillus casei	ATCC 334
	ATCC 55825
	ATCC 39392
Lactobacillus paracasei	ATCC 25598
	ATCC BAA-52
	ATCC 27092
Lactobacillus rhamnosus	ATCC 39595
	ATCC 53103
	ATCC 55915
Lactobacillus zeae	ATCC 15820
Listeria	
Listeria innocua	NCTC-11288
	ATCC 33090
Listeria ivanovii	ATCC 19119
	ATCC BAA-139
	ATCC 700402
Listeria monocytogenes	ATCC 10890
	ATCC 19111
	ATCC 13932
	ATCC 19114
	ATCC 7644
	ATCC 19112
	ATCC BAA-751
	ATCC 19118
	ATCC 19115
Listeria seeligeri	ATCC 35967
Listeria welshimeri	ATCC 35897
Listeria monocytogenes	
Listeria monocytogenes	ATCC 10890
	ATCC 19111
	ATCC 13932
Listeria monocytogenes	ATCC 19114
Listeria monocytogenes	ATCC 7644
	ATCC 19112
	ATCC BAA-751
	ATCC 19118
	ATCC 19115
Micrococcus	
Micrococcus luteus	ATCC 19212
	ATCC 10240
	ATCC 400
	ATCC 53598
	ATCC 49732
	ATCC 4698
Micrococcus lylae	ATCC 27566
Micrococcus yunnanensis	ATCC 7468

Organism	Strain
***Streptococcus anginosus* group**	
Streptococcus anginosus	ATCC 9895
	ATCC 33397
	NCTC-10713
Streptococcus constellatus	ATCC 27513
Streptococcus intermedius	ATCC 27335
Streptococcus pneumoniae	
Streptococcus pneumoniae	ATCC BAA-475
	ATCC 10357
	ATCC 49619
	ATCC 49136
	ATCC BAA-659
	ATCC 6315
	ATCC BAA-1667
	ATCC 700674
	ATCC 6321
	ATCC 700673
	ATCC 51916
	ATCC 8338
	ATCC 6301
	ATCC 8335
	NCIMB-13286
	ATCC BAA-1656
Streptococcus pyogenes	
Streptococcus pyogenes	ATCC 12384
	ATCC 49399
	ATCC 12344
	ATCC 19615
	NCIMB-13285
	ATCC 14289
Pan *Candida*	
Candida albicans	ATCC 24433
	ATCC MYA-4441
	ATCC 14053
Candida albicans	ATCC 90028
Candida glabrata	ATCC 66032
	ATCC 15126
	ATCC MYA-2950
	ATCC 2001
Candida krusei	ATCC 34135
	ATCC 32196
	ATCC 14243
Candida parapsilosis	ATCC 90018[D]
	ATCC 58895
	ATCC 22019
Pan Gram-Negative	
Acinetobacter baumannii	NCTC-13302
	NCTC-13422
Acinetobacter haemolyticus	ATCC 19002

Organism	Strain
Staphylococcus	
Staphylococcus arlettae	ATCC 43957
Staphylococcus aureus	ATCC 25923
	ATCC 29247
	ATCC 6538P
	ATCC 29213
	NR-45889
	NR-45890
	NR-46074
	NR-45881
	NR-46411
	NR-46414
	NR-46418
	NR-46417
Staphylococcus aureus (mecA+)	NR-13524
	NR-13527
	NR-13525
	NR-13526
	NRS-123
	NR-46805
	NRS-662
	ATCC BAA-1707
	ATCC 43300
Staphylococcus aureus (mecA+)	NRS-383
	NCTC-12493
	NRS-676
Staphylococcus aureus (mecA+)	NRS-678
	NRS-648
	NRS-651
	NRS-643
	NRS-484
	NRS-385
	NRS-384
	ATCC BAA-40
	ATCC 700698
	NRS-382
	NRS-659
	NRS-657
Staphylococcus aureus (mecA+)	NRS-655

Organism	Strain
Acinetobacter junii	ATCC 17908
Acinetobacter lwoffii	ATCC 15309
Acinetobacter ursingii	ATCC BAA-617
Bacteroides fragilis	NCTC-9343
Burkholderia cepacia	ATCC 25416
Cedecea davisiae	ATCC 43025
Citrobacter freundii	NCTC-9750
Citrobacter koseri	ATCC 27156
Cronobacter muytjensii	ATCC 51329
Cronobacter sakazakii	ATCC 12868
Edwardsiella tarda	ATCC 15947
Enterobacter aerogenes	ATCC 13048
Enterobacter amnigenus	ATCC 51816
Enterobacter asburiae	ATCC 35953
Enterobacter cloacae	ATCC 13047
	ATCC 23373
	ATCC 23355
	ATCC 35030
Enterobacter hormaechei	ATCC 700323
Erwinia aphidicola	ATCC 27991
Escherichia coli	ATCC 4157
	ATCC 14948
	ATCC 25922
Escherichia coli	ATCC BAA-196
Escherichia fergusonii	ATCC 35469
Escherichia hermannii	ATCC 700368
Escherichia vulneris	ATCC 33821
Fusobacterium necrophorum	ATCC 25286
Fusobacterium nucleatum	ATCC 25586
Haemophilus influenzae	ATCC 10211
	ATCC 49144
	ATCC 43065
Haemophilus influenzae	NCTC-8468
Haemophilus parainfluenzae	ATCC 9796
Hafnia alvei	ATCC 51815
Klebsiella oxytoca	ATCC 700324
	ATCC 43165
	ATCC 43863
Klebsiella ozaenae	ATCC 11296

Organism	Strain
	NRS-654
	NRS-647
	ATCC BAA-42
	ATCC BAA-41
	NRS-483
	NRS-675
	NRS-645
	NRS-687
	NRS-667
	NRS-677
	NRS-683
	NRS-688
	NRS-22
	NRS-387
	NRS-70
	ATCC 33591
Staphylococcus aureus (mecC+)	ATCC BAA-2312
	ATCC BAA-2313
Staphylococcus auricularis	ATCC 33750
	ATCC 33753
Staphylococcus capitis	ATCC 27840
	NRS-866
	ATCC 35661
Staphylococcus caprae	ATCC 51548
Staphylococcus carnosus	ATCC 51365
Staphylococcus chromogenes	ATCC 43764
Staphylococcus cohnii	ATCC 29974
Staphylococcus epidermidis	ATCC 12228
	ATCC 49134
	NCIMB-8853
	ATCC 700583
	ATCC 14990
Staphylococcus epidermidis (mecA+)	ATCC 35983
	ATCC 35984
	ATCC 29887
	ATCC 49461
	ATCC 700565
	ATCC 51625
Staphylococcus gallinarum	ATCC 700401

Organism	Strain
Klebsiella pneumoniae	ATCC BAA-1706
	NCTC-9633
	NCTC-13440
	ATCC 51503
Kluyvera ascorbata	ATCC 14236
Kluyvera cryocrescens	ATCC 14240
Legionella pneumophila	ATCC 33823
Moraxella catarrhalis	ATCC 23246
Moraxella nonliquefaciens	ATCC 17953
Moraxella osloensis	ATCC 10973
Morganella morganii	ATCC 25829
Neisseria lactamica	ATCC 23970
Neisseria meningitidis	ATCC 13090
	ATCC 13113
	ATCC 13077
	ATCC 13102
Neisseria mucosa	ATCC 19695
Neisseria sicca	ATCC 29193
Pantoea agglomerans	ATCC 14537
Pasteurella aerogenes	ATCC 27883
Proteus mirabilis	ATCC 43071
	CDC#0155
	CDC#0159
Proteus penneri	ATCC 35197
Proteus vulgaris	ATCC 6380
Providencia alcalifaciens	ATCC 9886
Providencia rettgeri	ATCC 9919
Providencia stuartii	ATCC 33672
Pseudomonas aeruginosa	ATCC 15442
	NCIMB-12469
	ATCC 10145
Pseudomonas fluorescens	ATCC 13525
Pseudomonas luteola	ATCC 35970
Pseudomonas putida	ATCC 31483
Raoultella terrigena	ATCC 55553
Salmonella bongori	ATCC 43975
Salmonella enterica subsp. *enterica*	ATCC 51957
Salmonella enterica Choleraesuis	ATCC 12011
Salmonella enterica Paratyphi	FSL S5-0447

Organism	Strain
	ATCC 35539
Staphylococcus haemolyticus	ATCC 29970
	ATCC 31874
Staphylococcus haemolyticus (mecA+)	NRS-62
	ATCC BAA-1693
	NRS-69
Staphylococcus hominis	NRS-871
	NRS-870
	ATCC 27844
Staphylococcus hominis (mecA+)	ATCC 700237
	ATCC 700236
Staphylococcus hyicus	ATCC 11249
Staphylococcus intermedius	ATCC 29663
	ATCC 49052

