December 2024

QIAstat-Dx® Gastrointestinal Panel 2 Summary of Safety and Performance

Version 1

IVD

For In vitro Diagnostic Use

For use with QIAstat-Dx Analyzer 1.0, QIAstat-Dx Analyzer 2.0, and QIAstat-Dx Rise

CE 0197

REF 691413

QIAGEN GmbH, QIAGEN Strasse 1, 40724 Hilden, GERMANY

R2

Summary of Safety and Performance

This Summary of Safety and Performance (SSP) is intended to provide public access to an up-to-date summary of the main aspects of the safety and performance of the device.

The SSP is not intended to replace the Instructions For Use as the main document to ensure the safe use of the device, nor is it intended to provide diagnostic or therapeutic suggestions to intended users.

The following information is intended for professional users.

Document revision: 002
Date issued: December 2024
Manufacturer's reference number for the SSP: HB-3462-SPR

1. Device identification and general information	
1.1 Device trade name(s)	QIAstat-Dx® Gastrointestinal Panel 2
1.2 Manufacturer's name and address	QIAGEN GmbH, QIAGEN Strasse 1, 40724 Hilden GERMANY
1.3 Manufacturer's single registration number (SRN)	DE-MF-000004949
1. 4 Basic UDI-DI	4053228RGI2QST000000001RK
1.5 European Medical Device Nomenclature (EMDN) description / text	W0105070504 GASTROINTESTINAL INFECTIONS MULTIPLEX NA REAGENTS
1.6 Risk Class of the device	C
1.7 Indication whether it is a device for near-patient testing and/or a companion diagnostic	The device is not for near patient testing. The device is not a companion diagnostic.

1.8 Year when the first certificate was issued under Regulation (EU) 2017/746 covering the device	2024
1.9 Authorised representative if applicable; name and the SRN	Not Applicable
1.10 Notified body and the single identification number (SIN)	TÜV Rheinland LGA Products GmbH, Tillystrase 2 90431 Nürnberg, GERMANY 0197
2. Intended use of the device	
2.1 Intended purpose	The QIAstat-Dx® Gastrointestinal Panel 2 is a multiplexed nucleic acid test intended for use with the QIAstat-Dx Analyzer 1.0, QIAstat-Dx Analyzer 2.0, or the QIAstat-Dx Rise for the simultaneous qualitative detection and identification of nucleic acids from multiple viruses, bacteria, and parasites directly from stool samples in Cary-Blair or modified Cary-Blair transport media obtained from individuals with signs and/or symptoms of gastrointestinal infection. The following viruses, bacteria (including several diarrheagenic *E.coli*/*Shigella* pathotypes), and parasites are identified with the QIAstat-Dx Gastrointestinal Panel 2: • Adenovirus F40/F41 • Astrovirus • Norovirus GI/GII • Rotavirus A

	• Sapovirus (GI, GII, GIV, GV) • *Campylobacter* (*C. jejuni*, *C. coli,* and *C. upsaliensis*) • *Clostridium difficile* (toxin A/B) • Enteroaggregative *Escherichia coli* (EAEC) • *Shigella*/Enteroinvasive *Escherichia coli* (EIEC) • Enteropathogenic *Escherichia coli* (EPEC) • Enterotoxigenic *Escherichia coli* (ETEC) *lt/st* • *Salmonella* • *Plesiomonas shigelloides* • *Vibrio cholerae* • *Vibrio parahaemolyticus* • *Vibrio vulnificus* • *Yersinia enterocolitica* • *Cryptosporidium* • *Cyclospora cayetanensis* • *Entamoeba histolytica*

	• *Giardia lamblia* *Shiga-like toxin-producing *Escherichia coli* (STEC) stx1/stx2* (including specific identification of *E. coli* O157 serogroup within STEC). Concomitant culture is necessary for organism recovery and further typing of bacterial agents. The QIAstat-Dx Gastrointestinal Panel 2 is indicated as an aid in the diagnosis of specific agents of gastrointestinal illness, in conjunction with other clinical, laboratory, and epidemiological data. Positive results do not rule-out co-infection with organisms not detected by the QIAstat-Dx Gastrointestinal Panel 2. The organisms detected may not be the sole or definitive cause of the disease. QIAstat-Dx Gastrointestinal Panel 2 is not intended to monitor or guide treatment for *C. difficile* infections. Negative QIAstat-Dx Gastrointestinal Panel 2 results in the setting of clinical illness compatible with gastroenteritis may be due to infection by pathogens that are not detected by this assay test or non-infectious causes such as ulcerative colitis, irritable bowel syndrome, or Crohn's disease. The QIAstat-Dx Gastrointestinal Panel 2 also aids in the detection and identification of acute gastroenteritis in the context of outbreaks. The QIAstat-Dx Gastrointestinal Panel 2 is intended for professional use only and is not intended for self-testing. The QIAstat-Dx Gastrointestinal Panel 2 is intended for in vitro diagnostic use.

2.2 Indication(s) and target population(s)	The QIAstat-Dx Gastrointestinal Panel 2 is a multiplexed nucleic acid test intended for use with the QIAstat-Dx Analyzer 1.0, QIAstat-Dx Analyzer 2.0, or the QIAstat-Dx Rise for the simultaneous qualitative detection and identification of nucleic acids from multiple viruses, bacteria, and parasites directly from stool samples in Cary-Blair or modified Cary-Blair transport media obtained from individuals with signs and/or symptoms of gastrointestinal infection. The QIAstat-Dx Gastrointestinal Panel 2 is intended for professional use only and is not intended for self-testing. The QIAstat-Dx Gastrointestinal Panel 2 is for in vitro diagnostic use.
2.3 Limitations and/or contra-indications	• Results from the QIAstat-Dx Gastrointestinal Panel 2 are not intended to be used as the sole basis for diagnosis, treatment or other patient management decisions. • Due to high rates of asymptomatic carriage of *Clostridium difficile,* especially in very young children and hospitalized patients, the detection of toxigenic *C. difficile* should be interpreted within the context of guidelines developed by the testing facility or other experts. • For prescription use only. • The QIAstat-Dx Gastrointestinal Panel 2 is not intended for testing of samples other than those described in these Instructions for Use. The performance of this test has only been validated with human stool collected in Cary- Blair transport medium, according to the media manufacturers' instructions. It has not been validated for use with other stool transport media, rectal swabs, raw stool, vomitus, or endoscopy stool aspirates. The QIAstat- Dx Gastrointestinal Panel 2 should not be used to test Cary-Blair vials from collection devices that have been overfilled

	with stool. Only stool resuspended following the collection device manufacturer's instructions should be used. • The detection of viral, bacterial, or parasitic sequences is dependent upon proper specimen collection, handling, transportation, storage, and preparation (including extraction). Failure to observe proper procedures in any one of these steps can lead to incorrect results. There is a risk of false negative values resulting from improperly collected, transported, or handled specimens. • Positive results do not rule out co-infection with organisms not included in the QIAstat-Dx Gastrointestinal Panel 2. The agent detected may not be the definitive cause of the disease. • Not all agents of acute gastrointestinal infection are detected by this assay. • The QIAstat-Dx Gastrointestinal Panel 2 is intended to be used in conjunction with standard of care culture for organism recovery, serotyping and/or antimicrobial susceptibility testing where applicable. • The QIAstat-Dx Gastrointestinal Panel 2 can be used only with the QIAstat-Dx Analyzer 1.0, the QIAstat-Dx Analyzer 2.0, and QIAstat-Dx Rise. • The identification of multiple diarrheagenic *E. coli* pathotypes has historically relied upon phenotypic characteristics, such as adherence patterns or toxigenicity in certain tissue culture cell lines. The QIAstat-Dx Gastrointestinal Panel 2 targets genetic determinants characteristic of most pathogenic strains of these organisms but may not detect all strains having phenotypic characteristics of a pathotype. In particular, the QIAstat- Dx Gastrointestinal Panel 2 will only detect Enteroaggregative *E. coli* (EAEC) strains carrying the *aggR*