A. Detected at 2 x 10^8 CFU/mL
B. Detected at 2 x 10^9 CFU/mL

Organism	Strain
Salmonella Typhi	ATCC 19430
Serratia fonticola	ATCC 29844
Serratia liquefaciens	ATCC 27592
Serratia marcescens	ATCC 8100
	ATCC 14756
	ATCC 13880
Serratia odorifera	ATCC 33077
Serratia rubidaea	ATCC 27593
Shigella boydii	ATCC 9207
Shigella dysenteriae	ATCC 13313
Shigella sonnei	ATCC 29930
Stenotrophomonas maltophilia	ATCC 13636
Tatumella ptyseos	ATCC 33302
Yersinia enterocolitica subsp. *enterocolitica*	ATCC 9610

C. Detected at 4 x 10^8 CFU/mL
D. Detected at 1 x 10^7 CFU/mL

Predicted (*in silico*) Reactivity for Genus and Group Assays

Note: the performance of the cobas eplex BCID-GP panel **has not been established for all of the organisms listed in the tables below. See the Analytical Reactivity (Inclusivity) and Limit of Detection (Analytical Sensitivity) sections for data on organisms for which performance characteristics have been established (indicated with an asterisk in Tables 57-68). Some species were not assessed *in silico* due to lack of sequence data, though they may appear in the analytical sensitivity or specificity studies.**

In addition to species-specific assays, the **cobas eplex** BCID-GP panel contains a number of broader genus or group-level assays; including *Bacillus cereus* group, *Bacillus subtilis* group, *Corynebacterium, Enterococcus*, *Lactobacillus*, *Listeria*, *Micrococcus*, *Staphylococcus, Streptococcus, Streptococcus anginosus* group, Pan *Candida* and Pan Gram-Negative assays. **Tables 57-68** summarize the predicted (*in silico*) reactivity (inclusivity) for these assay targets.

Table 57: Predicted (*in silico*) Reactivity (Inclusivity) Results for *Bacillus cereus* group

Detection Predicted for ≥95% of target sequences		
*Bacillus thuringiensis**	*Bacillus toyonensis*	*Bacillus weihenstephanensis*
Detection Predicted for 85%-94% of target sequences		
*Bacillus cereus**		
Detection Predicted for <85% of target sequences		
None Identified		
Detection Not Predicted		
*Bacillus mycoides**	*Bacillus pseudomycoides*	

Table 58: Predicted (*in silico*) Reactivity (Inclusivity) Results for *Bacillus subtilis* group

Detection Predicted for ≥95% of target sequences		
*Bacillus subtilis**	*Bacillus licheniformis**	*Bacillus siamensis*
*Bacillus amyloliquefaciens**	*Bacillus methylotrophicus* / *Bacillus velezensis*	*Bacillus tequilensis*
*Bacillus atrophaeus**	*Bacillus paralicheniformis*	*Bacillus vallismortis*
Detection Predicted for 85%-94% of target sequences		
None Identified		
Detection Predicted for <85% of target sequences		
Bacillus mojavensis (77.8%)	*Bacillus sonorensis* (83.3%)	
Detection Not Predicted		
None Identified		

Table 59: Predicted (*in silico*) Reactivity (Inclusivity) Results for *Corynebacterium*

Detection Predicted for ≥95% of target sequences		
Corynebacterium afermentans	*Corynebacterium glaucum*	*Corynebacterium renale*
Corynebacterium afermentans subsp. *afermentans**	*Corynebacterium halotolerans*	*Corynebacterium simulans**
Corynebacterium afermentans subsp. *lipophilium**	*Corynebacterium hansenii*	*Corynebacterium singulare*
Corynebacterium appendicis	*Corynebacterium humireducens*	*Corynebacterium sputi*
Corynebacterium auris	*Corynebacterium imitans**	*Corynebacterium striatum**
Corynebacterium auriscanis	*Corynebacterium lipophiloflavum*	*Corynebacterium suicordis*
Corynebacterium camporealensis	*Corynebacterium lowii*	*Corynebacterium terpenotabidum*
Corynebacterium casei	*Corynebacterium marinum*	*Corynebacterium testudinoris*
Corynebacterium ciconiae	*Corynebacterium massiliense*	*Corynebacterium timonense**
*Corynebacterium coyleae**	*Corynebacterium minutissimum**	*Corynebacterium tuscaniense*
Corynebacterium doosanense	*Corynebacterium mucifaciens*	*Corynebacterium ulceribovis*
*Corynebacterium falsenii**	*Corynebacterium mycetoides*	*Corynebacterium urealyticum**
Corynebacterium felinum	*Corynebacterium nuruki*	*Corynebacterium ureicelerivorans**
*Corynebacterium freneyi**	*Corynebacterium oculi*	*Corynebacterium xerosis*
Corynebacterium genitalium	*Corynebacterium pilosum*	
Detection Predicted for 85%-94% of target sequences		
None Identified		
Detection Predicted for <85% of target sequences		
Corynebacterium aurimucosum (50.0%)	*Corynebacterium jeikeium* (38.7%)*[A]	*Corynebacterium variabile* (75.0%)
Corynebacterium diphtheriae (76.4%)*	*Corynebacterium ulcerans* (47.4%)*[A]	*Corynebacterium vitaeruminis* (75.0%)
Detection Not Predicted		

Corynebacterium accolens	*Corynebacterium epidermidicanis*	*Corynebacterium propinquum*
Corynebacterium ammoniagenes	*Corynebacterium flavescens*	*Corynebacterium pseudodiphtheriticum*
Corynebacterium amycolatum	*Corynebacterium frankenforstense*	*Corynebacterium pseudogenitalium*
Corynebacterium aquilae	*Corynebacterium freiburgense*	*Corynebacterium pseudotuberculosis*
Corynebacterium argentoratense	*Corynebacterium glucuronolyticum*	*Corynebacterium pyruviciproducens*
Corynebacterium atypicum	*Corynebacterium glutamicum*	*Corynebacterium resistens*
Corynebacterium bovis	*Corynebacterium glyciniphilum*	*Corynebacterium riegelii*
Corynebacterium callunae	*Corynebacterium kroppenstedtii*	*Corynebacterium sphenisci*
Corynebacterium capitovis	*Corynebacterium kutscheri*	*Corynebacterium spheniscorum*
Corynebacterium caspium	*Corynebacterium lactis*	*Corynebacterium stationis*
Corynebacterium confusum	*Corynebacterium lubricantis*	*Corynebacterium sundsvallense*
Corynebacterium crenatum	*Corynebacterium maris*	*Corynebacterium thomssenii*
Corynebacterium cystitidis	*Corynebacterium mastitidis*	*Corynebacterium tuberculostearicum*
Corynebacterium deserti	*Corynebacterium matruchotii*	*Corynebacterium uropygiale*
Corynebacterium durum	*Corynebacterium mustelae*	*Corynebacterium uterequi*
Corynebacterium efficiens	*Corynebacterium phocae*	

A. 38.7% of sequences in NCBI for *C. jeikeium* were predicted to be detected bioinformatically; 47.4% of sequences in NCBI for *C. ulcerans* were predicted to be detected bioinformatically. All strains tested for these species were detected as a part of the Analytical Reactivity (Inclusivity) or Limit of Detection (Analytical Sensitivity) studies.