	and/or *aatA* markers on the pAA (aggregative adherence) plasmid; it will not detect all strains exhibiting an aggregative adherence pattern. • Genetic virulence markers associated with diarrheagenic *E. coli /Shigella* pathotypes are often carried on mobile genetic elements (MGEs) that can be transferred horizontally between different strains, therefore "Detected" results for multiple diarrheagenic *E. coli/Shigella* may be due to co-infection with multiple pathotypes or, less frequently, may be due to the presence of a single organism containing genes characteristic of multiple pathotypes. An example of the latter is the 2019 *E. coli* hybrid ETEC/STEC strains found in Sweden. • The QIAstat-Dx Gastrointestinal Panel 2 detects Enteropathogenic *E. coli* (EPEC) through targeting of the *eae* gene, which encodes the adhesin intimin. As some Shiga-like toxin- producing *E. coli* (STEC) also carry *eae* (in particular, strains identified as enterohemorrhagic *E. coli*; EHEC), the QIAstat- Dx Gastrointestinal Panel 2 cannot distinguish between STEC containing *eae* and a co-infection of EPEC and STEC. Therefore, the EPEC result is not applicable (N/A) and not reported for specimens in which STEC has also been detected. In rare cases, STEC may be reported as EPEC when a STEC carrying *eae* (EHEC) is present in a specimen below the LoD of the STEC oligonucleotide design(s). Rare instances of other organisms carrying *eae* have been documented; e.g., *Escherichia albertii*, and *Shigella boydii*. • *Shigella dysenteriae* serotype 1 possess a shiga toxin gene (*stx*) that is identical to the *stx1* gene of STEC. Stx genes have been more recently found in other Shigella species (e.g., *S. sonnei* and *S. flexneri*). The detection of

	both *Shigella*/Enteroinvasive *E. coli* (EIEC) and STEC *stx1/stx2* analytes in the same specimen may indicate the presence of *Shigella* species such as *S. dysenteriae*. Rare instances of the detection of Shiga-like toxin genes in other genera/species have been reported; e.g., *Acinetobacter haemolyticus*, *Enterobacter cloacae* and *Citrobacter freundii*. • *E. coli* O157 result is only reported as specific serogroup identification in association with STEC *stx1/stx2*. While non-STEC O157 strains have been detected in human stool, their role in disease has not been established. Serotype O157 EPEC has been identified and will be detected by the QIAstat-Dx Gastrointestinal Panel 2 (by the EPEC oligonucleotides design) due to their carriage of the *eae* gene. • The QIAstat-Dx Gastrointestinal Panel 2 cannot distinguish between infections with a single toxigenic STEC O157 or rare co-infections of STEC (non-O157) with a *stx1/stx2*-negative E. coli O157. • This test only detects *Campylobacter jejuni*, *C. coli*, and *C. upsaliensis* and does not differentiate between these three species of *Campylobacter*. Additional testing is required to differentiate between these species and to detect other *Campylobacter* species that may be present in stool specimens. In particular the *Campylobacter upsaliensis* oligonucleotides design may cross- react with the *Campylobacter* species *C. lari* and *C. helveticus* organisms. • Negative results do not exclude the possibility of gastrointestinal infection. Negative test results may occur from sequence variants in the region targeted by the assay, the presence of inhibitors, technical errors, sample

	mix-ups, or an infection caused by an organism not detected by the panel. Test results may also be affected by use of certain medications (e.g., calcium carbonate), concurrent antimicrobial therapy or levels of organism in the sample that are below the limit of detection for the test. Sensitivity in some clinical settings may differ from that described in the Instructions for Use. Negative results should not be used as the sole basis for diagnosis, treatment, or other management decisions. • Organism and amplicon contamination may produce erroneous results for this test. Particular attention should be given to the Laboratory Precautions noted under the Laboratory Precautions section. • There is a risk of false- positive values resulting from cross-contamination by target organisms, their nucleic acids or the amplified product, or from non-specific signals in the assay. • There is a risk of false negative results due to the presence of strains with sequence variability in the target regions of the oligonucleotides design. Refer to the inclusivity testing section of the Instructions for Use for additional information. • The performance of the QIAstat-Dx Gastrointestinal Panel 2 has not been established in individuals who received Rotavirus A vaccine. Recent oral administration of a Rotavirus A vaccine may cause positive results for Rotavirus A if the virus is passed in the stool. • The performance of this test has not been evaluated for immunocompromised individuals. • The performance of this test has not been established for monitoring treatment of infection with any of the targeted microorganisms.

	• Analyte targets (virus, bacteria, or parasite nucleic acid sequences) may persist in vivo, independent of virus, bacteria, or parasite viability. Detection of analyte target(s) does not guarantee that the corresponding live organism(s) is present, or that the corresponding organism(s) is the causative agent for clinical symptoms. • Underlying polymorphisms in primer-binding regions can affect the targets being detected and subsequently the test results returned. • Positive and negative predictive values are highly dependent on prevalence. False negative test results are more likely when prevalence of disease is high. False positive test results are more likely when prevalence is low. • The effect of interfering substances has only been evaluated for those listed in the labeling at its indicated amount or concentration. Interference by substances other than those described in the "Interfering Substances" section of the Instruction for Use can lead to erroneous results. • Cross- reactivity with gastrointestinal tract organisms other than those listed in the "Analytical Specificity" section of the package insert may lead to erroneous results. • This test is a qualitative test and does not provide the quantitative value of detected organism present. • The assay sensitivity to detect *Cyclospora cayetanensis*, Adenovirus F41, *Entamoeba histolytica,* and the Shiga-like toxin- producing *Escherichia coli* (STEC) might be reduced up to 3.16-fold when using half-input sample volume (100 µL) workflow detailed in "Appendix C: Additional instructions for use" of the Instruction for Use.

3. Device description	
3.1 Description of the device, including the conditions to use the device	**a) General description of the device, including its intended purpose and intended users** The QIAstat-Dx Gastrointestinal Panel 2 Cartridge is a disposable plastic device that allows performance of fully automated molecular assays for the detection of gastrointestinal pathogens. The main features of the QIAstat-Dx Gastrointestinal Panel 2 Cartridge include compatibility with a liquid sample type, hermetical containment of the pre-loaded reagents necessary for testing, and true walk-away operation. All sample preparation and assay testing steps are performed within the cartridge. All reagents required for the complete execution of a test run are pre-loaded and self-contained in the QIAstat-Dx Gastrointestinal Panel 2 Cartridge. The user does not need to come in contact with and/or manipulate any reagents. After the sample is manually loaded, the diagnostic tests with the QIAstat-Dx Gastrointestinal Panel 2 are performed on the QIAstat-Dx Analyzer 1.0, the QIAstat-Dx Analyzer 2.0, or QIAstat-Dx Rise. All of the sample preparation and analysis steps are performed automatically by the QIAstat-Dx Analyzer 1.0, the QIAstat-Dx Analyzer 2.0, or QIAstat-Dx Rise. The QIAstat-Dx Analyzer 1.0, QIAstat-Dx Analyzer 2.0 and QIAstat-Dx Rise house air filters for both incoming and outgoing air, further safeguarding the environment. After testing, the cartridge stays hermetically closed at all times, greatly enhancing its safe disposal.