Table 60: Predicted (*in silico*) Reactivity (Inclusivity) Results for *Enterococcus*

Detection Predicted for ≥95% of target sequences		
*Enterococcus avium**	*Enterococcus flavescens*	*Enterococcus raffinosus*
*Enterococcus dispar**	*Enterococcus italicus**	*Enterococcus saccharolyticus**
Enterococcus durans	*Enterococcus lactis*	*Enterococcus thailandicus*
*Enterococcus faecalis**	*Enterococcus malodoratus*	
*Enterococcus faecium**	*Enterococcus pseudoavium*	
Detection Predicted for 85%-94% of target sequences		
Enterococcus casseliflavus	*Enterococcus gallinarum*	
Enterococcus cecorum	*Enterococcus hirae**	
Detection Predicted for <85% of target sequences		
Enterococcus mundtii (9.1%)		
Detection Not Predicted		
Enterococcus aquimarinus	*Enterococcus hawaiiensis*	*Enterococcus rotai*
Enterococcus asini	*Enterococcus hermanniensis*	*Enterococcus silesiacus*
Enterococcus caccae	*Enterococcus pallens*	*Enterococcus sulfureus*

Enterococcus camelliae	*Enterococcus pernyi*	*Enterococcus termitis*
Enterococcus canintestini	*Enterococcus phoeniculicola*	*Enterococcus ureasiticus*
Enterococcus canis	*Enterococcus plantarum*	*Enterococcus ureilyticus*
Enterococcus columbae	*Enterococcus quebecensis*	*Enterococcus villorum*
Enterococcus devriesei	*Enterococcus ratti*	
Enterococcus haemoperoxidus	*Enterococcus rivorum*	

Table 61: Predicted (*in silico*) Reactivity (Inclusivity) Results for *Lactobacillus*

Detection Predicted for ≥95% of target sequences		
*Lactobacillus casei**	*Lactobacillus rhamnosus**	
*Lactobacillus paracasei**	*Lactobacillus zeae**	
Detection Predicted for 85%-94% of target sequences		
None Identified		
Detection Predicted for <85% of target sequences		
None Identified		
Detection Not Predicted		
Lactobacillus acetotolerans	*Lactobacillus ghanensis*	*Lactobacillus panis*
Lactobacillus acidifarinae	*Lactobacillus gigeriorum*	*Lactobacillus pantheris*
Lactobacillus acidipiscis	*Lactobacillus ginsenosidimutans*	*Lactobacillus parabrevis*
Lactobacillus acidophilus	*Lactobacillus gorillae*	*Lactobacillus parabuchneri*
Lactobacillus agilis	*Lactobacillus graminis*	*Lactobacillus paracollinoides*
Lactobacillus algidus	*Lactobacillus hammesii*	*Lactobacillus parafarraginis*
Lactobacillus alimentarius	*Lactobacillus hamsteri*	*Lactobacillus parakefiri*
Lactobacillus amylolyticus	*Lactobacillus harbinensis*	*Lactobacillus paralimentarius*
Lactobacillus amylophilus	*Lactobacillus hayakitensis*	*Lactobacillus paraplantarum*
Lactobacillus amylotrophicus	*Lactobacillus heilongjiangensis*	*Lactobacillus pasteurii*
Lactobacillus amylovorus	*Lactobacillus helsingborgensis*	*Lactobacillus paucivorans*
Lactobacillus animalis	*Lactobacillus helveticus*	*Lactobacillus pentosus*
Lactobacillus antri	*Lactobacillus herbarum*	*Lactobacillus perolens*
Lactobacillus apinorum	*Lactobacillus hilgardii*	*Lactobacillus plantarum*
Lactobacillus apis	*Lactobacillus hokkaidonensis*	*Lactobacillus pobuzihii*
Lactobacillus apodemi	*Lactobacillus hominis*	*Lactobacillus pontis*
Lactobacillus aquaticus	*Lactobacillus homohiochii*	*Lactobacillus psittaci*
Lactobacillus aviarius	*Lactobacillus hordei*	*Lactobacillus rapi*
Lactobacillus backii	*Lactobacillus iners*	*Lactobacillus rennini*
Lactobacillus bifermentans	*Lactobacillus ingluviei*	*Lactobacillus reuteri*
Lactobacillus bombi	*Lactobacillus intestinalis*	*Lactobacillus rodentium*
Lactobacillus bombicola	*Lactobacillus jensenii*	*Lactobacillus rossiae*

Lactobacillus brantae	*Lactobacillus johnsonii*	*Lactobacillus ruminis*
Lactobacillus brevis	*Lactobacillus kalixensis*	*Lactobacillus saerimneri*
Lactobacillus buchneri	*Lactobacillus kefiranofaciens*	*Lactobacillus sakei*
Lactobacillus cacaonum	*Lactobacillus kefiri*	*Lactobacillus salivarius*
Lactobacillus camelliae	*Lactobacillus kimbladii*	*Lactobacillus sanfranciscensis*
Lactobacillus capillatus	*Lactobacillus kimchicus*	*Lactobacillus saniviri*
Lactobacillus ceti	*Lactobacillus kimchiensis*	*Lactobacillus satsumensis*
Lactobacillus coleohominis	*Lactobacillus kisonensis*	*Lactobacillus secaliphilus*
Lactobacillus collinoides	*Lactobacillus kitasatonis*	*Lactobacillus selangorensis*
Lactobacillus composti	*Lactobacillus koreensis*	*Lactobacillus senioris*
Lactobacillus concavus	*Lactobacillus kullabergensis*	*Lactobacillus senmaizukei*
Lactobacillus coryniformis	*Lactobacillus kunkeei*	*Lactobacillus sharpeae*
Lactobacillus crispatus	*Lactobacillus letivazi*	*Lactobacillus shenzhenensis*
Lactobacillus crustorum	*Lactobacillus lindneri*	*Lactobacillus silagei*
Lactobacillus curieae	*Lactobacillus malefermentans*	*Lactobacillus siliginis*
Lactobacillus curvatus	*Lactobacillus mali*	*Lactobacillus similis*
Lactobacillus delbrueckii	*Lactobacillus manihotivorans*	*Lactobacillus spicheri*
Lactobacillus dextrinicus	*Lactobacillus mellifer*	*Lactobacillus sucicola*
Lactobacillus diolivorans	*Lactobacillus mellis*	*Lactobacillus suebicus*
Lactobacillus equi	*Lactobacillus melliventris*	*Lactobacillus sunkii*
Lactobacillus equicursoris	*Lactobacillus mindensis*	*Lactobacillus suntoryeus*
Lactobacillus equigenerosi	*Lactobacillus mucosae*	*Lactobacillus taiwanensis*
Lactobacillus fabifermentans	*Lactobacillus murinus*	*Lactobacillus thailandensis*
Lactobacillus farciminis	*Lactobacillus nagelii*	*Lactobacillus tucceti*
Lactobacillus farraginis	*Lactobacillus namurensis*	*Lactobacillus ultunensis*
Lactobacillus fermentum	*Lactobacillus nantensis*	*Lactobacillus uvarum*
Lactobacillus floricola	*Lactobacillus nasuensis*	*Lactobacillus vaccinostercus*
Lactobacillus florum	*Lactobacillus nodensis*	*Lactobacillus vaginalis*
Lactobacillus fructivorans	*Lactobacillus odoratitofui*	*Lactobacillus versmoldensis*
Lactobacillus frumenti	*Lactobacillus oeni*	*Lactobacillus vini*
Lactobacillus fuchuensis	*Lactobacillus oligofermentans*	*Lactobacillus wasatchensis*
Lactobacillus futsaii	*Lactobacillus oris*	*Lactobacillus xiangfangensis*
Lactobacillus gallinarum	*Lactobacillus oryzae*	*Lactobacillus zymae*
Lactobacillus gasseri	*Lactobacillus otakiensis*	
Lactobacillus gastricus	*Lactobacillus ozensis*	

Table 62: Predicted (*in silico*) Reactivity (Inclusivity) Results for *Listeria*

Detection Predicted for ≥95% of target sequences		
*Listeria monocytogenes**	*Listeria marthii*	*Listeria welshimeri**
*Listeria ivanovii**	*Listeria seeligeri**	
Detection Predicted for 85%-94% of target sequences		
*Listeria innocua**		
Detection Predicted for <85% of target sequences		
None Identified		
Detection Not Predicted		
Listeria grayi		

Table 63: Predicted (*in silico*) Reactivity (Inclusivity) Results for *Micrococcus*

Detection Predicted for ≥95% of target sequences		
*Micrococcus luteus**	*Micrococcus aquilus*	*Micrococcus yunnanensis**
Micrococcus alkanovora	*Micrococcus flavus*	
Micrococcus aloeverae	*Micrococcus thailandicus*	
Detection Predicted for 85%-94% of target sequences		
Micrococcus endophyticus	*Micrococcus indicus*	
Detection Predicted for <85% of target sequences		
Micrococcus lylae (50.0%)*		
Detection Not Predicted		
Micrococcus antarcticus	*Micrococcus lactis*	
Micrococcus chenggongense	*Micrococcus terreus*	

Table 64: Predicted (*in silico*) Reactivity (Inclusivity) Results for *Staphylococcus*