	Within the cartridge, multiple steps are automatically performed in sequence using pneumatic pressure to transfer samples and fluids via the transfer chamber to their intended destinations. Stool samples should be collected and handled according to the Cary-Blair transport medium manufacturer's recommended procedures. This kit is intended for professional use. The product is to be used only by personnel specifically instructed and trained in molecular biology techniques and familiar with this technology. **b) Description of the principle of the assay method or principles of operation of the instrument** Stool samples are transferred to Cary-Blair transport media following the collection device manufacturer's instructions. Once the sample is loaded into the cartridge it can be inserted into the instrument The principle of the assay is a multiplex PCR test carried out within different reaction chamber in the cartridge: The following steps occur: - Sample pre-treatment using chemical buffers to remove commonly found inhibitory substances in stool from DNA/RNA - Resuspension of Internal Control (IC) and Proteinase K - Cell Lysis: a mechanical lysis (rotation of beads) and a chemical lysis

<table>
<tr><td></td><td>- Purification via a silica membrane as the DNA/RNA binds to it

- Mixing purified nucleic acid with lyophilized components of the PCR (Master Mix)

- Aliquoting and PCR – the sample is distributed to the reaction chambers within the cartridge where the air-dried primers and probes are. Within each reaction chamber, a reverse-transcription step followed by real time, multiplex PCR (RT-PCR) is performed.</td></tr>
<tr><td>3.2 In case the device is a kit, description of the components (including regulatory status of components, for example, IVDs, medical devices and any Basic UDI-DIs)</td><td>The kit contents are:

6 individually packaged cartridges containing all reagents needed for sample preparation and multiplex real-time RT-PCR, plus Internal Control.
6 individually packaged transfer pipettes for dispensing liquid sample into the QIAstat-Dx Gastrointestinal Panel 2 Cartridge.

The kit contents are not sold separately.

The QIAstat-Dx Gastrointestinal Panel 2 meets the definition of an in vitro diagnostic device (IVDR Article 2(2)) since it is intended for the detection and identification of pathogens associated with gastrointestinal illness and therefore provides information on the physiological state.

Risk Class C (Annex VIII Rule 3 (c))</td></tr>
<tr><td>3.3 A reference to previous generation(s) or variants if such exists, and a description of the differences</td><td>The difference between the subject device, QIAstat-Dx Gastrointestinal Panel 2, and the previous version, QIAstat-Dx Gastrointestinal Panel, are listed in the table below.

<table><tr><td></td><td>QIAstat-Dx Gastrointestinal Panel 2 (Cat. No.</td><td>QIAstat-Dx Gastrointestinal</td></tr></table></td></tr>
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	691413 and Cat. No 691412 IVDD version)	**Panel (Cat. No. 691411)**
Sample collection, preparation and processing	No specific collection device is required. Clinical performance was established using Para-Pak® C&S collection devices and FecalSwab™ #4C024S from Copan.	No specific collection device is required. Clinical performance was established using FecalSwab #4C024S from Copan collection device.
Internal control	The internal control was moved to its own reaction chamber, enabling it to be run as a singleplex reaction. This improves the robustness of the control assay.	The internal control shares a reaction chamber with other targets.
Target differentiation	The panel differentiates the Shiga-like toxin genes stx1 and stx2, produced by diarrheagenic Shiga toxin-producing *E. coli* (EHEC/STEC). This information can be used to determine the risk of certain patient populations to hemolytic uremic syndrome (HUS) and therefore can help provide	The panel does not differentiate the STEC toxin genes stx1 and stx2

		improved patient monitoring.	
	Inclusivity	The inclusivity of some targets was upgraded to cover a wider range of genetic variability.	The inclusivity of some targets was limited due to the smaller number of strains covered.
	Shelf Life	9 months	6 months
3.4 Description of accessories intended to be used in combination with the device	Not applicable.		
3.5 Description of any other devices and products which are intended to be used in combination with the device	QIAstat-Dx Gastrointestinal Panel 2 is designed for use with the QIAstat-Dx Analyzer 1.0, the QIAstat-Dx Analyzer 2.0, and QIAstat-Dx Rise. Please note that the Assay Definition File (ADF) for the QIAstat-Dx Gastrointestinal Panel 2 is available at www.qiagen.com.		
4. Reference to any harmonised standards and CS applied			
4 Harmonised standards and Common Specifications (CS) applied	• EN ISO 13485:2016 + AC:2018 + A11:2021 Medical devices - Quality management systems - Requirements for regulatory purposes (ISO 13485:2016) • EN ISO 14971:2019+A11:2021 Medical devices – Application of risk management to medical devices		

	• EN ISO 15223-1:2021 Medical devices – Symbols to be used with information to be supplied by the manufacturer – Part 1: General requirements (ISO 15223-1:2021) • EN 13612:2002 Performance Evaluation of In vitro Diagnostic Medical Devices • EN ISO 18113-1:2011 In vitro diagnostic medical devices – Information supplied by the manufacturer (labelling) – Part 1: Terms, definitions and general requirements • EN ISO 18113-2:2011 *In vitro* diagnostic medical devices - Information supplied by the manufacturer (labelling) - Part 2: In vitro diagnostic reagents for professional use. In vitro diagnostic medical devices – Information supplied by the manufacturer (labelling) • EN 62304:2006+A1:2015 Medical device software – Software life-cycle processes • EN 62366-1:2015 +AC:2015+AC:2016+ A1:2020 Medical devices Part 1: Application of usability engineering to medical devices • ISO 20916:2019 *In vitro* diagnostic medical devices - Clinical performance studies using specimens from human subjects - Good study practice (ISO 20916) • EN ISO 23640:2015 In vitro diagnostic medical devices - Evaluation of stability of in vitro diagnostic reagents

	• EN 13975:2003 Sampling Procedures used for acceptance testing of in vitro diagnostic medical devices – statistical aspects (the list includes existing harmonized standards and ones listed to be harmonized)
5. Risks and warnings	
5.1 Residual risks and undesirable effects	Risks have been mitigated as far as possible and deemed as acceptable. There are no undesirable effects.
5.2 Warnings and precautions	For in vitro diagnostic use. The QIAstat-Dx Gastrointestinal Panel 2 is to be used by laboratory professionals trained in the use of QIAstat-Dx Analyzer 1.0, the QIAstat-Dx Analyzer 2.0, and the QIAstat-Dx Rise. Please be aware that you may be required to consult your local regulations for reporting serious incidents that have occurred in relation to the device to the manufacturer and the regulatory authority in which the user and/or the patient is established. When working with chemicals, always wear a suitable lab coat, disposable gloves, and protective goggles. For more information, please consult the appropriate safety data sheets (SDSs). These are available online in convenient and compact PDF format at www.qiagen.com/safety, where you can find, view, and print the SDS for each QIAGEN kit and kit component. Observe standard laboratory procedures for keeping the working area clean and contamination-free. Guidelines are outlined in publications such as the Biosafety in Microbiological and Biomedical Laboratories from the Centers for Disease Control and Prevention and the National Institutes of Health".

	Specimens and samples are potentially infectious. Discard sample and assay waste according to your local safety procedures. Always wear appropriate personal protective equipment and follow your institution's safety procedures for handling biological samples. Handle all samples, used cartridges, and transfer pipettes as if they are capable of transmitting infectious agents. Always observe safety precautions as outlined in relevant guidelines, such as the Clinical and Laboratory Standards Institute® (CLSI) *Protection of Laboratory Workers from Occupationally Acquired Infections; Approved Guideline* (M29), or other appropriate documents provided by local authorities. The QIAstat-Dx Gastrointestinal Panel 2 Cartridge is a closed, single-use device that contains all reagents needed for sample preparation and multiplex real-time RT-PCR within the QIAstat Dx Analyzer 1.0, the QIAstat-Dx Analyzer 2.0, and QIAstat-Dx Rise. Do not use a QIAstat-Dx Gastrointestinal Panel 2 Cartridge that is past its expiration date, appears damaged, or leaks fluid. Dispose of used or damaged cartridges in accordance with all national, state, and local health and safety regulations and laws. The following hazard and precautionary statements apply to components of the QIAstat-Dx Gastrointestinal Panel 2. 