Detection Predicted for ≥95% of target sequences		
*Staphylococcus aureus**	*Staphylococcus haemolyticus**	*Staphylococcus pseudintermedius**
Staphylococcus agnetis	*Staphylococcus hominis**	*Staphylococcus pseudolugdunensis*
Staphylococcus argensis	*Staphylococcus hominis* subsp. *novobiosepticus*	*Staphylococcus pulvereri*
Staphylococcus argenteus	*Staphylococcus hyicus**	*Staphylococcus rostri*
*Staphylococcus auricularis**	*Staphylococcus jettensis*	*Staphylococcus saprophyticus**
*Staphylococcus capitis**	*Staphylococcus kloosii*	*Staphylococcus schleiferi**
*Staphylococcus caprae**	*Staphylococcus lentus**	*Staphylococcus schweitzeri*
*Staphylococcus carnosus**	*Staphylococcus lugdunensis**	*Staphylococcus sciuri**
*Staphylococcus chromogenes**	*Staphylococcus lutrae*	*Staphylococcus simiae*
*Staphylococcus cohnii**	*Staphylococcus massiliensis*	*Staphylococcus simulans**
Staphylococcus delphini	*Staphylococcus microti*	*Staphylococcus stepanovicii*

Staphylococcus devriesei	*Staphylococcus muscae**	*Staphylococcus succinus*
*Staphylococcus epidermidis**	*Staphylococcus nepalensis*	*Staphylococcus vitulinus**
Staphylococcus equorum	*Staphylococcus pasteuri**	*Staphylococcus warneri **
Staphylococcus felis	*Staphylococcus petrasii*	*Staphylococcus xylosus**
Staphylococcus fleurettii	*Staphylococcus pettenkoferi**	
*Staphylococcus gallinarum**	*Staphylococcus piscifermentans*	
Detection Predicted for 85%-94% of target sequences		
Staphylococcus arlettae	*Staphylococcus intermedius**	
Staphylococcus condimenti	*Staphylococcus saccharolyticus**	
Detection Predicted for <85% of target sequences		
None Identified		
Detection Not Predicted		
Staphylococcus caseolyticus[A]		

A. Data for only one strain available in NCBI.

Table 65: Predicted (*in silico*) Reactivity (Inclusivity) Results for *Streptococcus*

Detection Predicted for ≥95% of target sequences		
*Streptococcus agalactiae**	*Streptococcus infantarius**	*Streptococcus phocae*
Streptococcus alactolyticus	*Streptococcus infantis**	*Streptococcus pneumoniae**
*Streptococcus anginosus**	*Streptococcus intermedius**	*Streptococcus porcinus*
Streptococcus australis	*Streptococcus intestinalis*	*Streptococcus porcorum*
Streptococcus caballi	*Streptococcus lactarius*	*Streptococcus pseudopneumoniae*
*Streptococcus constellatus**	*Streptococcus loxodontisalivarius*	*Streptococcus pseudoporcinus*
*Streptococcus criceti**	*Streptococcus luteciae*	*Streptococcus pyogenes**
Streptococcus cristatus	*Streptococcus lutetiensis*	*Streptococcus rifensis*
Streptococcus danieliae	*Streptococcus macedonicus*	*Streptococcus rubneri*
Streptococcus dentasini	*Streptococcus marimammalium*	*Streptococcus salivarius**
Streptococcus dentisani	*Streptococcus massiliensis*	*Streptococcus saliviloxodontae*
Streptococcus didelphis	*Streptococcus mitis**	*Streptococcus sanguinis**
Streptococcus difficilis	*Streptococcus moroccensis*	*Streptococcus seminale*
Streptococcus dysgalactiae subsp. *dysgalactiae*	*Streptococcus oligofermentans*	*Streptococcus sinensis*
Streptococcus dysgalactiae subsp. *equisimilis*	*Streptococcus oralis**	*Streptococcus suis*
*Streptococcus dysgalactiae**	*Streptococcus oricebi*	*Streptococcus thermophilus*
*Streptococcus equi**	*Streptococcus orisratti*	*Streptococcus thoraltensis**
*Streptococcus equinus**	*Streptococcus panodentis*	*Streptococcus tigurinus*
Streptococcus fryi	*Streptococcus parasanguinis**	*Streptococcus troglodytae*

*Streptococcus gallolyticus**	*Streptococcus parasuis*	*Streptococcus troglodytidis*
*Streptococcus gordonii**	*Streptococcus parauberis*	*Streptococcus urinalis*
Streptococcus himalayensis	*Streptococcus pasteuri*	*Streptococcus ursoris*
Streptococcus hongkongensis	*Streptococcus pasteurianus*	*Streptococcus vestibularis*
Streptococcus hyointestinalis	*Streptococcus peroris**	*Streptococcus waiu*
Detection Predicted for 85%-94% of target sequences		
*Streptococcus bovis**	*Streptococcus uberis*	
Detection Predicted for <85% of target sequences		
Streptococcus canis (15.8%)	*Streptococcus henryi* (10.0%)	*Streptococcus ratti* (75.0%)
Streptococcus halichoeri (66.7%)	*Streptococcus iniae* (6.9%)	
Detection Not Predicted		
Streptococcus acidominimus	*Streptococcus entericus*	*Streptococcus oriloxodontae*
Streptococcus azizii	*Streptococcus ferus*	*Streptococcus orisasini*
Streptococcus cameli	*Streptococcus gallinaceus*	*Streptococcus orisuis*
Streptococcus castoreus	*Streptococcus hyovaginalis*	*Streptococcus ovis*
Streptococcus cremoris	*Streptococcus ictaluri*	*Streptococcus pharyngis*
Streptococcus criae	*Streptococcus lactis*	*Streptococcus pluranimalium*
Streptococcus cuniculi	*Streptococcus macacae*	*Streptococcus plurextorum*
Streptococcus dentapri	*Streptococcus marmotae*	*Streptococcus plutanimalium*
Streptococcus dentiloxodontae	*Streptococcus merionis*	*Streptococcus porci*
Streptococcus dentirousetti	*Streptococcus milleri*	*Streptococcus rupicaprae*
Streptococcus devriesei	*Streptococcus minor*	*Streptococcus sobrinus*
Streptococcus downei	*Streptococcus mutans*	*Streptococcus tangierensis*

Table 66: Predicted (*in silico*) Reactivity (Inclusivity) Results for *Streptococcus anginosus* group

Detection Predicted for ≥95% of target sequences		
*Streptococcus anginosus**	*Streptococcus constellatus**	*Streptococcus intermedius**
Detection Predicted for 85%-94% of target sequences		
None Identified		
Detection Predicted for <85% of target sequences		
None Identified		
Detection Not Predicted		
None Identified		

Table 67: Predicted (*in silico*) Reactivity (Inclusivity) Results for Pan *Candida*

Detection Predicted for ≥95% of target sequences		
*Candida albicans**	*Candida glabrata**	*Candida krusei**
*Candida parapsilosis**		
Detection Predicted for 85%-94% of target sequences		
None Identified		
Detection Predicted for <85% of target sequences		
None Identified		
Detection Not Predicted		
*Candida lusitaniae**	*Candida orthopsilosis**	
*Candida metapsilosis**	*Candida tropicalis**	

Table 68:Predicted (*in silico*) Reactivity (Inclusivity) Results for Pan Gram-Negative

The Pan Gram-Negative assay was designed to be broadly inclusive of the majority of gram-negative organisms.

Analytical Specificity (Cross-Reactivity and Exclusivity)

Cross-reactivity of on-panel and off-panel analytes was evaluated with the BCID-GP panel. Bacterial targets were tested in triplicate at a concentration of ≥1x10^9 CFU/mL while fungi were tested in triplicate at a concentration of ≥1x10^7 CFU/mL. If the target concentration could not be reached, the organism was diluted 2-fold from stock for use.

No cross reactivity was observed for any of the on-panel gram-positive organisms. Three organisms showed cross-reactivity, *Burkholderia cepacia* cross reacts with the *Corynebacterium* assay at levels ≥1x10^7 CFU/mL, an unspeciated *Rhodococcus* strain (ATCC 49988) cross reacts with the *Micrococcus* assay at levels ≥1x10^7 CFU/mL and *Bacillus badius* cross reacts with the *Bacillus subtilis* group assay at 7 x 10^7 CFU/mL. See **Table 55** and **Table 56** for summaries of the on-panel strains tested as a part of the Limit of Detection (Analytical Sensitivity) and Analytical Reactivity (Inclusivity) studies and **Table 69** for a summary of off-panel strains tested.

Off-panel Exclusivity

Table 69: Targets Assessed for Cross-Reactivity with the cobas eplex BCID-GP panel (Exclusivity)

Organism	Strain ID	Organism	Strain ID
Abiotrophia defectiva	ATCC 49176	*Granulicatella elegans*	ATCC 700633[C]
Actinomyces odontolyticus	ATCC 17929	*Kocuria kristinae*	ATCC BAA-752
Aerococcus sanguinicola	ATCC BAA-465	*Kocuria rhizophila*	ATCC 9341
Aerococcus urinae	ATCC 700306	*Kytococcus sedentarius*	ATCC 27575
Aerococcus viridans	ATCC 10400	*Lactococcus garvieae*	ATCC 43921[D]
Anaerococcus prevotii	ATCC 9321	*Lactococcus lactis*	ATCC 49032
Arcanobacterium bernardiae	ATCC 51728	*Leuconostoc carnosum*	ATCC 49367

Organism	Strain ID
Arcanobacterium haemolyticum	ATCC BAA-1784[A]
Arthrobacter psychrolactophilus	ATCC 700733
Aspergillus fumigatus	ATCC 204305[B]
Bacillus badius	ATCC 14574
Bacillus pumilus	ATCC 14884
Brochothrix thermosphacta	ATCC 11509
Candida lusitaniae	ATCC 34449
Candida metapsilosis	ATCC 96144
Candida orthopsilosis	ATCC 96139
Candida tropicalis	ATCC 1369
Carnobacterium divergens	ATCC 35677
Carnobacterium maltaromaticum	ATCC 27865[C]
Cellulomonas turbata	ATCC 25835
Cellulosimicrobium cellulans	ATCC 27402
Clostridium clostridioforme	ATCC 25537
Clostridium perfringens	ATCC 13124
Clostridium ramosum	ATCC 25582
Cryptococcus gattii	ATCC 76108
Cryptococcus grubii	ATCC 208821
Cryptococcus neoformans	ATCC 14116
Cutibacterium granulosum	ATCC 11829
Erysipelothrix rhusiopathiae	ATCC 35457
Gemella haemolysans	ATCC 10379
Gemella morbillorum	ATCC 27824
Geotrichum capitatum	ATCC 10663
Granulicatella adiacens	ATCC 43205

Organism	Strain ID
Leuconostoc citreum	ATCC 13146
Leuconostoc mesenteroides	ATCC 8293
Macrococcus caseolyticus	ATCC 29750
Macrococcus caseolyticus	ATCC 51834
Mycobacterium avium complex	ATCC 15769
Mycobacterium fortuitum	ATCC 6841
Mycobacterium mucogenicum	ATCC 49650
Mycobacterium tuberculosis	ATCC 25177
Mycoplasma pneumoniae	ATCC 39505
Pediococcus acidilactici	ATCC 8042
Pediococcus pentosaceus	ATCC 33316
Penicillium marneffei	ATCC 200050
Peptostreptococcus anaerobius	ATCC 27337
Planococcus species	ATCC 35671
Propionibacterium propionicum	ATCC 14157
Rhodococcus equi	ATCC 6939
Rhodococcus species	ATCC 49988
Rhodotorula glutinis	ATCC 32766
Rhodotorula minuta	ATCC 36236
Rhodotorula mucilaginosa	ATCC 9449
Rothia dentocariosa	ATCC 31918
Rothia mucilaginosa	ATCC 25296
Saccharomyces cerevisiae	ATCC 18824
Trichosporon asahii	ATCC 201110
Vagococcus fluvialis	ATCC 49515
Weissella paramesenteroides	ATCC 33313

A. Final testing concentration of 4.05×10^8 CFU/mL
B. Final testing concentration of 2.5×10^6 CFU/mL
C. Final testing concentration of 3.63×10^8 CFU/mL
D. Final testing concentration of 2.78×10^8 CFU/mL

Bottle Positivity

Several representative bacterial and fungal organisms were spiked into blood culture bottles along with the manufacturer's recommended volume of human whole blood and grown to positivity in a commercially-available continuously monitoring blood culture system. Bottles were removed from the incubator within two hours of being identified as positive as well as eight hours after bottle positivity. At least two independent positive blood culture replicates were quantified for each organism on culture plates. Organisms tested and approximate bottle positivity concentrations are summarized in **Table 70**. Concentrations shown below represent approximate levels that may be observed in a clinical setting. All estimated bottle positivity concentrations are equivalent or greater than the established Limit of Detection (LOD) for each of the assays of the **cobas eplex** BCID-GP panel.

Table 70: Bottle Positivity Concentrations

Organism	Strain ID	Mean Bottle Positivity Concentration	Mean Bottle Positivity +8 hours Concentration
Gram-positive Organisms			
Corynebacterium striatum	ATCC BAA-1293	4.5 x 10^6 CFU/mL	2.7 x 10^9 CFU/mL
Cutibacterium acnes (P. acnes)	ATCC 6919	3.0 x 10^8 CFU/mL	3.5 x 10^8 CFU/mL
Enterococcus faecium	ATCC BAA-2317	4.9 x 10^7 CFU/mL	3.6 x 10^7 CFU/mL
Lactobacillus casei	ATCC 39392	4.8 x 10^7 CFU/mL	3.1 x 10^{11} CFU/mL
Staphylococcus aureus	NRS 483	2.8 x 10^7 CFU/mL	2.1 x 10^7 CFU/mL
Streptococcus anginosus	ATCC 33397	4.1 x 10^7 CFU/mL	4.0 x 10^8 CFU/mL
Gram-negative Organisms			
Acinetobacter baumannii	NCTC 13301	4.4 x 10^8 CFU/mL	3.8 x 10^8 CFU/mL
Bacteroides fragilis	ATCC 700786	4.7 x 10^8 CFU/mL	6.7 x 10^9 CFU/mL
Enterobacter cloacae	NCTC 13464	2.8 x 10^8 CFU/mL	7.7 x 10^8 CFU/mL
Escherichia coli	NCTC 13476	2.3 x 10^8 CFU/mL	1.5 x 10^9 CFU/mL
Fusobacterium nucleatum	ATCC 31647	6.5 x 10^7 CFU/mL	4.9 x 10^8 CFU/mL
Haemophilus influenzae	ATCC 19418	6.9 x 10^8 CFU/mL	1.2 x 10^9 CFU/mL
Klebsiella oxytoca	CDC #0147	9.3 x 10^8 CFU/mL	1.5 x 10^9 CFU/mL
Neisseria meningitidis	ATCC 13102	3.1 x 10^7 CFU/mL	2.1 x 10^8 CFU/mL
Pseudomonas aeruginosa	NCTC 13476	1.6 x 10^8 CFU/mL	8.4 x 10^8 CFU/mL
Serratia marcescens	ATCC 14041	1.2 x 10^9 CFU/mL	2.2 x 10^9 CFU/mL
Fungal Organism			
Candida albicans	ATCC 90082	1.6 x 10^6 CFU/mL	1.4 x 10^6 CFU/mL

Reproducibility

Four positive mixes including 9 on-panel organisms and 3 antibiotic resistance genes representing 15 targets at two concentrations and one negative mix including an off-panel organism were tested. Two positive mixes were prepared by spiking cultured isolates into negative sample matrix in BD BACTEC Standard/10 Aerobic/F blood culture bottles at concentrations reflecting those observed at time of bottle positivity plus 8 hours (BP+8) and time of bottle positivity (BP). For the remaining two positive mixes, *Cutibacterium acnes* was grown in BD BACTEC Standard/10 Aerobic/F blood culture bottles until BP and BP+8, then cultured isolates for the remaining organisms were spiked in at concentrations reflecting those observed at BP and BP+8. The negative mix contained *Cutibacterium granulosum* grown in BD BACTEC Lytic/10 Anaerobic/F blood culture bottles to BP and BP+8, which is expected to yield a negative result. Bottle concentrations used in this study are summarized in **Table 71**. Each of the four positive mixes at two concentrations and the one negative mix were tested a minimum of 108 times. Testing occurred at three sites, with two operators testing the mixes over six days using three cartridge lots. For the negative mix, agreement with the expected negative result was 100% for all targets in the **cobas eplex** BCID-GP panel, except Pan Gram-Negative at 99.1%.

Table 71: Bottle Positivity Concentrations

Organism	Bottle Positivity Concentration	Bottle Positivity +8 Hours Concentration
Corynebacterium striatum	4 x 10^6 CFU/mL	1 x 10^8 CFU/mL
Cutibacterium acnes (P. acnes)	1 x 10^8 CFU/mL	4.4 x 10^7 CFU/mL
Enterococcus faecium (vanA+)	1 x 10^7 CFU/mL	1 x 10^8 CFU/mL
Enterococcus faecalis (vanB+)	1 x 10^7 CFU/mL	1 x 10^8 CFU/mL
Lactobacillus casei	1 x 10^7 CFU/mL	1 x 10^8 CFU/mL
Staphylococcus aureus (mecA+)	1 x 10^7 CFU/mL	1 x 10^8 CFU/mL
Streptococcus anginosus	1 x 10^7 CFU/mL	1 x 10^8 CFU/mL
Candida albicans (Pan *Candida* target)	1 x 10^6 CFU/mL	1 x 10^7 CFU/mL
Klebsiella pneumoniae (Pan Gram-Negative target)	1 x 10^8 CFU/mL	1 x 10^9 CFU/mL

The percent agreement of each target with the expected result is summarized in **Tables 72-86.** The **cobas eplex** BCID-GP panel demonstrates a high level of agreement with the expected results.