	Contains: ethanol; guanidine hydrochloride; guanidine thiocyanate; isopropanol; proteinase K; t-Octylphenoxypolyethoxyethanol. Danger! Highly flammable liquid and vapor. Harmful if swallowed or if inhaled. May be harmful in contact with skin. Causes severe skin burns and eye damage. May cause allergy or asthma symptoms or breathing difficulties if inhaled. May cause drowsiness or dizziness. Harmful to aquatic life with long lasting effects. Contact with acids liberates very toxic gas. Corrosive to the respiratory tract. Keep away from heat, hot surfaces, sparks, open flames and other ignition sources. No smoking. Avoid breathing dust/fume/gas/mist/vapors/spray. Wear protective gloves/ protective clothing/ eye protection/ face protection. Wear respiratory protection. IF IN EYES: Rinse cautiously with water for several minutes. Remove contact lenses, if present and easy to do. Continue rinsing. IF exposed or concerned: Immediately call a POISON CENTER/ doctor. Rinse mouth. Do NOT induce vomiting. Remove person to fresh air and keep comfortable for breathing. Wash contaminated clothing before reuse. Store in a well-ventilated place. Keep container tightly closed. To reduce the risk of contamination when handling stool samples, it is recommended that the below guidelines are applied: • When handling the stool sample, a biosafety cabinet, dead air box, splash shield, or face shield should be used. • The work area used for cartridge loading should be separate from the work area used for stool pathogen testing (i.e., pathogen culture, EIA) to prevent cross-contamination.

	• Prior to sample handling, the work area should be thoroughly cleaned using 10% bleach or similar disinfectant. • QIAstat-Dx Gastrointestinal Panel 2 Cartridges and samples should be processed one at a time. • Change gloves prior to removing cartridges from shipping boxes. • Change gloves and clean the work area between processing each sample. • Dispose of used cartridges in a biohazard container immediately after the run is completed and avoid excessive handling. **Precautions Related to Public Health Reporting** State and local public health authorities have published guidelines for notification of reportable diseases in their jurisdictions (e.g., following the *Official Journal of the European Union 6.7.2018 L 170/1*, the list includes *Campylobacter enteritis*, Cholera, *Clostridium difficile* nosocomial infection, Cryptosporidiosis, Giardiasis (lambliasis), *Salmonella enteritis*, Shiga toxin/verocytotoxin-producing *E. coli* infection (STEC/VTEC), including Haemolytic-uraemic syndrome (HUS), Shigellosis and enteritis due to *Yersinia enterocolitica*) to determine necessary measures for verification of results to identify and trace outbreaks and for epidemiological investigations. Laboratories are responsible for following their state or local regulations for submission of clinical material or isolates on positive specimens to their state public health laboratories.
5.3 Other relevant aspects of safety, including a summary of any field safety	Not applicable.

corrective action (FSCA including FSN), if applicable	
6. Summary of the performance evaluation and post-market performance follow-up (PMPF)	
6.1 Summary of scientific validity of the device	Acute gastroenteritis (AGE; also called acute diarrhea, acute enteritis, enteral infection or infectious diarrhea) is prevalent globally and contributes to substantial morbidity and mortality, with an estimated 2 billion new cases each year and 1.9 million deaths among children under the age of 5 years. The majority of childhood fatalities occur in developing countries; for example, over 70% of diarrhea-related deaths among children less than 5 years old occur in Africa and South - East Asia. However, it is also a major public health issue in developed countries, responsible for approximately 76 million illnesses per year and 1,000 deaths annually in children under the age of 5 years in the United States. AGE is suspected when there is a decrease and abrupt onset of stool consistency and/or an increase in evacuation frequency, associated or not with sudden onset of vomiting, and ultimately with the presence of blood. In most children, AGE is typically present for less than 7 days and no more than 14 days. The term dysentery often appears as a synonym for AGE with bloody stools, and has also been characterized as the presence of stools with blood and/or mucus, associated with fever and abdominal cramps. AGE is caused by bacterial, viral, parasitic, and in rare cases, fungal infections. Enteric pathogens can be transmitted from contaminated food and water sources or from close contact with an infectious person. Many infectious gastroenteritis cases in the United States are associated with improperly prepared food, with