Table 72: Percent Agreement for *Corynebacterium*

Concentration of *Corynebacterium striatum*	Site	Agreement with Expected Results		
		Agreed / N	%	95% CI
Bottle Positive + 8 Hours (1x10^8 CFU/mL)	1	36/36	100	(90.4-100)
	2	36/36	100	(90.4-100)
	3	36/36	100	(90.4-100)
	All	**108/108**	**100**	**(96.6-100)**
Bottle Positive (4x10^6 CFU/mL)	1	35/36	97.2	(85.8-99.5)
	2	35/36	97.2	(85.8-99.5)
	3	33/36	91.7	(78.2-97.1)
	All	**103/108**	**95.4**	**(89.6-98.0)**
Negative	1	108/108	100	(96.6-100)
	2	107/108	99.1	(94.9-99.8)
	3	107/107	100	(96.5-100)
	All	**322/323**	**99.7**	**(98.3-99.9)**

CI=Confidence Interval

Table 73: Percent Agreement for *Cutibacterium acnes* (*Propionibacterium acnes*)

Concentration of *Cutibacterium acnes*	Site	Agreement with Expected Results		
		Agreed / N	%	95% CI
Bottle Positive + 8 Hours ($4.4x10^7$ CFU/mL)	1	32/36	88.9	(74.7-95.6)
	2	33/36	91.7	(78.2-97.1)
	3	36/36	100	(90.4-100)
	All	**101/108**	**93.5[A]**	**(87.2-96.8)**
Bottle Positive ($1.1x10^8$ CFU/mL)	1	36/36	100	(90.4-100)
	2	33/36	91.7	(78.2-97.1)
	3	35/36	97.2	(85.8-99.5)
	All	**104/108**	**96.3[B]**	**(90.9-98.6)**
Negative	1	108/108	100	(96.6-100)
	2	108/108	100	(96.6-100)
	3	107/107	100	(96.5-100)
	All	**323/323**	**100**	**(98.8-100)**

A. <95% agreement is expected because the *C. acnes* organism concentration is more than 0.5 log below the limit of detection of this assay (1.0×10^8 CFU/mL).
B. 95% agreement is expected because the *C. acnes* organism concentration is approximately equal to the limit of detection of this assay (1.0×10^8 CFU/mL).

Table 74: Percent Agreement for *Enterococcus*

Concentration of *Enterococcus*	Site	Agreement with Expected Results		
		Agreed / N	%	95% CI
Bottle Positive + 8 Hours ($1x10^8$ CFU/mL)	1	72/72	100	(94.9-100)
	2	72/72	100	(94.9-100)
	3	72/72	100	(94.9-100)
	All	**216/216**	**100**	**(98.3-100)**
Bottle Positive ($1x10^7$ CFU/mL)	1	72/72	100	(94.9-100)
	2	72/72	100	(94.9-100)
	3	72/72	100	(94.9-100)
	All	**216/216**	**100**	**(98.3-100)**
Negative	1	36/36	100	(90.4-100)
	2	36/36	100	(90.4-100)
	3	35/35	100	(90.1-100)
	All	**107/107**	**100**	**(96.5-100)**

Table 75: Percent Agreement for *Enterococcus faecalis*

Concentration of *Enterococcus faecalis*	Site	Agreement with Expected Results		
		Agreed / N	%	95% CI
Bottle Positive + 8 Hours ($1x10^8$ CFU/mL)	1	36/36	100	(90.4-100)
	2	36/36	100	(90.4-100)
	3	36/36	100	(90.4-100)
	All	**108/108**	**100**	**(96.6-100)**
Bottle Positive ($1x10^7$ CFU/mL)	1	36/36	100	(90.4-100)
	2	36/36	100	(90.4-100)
	3	36/36	100	(90.4-100)
	All	**108/108**	**100**	**(96.6-100)**
Negative	1	108/108	100	(96.6-100)
	2	108/108	100	(96.6-100)
	3	107/107	100	(96.5-100)
	All	**323/323**	**100**	**(98.8-100)**

Table 76: Percent Agreement for *Enterococcus faecium*

Concentration of *Enterococcus faecium*	Site	Agreement with Expected Results		
		Agreed / N	%	95% CI
Bottle Positive + 8 Hours ($1x10^8$ CFU/mL)	1	36/36	100	(90.4-100)
	2	36/36	100	(90.4-100)
	3	36/36	100	(90.4-100)
	All	**108/108**	**100**	**(96.6-100)**
Bottle Positive ($1x10^7$ CFU/mL)	1	36/36	100	(90.4-100)
	2	36/36	100	(90.4-100)
	3	36/36	100	(90.4-100)
	All	**108/108**	**100**	**(96.6-100)**
Negative	1	108/108	100	(96.6-100)
	2	108/108	100	(96.6-100)
	3	107/107	100	(96.5-100)
	All	**323/323**	**100**	**(98.8-100)**

Table 77: Percent Agreement for *Lactobacillus*

Concentration of *Lactobacillus casei*	Site	Agreement with Expected Results		
		Agreed / N	%	95% CI
Bottle Positive + 8 Hours ($1x10^8$ CFU/mL)	1	36/36	100	(90.1-100)
	2	36/36	100	(89.8-100)
	3	36/36	100	(90.4-100)
	All	**108/108**	**100**	**(96.5-100)**
Bottle Positive ($1x10^7$ CFU/mL)	1	36/36	100	(89.8-100)
	2	36/36	100	(90.4-100)
	3	36/36	100	(90.1-100)
	All	**108/108**	**100**	**(96.5-100)**
Negative	1	108/108	100	(90.4-100)
	2	108/108	100	(89.8-100)
	3	107/107	100	(90.1-100)
	All	**323/323**	**100**	**(96.5-100)**

Table 78: Percent Agreement for *Staphylococcus*

Concentration of *Staphylococcus*	Site	Agreement with Expected Results		
		Agreed / N	%	95% CI
Bottle Positive + 8 Hours ($1x10^8$ CFU/mL)	1	36/36	100	(90.4-100)
	2	36/36	100	(90.4-100)
	3	36/36	100	(90.4-100)
	All	**108/108**	**100**	**(96.6-100)**
Bottle Positive ($1x10^7$ CFU/mL)	1	36/36	100	(90.4-100)
	2	36/36	100	(90.48-100)
	3	36/36	100	(90.4-100)
	All	**108/108**	**100**	**(96.6-100)**
Negative	1	108/108	100	(96.6-100)
	2	106/108	98.1	(93.5-99.5)
	3	107/107	100	(96.5-100)
	All	**321/323**	**99.4**	**(97.8-99.8)**

Table 79: Percent Agreement for *Staphylococcus aureus*

Concentration of *Staphylococcus aureus*	Site	Agreement with Expected Results		
		Agreed / N	%	95% CI
Bottle Positive + 8 Hours ($1x10^8$ CFU/mL)	1	36/36	100	(90.4-100)
	2	36/36	100	(90.4-100)
	3	36/36	100	(90.4-100)
	All	**108/108**	**100**	**(96.6-100)**
Bottle Positive ($1x10^7$ CFU/mL)	1	36/36	100	(90.4-100)
	2	36/36	100	(90.4-100)
	3	36/36	100	(90.4-100)
	All	**108/108**	**100**	**(96.6-100)**
Negative	1	108/108	100	(96.6-100)
	2	108/108	100	(96.6-100)
	3	107/107	100	(96.5-100)
	All	**323/323**	**100**	**(98.8-100)**

Table 80: Percent Agreement for *Streptococcus*

Concentration of Streptococcus	Site	Agreement with Expected Results		
		Agreed / N	%	95% CI
Bottle Positive + 8 Hours ($1x10^8$ CFU/mL)	1	36/36	100	(90.4-100)
	2	36/36	100	(90.4-100)
	3	36/36	100	(90.4-100)
	All	**108/108**	**100**	**(96.6-100)**
Bottle Positive ($1x10^7$ CFU/mL)	1	36/36	100	(90.4-100)
	2	35/36	97.2	(85.8-99.5)
	3	36/36	100	(90.4-100)
	All	**107/108**	**99.1**	**(94.9-99.8)**
Negative	1	108/108	100	(96.6-100)
	2	107/108	99.1	(94.9-99.8)
	3	107/107	100	(96.5-100)
	All	**322/323**	**99.7**	**(98.3-99.9)**

Table 81: Percent Agreement for *Streptococcus anginosus* group

Concentration of *Streptococcus anginosus*	Site	Agreement with Expected Results		
		Agreed / N	%	95% CI
Bottle Positive + 8 Hours ($1x10^8$ CFU/mL)	1	36/36	100	(90.4-100)
	2	36/36	100	(90.4-100)
	3	36/36	100	(90.4-100)
	All	**108/108**	**100**	**(96.6-100)**
Bottle Positive ($1x10^7$ CFU/mL)	1	36/36	100	(90.4-100)
	2	35/36	97.2	(85.8-99.5)
	3	36/36	100	(90.4-100)
	All	**107/108**	**99.1**	**(94.9-99.8)**
Negative	1	108/108	100	(96.6-100)
	2	108/108	100	(96.6-100)
	3	107/107	100	(96.5-100)
	All	**323/323**	**100**	**(98.8-100)**

Table 82: Percent Agreement for Pan *Candida*

Concentration of *Candida albicans*	Site	Agreement with Expected Results		
		Agreed / N	%	95% CI
Bottle Positive + 8 Hours ($1x10^7$ CFU/mL)	1	36/36	100	(90.4-100)
	2	36/36	100	(90.4-100)
	3	36/36	100	(90.4-100)
	All	**108/108**	**100**	**(96.6-100)**
Bottle Positive ($1x10^6$ CFU/mL)	1	36/36	100	(90.4-100)
	2	36/36	100	(90.4-100)
	3	36/36	100	(90.4-100)
	All	**108/108**	**100**	**(96.6-100)**
Negative	1	108/108	100	(96.6-100)
	2	108/108	100	(96.6-100)
	3	107/107	100	(96.5-100)
	All	**323/323**	**100**	**(98.8-100)**

Table 83: Percent Agreement for Pan Gram-Negative

Concentration of *Klebsiella pneumoniae*	Site	Agreement with Expected Results		
		Agreed / N	%	95% CI
Bottle Positive + 8 Hours ($1x10^9$ CFU/mL)	1	36/36	100	(90.4-100)
	2	36/36	100	(90.4-100)
	3	36/36	100	(90.4-100)
	All	**108/108**	**100**	**(96.6-100)**
Bottle Positive ($1x10^8$ CFU/mL)	1	36/36	100	(90.4-100)
	2	36/36	100	(90.4-100)
	3	36/36	100	(90.4-100)
	All	**108/108**	**100**	**(96.6-100)**
Negative	1	108/108	100	(96.6-100)
	2	107/108	99.1	(94.9-99.8)
	3	107/107	100	(96.5-100)
	All	**322/323**	**99.7**	**(98.3-99.9)**

Table 84: Percent Agreement for *mecA*

Concentration of *Staphylococcus aureus*	Site	Agreement with Expected Results		
		Agreed / N	%	95% CI
Bottle Positive + 8 Hours ($1x10^8$ CFU/mL)	1	36/36	100	(90.4-100)
	2	36/36	100	(90.4-100)
	3	36/36	100	(90.4-100)
	All	**108/108**	**100**	**(96.6-100)**
Bottle Positive ($1x10^7$ CFU/mL)	1	36/36	100	(90.4-100)
	2	36/36	100	(90.4-100)
	3	36/36	100	(90.4-100)
	All	**108/108**	**100**	**(96.6-100)**
Negative	1	108/108	100	(96.6-100)
	2	108/108	100	(96.6-100)
	3	107/107	100	(96.5-100)
	All	323/323	100	(98.8-100)

Table 85: Percent Agreement for *vanA*

Concentration of *Enterococcus faecium*	Site	Agreement with Expected Results		
		Agreed / N	%	95% CI
Bottle Positive + 8 Hours ($1x10^8$ CFU/mL)	1	36/36	100	(90.4-100)
	2	36/36	100	(90.4-100)
	3	36/36	100	(90.4-100)
	All	**108/108**	**100**	**(96.6-100)**
Bottle Positive ($1x10^7$ CFU/mL)	1	36/36	100	(90.4-100)
	2	36/36	100	(90.4-100)
	3	36/36	100	(90.4-100)
	All	**108/108**	**100**	**(96.6-100)**
Negative	1	108/108	100	(96.6-100)
	2	108/108	100	(96.6-100)
	3	107/107	100	(96.5-100)
	All	323/323	100	(98.8-100)

Table 86: Percent Agreement for *vanB*

Concentration of *Enterococcus faecalis*	Site	Agreement with Expected Results		
		Agreed / N	%	95% CI
Bottle Positive + 8 Hours ($1x10^8$ CFU/mL)	1	36/36	100	(90.4-100)
	2	36/36	100	(90.4-100)
	3	36/36	100	(90.4-100)
	All	**108/108**	**100**	**(96.6-100)**
Bottle Positive ($1x10^7$ CFU/mL)	1	36/36	100	(90.4-100)
	2	36/36	100	(90.4-100)
	3	36/36	100	(90.4-100)
	All	**108/108**	**100**	**(96.6-100)**
Negative	1	108/108	100	(96.6-100)
	2	108/108	100	(96.6-100)
	3	107/107	100	(96.5-100)
	All	323/323	100	(98.8-100)

Interfering Substances and Sample Matrix Equivalency (Bottle Evaluation)

Two organism mixes consisting of 9 on-panel organisms representing 14 targets and negative blood matrix were used to assess potentially interfering substances and bottle types for interference. The concentration of each organism tested is summarized in **Table 87.**

Table 87: Interfering Substance and Bottle Equivalency Concentrations

Organism	Concentration
Cutibacterium acnes	3 x 10^8 CFU/mL
Enterococcus faecalis (*vanB*+)	4 x 10^7 CFU/mL
Enterococcus faecium (*vanA*+)	4 x 10^7 CFU/mL
Lactobacillus casei	4 x 10^7 CFU/mL
Staphylococcus aureus	2 x 10^7 CFU/mL
Staphylococcus epidermidis	2 x 10^7 CFU/mL
Streptococcus pneumoniae	4 x 10^7 CFU/mL
Klebsiella pneumoniae (Pan Gram-Negative target)	5 x 10^8 CFU/mL
Candida albicans (Pan *Candida* target)	1 x 10^6 CFU/mL

Interfering Substances

Eighteen substances were used to assess the **cobas eplex** BCID-GP panel for potential interference. The organisms in **Table 87** were spiked into negative blood matrix and tested in triplicate with and without each potentially interfering substance. Negative blood matrix was tested to control for potential positive interference. Potentially interfering substances are summarized in **Table 88**. None of the eighteen substances commonly found in blood culture specimens or as medications commonly used to treat skin or bloodstream infections were found to inhibit the **cobas eplex** BCID-GP panel at clinically relevant concentrations. The effect of interfering substances has only been evaluated for the organisms listed in **Table 87**. Interference due to substances other than those described in this section can lead to erroneous results.

Table 88: Potentially Interfering Substances: Substance List

Endogenous Substances	Testing Concentration
Bilirubin	60 µg/mL
Hemoglobin	0.6 g/L
Human Genomic DNA	6 x 10^5 copies/mL
Triglycerides	1000 mg/dL
γ-globulin	0.425 g/dL

Exogenous Substances	Testing Concentration
Amoxicillin/Clavulanate	3.5 µg/mL
Amphotericin B	2 µg/mL
Caspofungin	5 µg/mL
Ceftriaxone	0.23 mg/mL
Ciprofloxacin	3 mg/L
Fluconazole	25 mg/L
Flucytosine	90 µg/mL
Gentamicin sulfate	3 µg/mL
Heparin	0.9 U/mL
Imipenem	83 µg/mL
Sodium Polyanethol Sulfonate	0.25% w/v
Tetracycline	5 mg/L
Vancomycin	30 mg/L

Sample Matrix Equivalency (Bottle Evaluation)

Thirteen bottle types were tested for interference with each of the organisms listed in **Table 87**. Five replicates of each organism were tested in each of two bottle lots. Negative blood matrix was run as a negative control. Eleven of the bottle types tested showed no interference for any of the targets tested. One lot of the BACTEC™ Plus Anaerobic bottles showed false positive results for Pan Gram-Negative. The BacT/ALERT® FN Plus bottle type showed lower sensitivity for some targets (Pan Gram-Negative and *E. faecium* with *vanA*). A summary of the bottle types assessed and the study outcomes is found in **Table 89**.

Table 89: Sample Matrix Equivalency (Bottle Evaluation) Bottle Types

Manufacturer	Bottle Brand	Bottle Type	Study Outcome
BD	BACTEC™	Plus Aerobic	No interference observed
BD	BACTEC™	Plus Anaerobic	False positive results for Pan Gram-Negative target were observed in one lot.
BD	BACTEC™	Standard Aerobic	No interference observed
BD	BACTEC™	Standard Anaerobic	No interference observed
BD	BACTEC™	Peds Plus™	No interference observed
BD	BACTEC™	Lytic Anaerobic	No interference observed
bioMérieux	BACT/ALERT®	SA Standard Aerobic	No interference observed
bioMérieux	BACT/ALERT®	SN Standard Anaerobic	No interference observed
bioMérieux	BACT/ALERT®	FA Plus	No interference observed
bioMérieux	BACT/ALERT®	FN Plus	False negative results were observed for Pan Gram-Negative and *E. faecium/vanA* targets
bioMérieux	BACT/ALERT®	PF Plus	No interference observed
Thermo Scientific™	VersaTREK™	REDOX™ 1 EZ Draw Aerobic	No interference observed
Thermo Scientific™	VersaTREK™	REDOX™ 2 EZ Draw Anaerobic	No interference observed

Carryover and Cross-Contamination

Carryover and cross-contamination were evaluated for the **cobas eplex** BCID-GP panel within and between runs by alternating high positive and negative samples across multiple runs over 5 rounds of testing. A high-titer mix of *mecA* positive *Staphylococcus aureus*, *vanA* positive *Enterococcus faecium* and *Klebsiella pneumoniae* (a Pan Gram-Negative target organism) was prepared at 1 x 10^9 CFU/mL each as well as *Candida albicans* (a Pan *Candida* target organism) at 1x10^7 CFU/mL to simulate clinically relevant high positive samples for positive testing. Negative blood culture matrix was used to represent negative samples. Over 120 runs, all valid positive runs resulted in detection of *Staphylococcus aureus*, *mecA*, *Enterococcus faecium*, *vanA*, Pan Gram-Negative and Pan *Candida* and no false positives were detected in the negative runs.

Competitive Inhibition Study

Competitive inhibition was evaluated for the **cobas eplex** BCID-GP panel by pairing eight clinically relevant organisms (including a Pan Gram-Negative assay target, a Pan *Candida* assay target, and an off-panel gram-positive organism) in four simulated dual infection sample mixes. Each dual infection mix was tested in combination with each of the three other mixes, such that all organisms were tested at low titer (concentrations expected at bottle positivity) while in the presence of other organisms at higher titer (concentrations expected at 8 hours beyond bottle positivity, or one log higher than that expected at bottle positivity). No competitive inhibition was observed in any replicates of the twelve testing conditions. A summary of the organisms assessed and testing concentrations is found in **Table 90**.

Table 90: Competitive Inhibition Organisms and Concentrations Tested

Organism	High Concentration	Low Concentration
Enterococcus faecium	1 x 10^8 CFU/mL	4 x 10^7 CFU/mL
Staphylococcus aureus	1 x 10^8 CFU/mL	2 x 10^7 CFU/mL
Staphylococcus epidermidis	1 x 10^8 CFU/mL	2 x 10^7 CFU/mL
Streptococcus agalactiae	4 x 10^8 CFU/mL	4 x 10^7 CFU/mL
Streptococcus pneumoniae	4 x 10^8 CFU/mL	4 x 10^7 CFU/mL
Candida albicans	1 x 10^7 CFU/mL	1 x 10^6 CFU/mL
Escherichia coli	1 x 10^9 CFU/mL	2 x 10^8 CFU/mL
Cutibacterium granulosum[A]	1 x 10^9 CFU/mL	3 x 10^8 CFU/mL

A. Off-panel organism

TROUBLESHOOTING

Table 91: Troubleshooting Table

For a complete list of all **cobas eplex** error messages and a description of the messages, please refer to the **cobas eplex** Operator Manual.

Error	Error Messages	Description	Re-test Recommendations
Test did not start	"Cartridge failure" "The cartridge initialization test failed" "Cartridge not present" "Bay heater failure" "Unknown error" "Bay main / fluid motor failure" "Bay over pressured" "Bay temperature out of range" "The system was unable to read the cartridge" "Cartridge inserted doesn't match the serial number of the cartridge scanned" "The system is not ready to accept the cartridge" "The system was unable to enable cartridge insertion for the bay" "The system failed to prepare the cartridge for processing"	An error that occurs during pre-flight check (initialization) of cartridge upon insertion into bay. Pre-flight or cartridge initialization occurs when the cartridge is first inserted into the bay and takes approximately 90 seconds. Upon completion of preflight testing or cartridge initialization, the cartridge cannot be re-used, but prior to this point, the cartridge can be re-tested. To verify cartridge initialization has completed, examine the cartridge label upon removal. If the **cobas eplex** BCID-GP cartridge label has been pierced, initialization started and cartridge cannot be re-tested. If the label has not been pierced, follow the recommendation as stated.	1. Remove cartridge from bay. a. Reset bay to clear the error b. Re-insert cartridge in any available bay 2. If the cartridge is not able to be initialized on the second try and again generates an error during pre-flight check, this indicates an issue with the cartridge. This cartridge should be discarded following laboratory procedures and the sample should be repeated using a new cartridge. Bay(s) should be reset to clear the errors. Please contact Technical support to alert them of the issue If the bay remains in an error state (flashing red) after the cartridge has been removed, then it must be reset through the Bay Configuration menu before it can be used to run cartridges.
Test did not finish	"Bay heater failure" "Bay main / fluid motor failure" "Bay voltage failure" "Bay sub-system communication timeout" "Cartridge failure" "The cartridge initialization test failed" "Bay over pressured" "Bay auto-calibration failure" "Bay temperature out of range" "The system rejected an attempt to process a previously used cartridge" "The system was unable to eject the cartridge from the bay"	This type of error occurs during the run, after pre-flight checks completed and prevents the cartridge from being processed to completion.	Reagents have been consumed and the cartridge cannot be reused. Contact Roche Technical Support and proceed with repeat testing the sample using a new cartridge. If the bay remains in an error state (flashing red) after the cartridge has been removed, then it must be reset through the Bay Configuration menu before it can be used to run cartridges.
Invalid		This is an error that results in no valid results being generated. A test report will be generated, but all targets and internal control will be invalid.	Reagents have been consumed and the cartridge cannot be reused. Contact Roche Technical Support and proceed with repeat testing the sample using a new cartridge.

Technical Support (United States)

Roche Technical support is available 24 hours a day, 7 days a week to provide the highest level of customer support and satisfaction.

GenMark Diagnostics, Inc. A Member of the Roche Group
5964 La Place Court
Carlsbad, CA 92008 USA

In the US, please contact:
Technical support: 833.943.6627 (833.9GENMAR) or cad.technical_support_us@roche.com.
Customer service: 1-800-428-5076

Technical Support (International)

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

GLOSSARY OF SYMBOLS

Symbol	Description	Symbol	Description
LOT	Batch Code	C. LOT	Cartridge Lot
IVD	In vitro diagnostic medical device	EC REP	Authorized representative in the European Community
SN	Serial number	REF	Catalog number
CE	European Union Conformity		Consult instructions for use
	Manufacturer		Use by date YYYY-MM-DD
Σ	Contains sufficient for <n> tests		Caution
	Oxidizers		Irritant, dermal sensitizer, acute toxicity (harmful), narcotic effects, respiratory tract irritation
Rx Only	For prescription use only	UK CA	UK Conformity Assessed
	Biological risks		Lower limit of temperature
	Upper limit of temperature		Temperature range
UDI	Unique Device Identifier	GTIN	Global Trade Identification Number
	Single Use		Importer
Roche PN	Roche Part Number		

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DOCUMENT REVISION

Document Revision Information	
Rev. A 01/2019	Original document
Rev. B 11/2019	Updated technical support contact info; Reporting of N/A for resistance genes and external control information
Rev. C 02/2020	Updated errors in table numbering
Rev. D 04/2021	Added limitation about cross-reactivity of S. pneumoniae and S. mitis; updated specimen stability dating
Rev. E 06/2023	IVDR requirement updates. Updated Emergo address. UKCA requirement updates. Updated technical support contact, website, part number information, and Glossary of Symbols.
Doc Rev. 1.0 12/2023	First publishing for Branchburg based on IFU PI1079-E. Updated branding from GenMark's ePlex® to cobas® eplex. Updated SDS website information in **Safety** section. 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

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