	the increasing globalization of food distribution providing new opportunities for pathogens to spread. For example, *Cyclospora cayetanensis* outbreaks in the United States have been linked to cilantro and salad mixes imported from Mexico. Increases in international travel and immigration have also expanded the breadth of enteric pathogens that clinicians need to consider in their patient population. The major viral pathogens responsible for AGE are rotavirus, norovirus, astrovirus, adenovirus and sapovirus, with rotavirus being a leading cause. The prevalence of viral gastroenteritis is similar in developed and developing countries, although infection rates change seasonally and are influenced by local weather factors including temperature, relative humidity and rainfall. Bacterial pathogens responsible for AGE include *Campylobacter, C. difficile, E. coli, Salmonella, P. shigelloides, V. cholerae. V. parahaemolyticus, V. vulnificus, Y. enterocolitica, Cryptosporidium, C. cayetanensis, E. histolytica* and *G. lambia*. Transmission depends on the pathogen but may be foodborne or waterborne and occur via the fecal-oral route. Coinfection exists between enteric bacteria and viruses, and this may play a critical role in disease progression. The etiological agents of AGE in developing countries are usually unknown and can lead to overuse or misuse of antibiotics, which may increase antibiotic resistance. Timely detection and treatment of gastrointestinal (GI) pathogens may prevent adverse patient outcomes, mitigate disease transmission, and inform on appropriate. Identifying the infectious agent may aid decision-making in terms of treatment, isolation, management in the

	community or hospital, and further investigations for non-infectious causes of diarrhea. Treatment for AGE depends on the etiology of the disease, and diagnosis of the responsible pathogen is important for guiding treatment decisions.
6.2 Summary of performance data from the equivalent device, if applicable	Not Applicable
6.3 Summary of performance data from conducted studies of the device prior to CE-marking	See Appendix 01 (Analytical), Appendix 02 (Clinical) - extracted from the Instruction for Use
6.4 Summary of performance data from other sources, if applicable	Not Applicable
6.5 An overall summary of the performance and safety	The overall performance and safety of the QIAstat-Dx Gastrointestinal Panel 2 is based on: Scientific Validity Assessment of available and retrieved data relevant to QIAstat-Dx Gastrointestinal Panel 2 and its intended purpose and consensus expert opinions from international guidelines demonstrate the scientific validity of the QIAstat-Dx Gastrointestinal Panel 2 for its Intended Use. Analytical Performance

	The assessment of these studies showed that the analytical performance of QIAstat-Dx Gastrointestinal Panel 2 is adequate for its Intended Use. Clinical Performance Assessment based on clinical performance studies demonstrating clinical performance indicators for sensitivity or positive percent agreement value (PPA) and specificity or negative percent agreement (NPA) meets user needs and/or customer requirements and intended use of the assay — overall QIAstat Gastrointestinal Panel 2 PPA is 95.31% (95% CI 94.13%-96.31 %) and NPA is 99.80% (95% CI 99.75%-99.84%). A systematic literature review was also carried out and evidence of similar device QIAstat-Dx Gastrointestinal Panel was demonstrated. The assessment of these sources and data showed that the clinical performance of the QIAstat-Dx Gastrointestinal Panel 2 is adequate for its Intended Use. The assessment of scientific validity, analytical performance, and clinical performance allows to constitute the clinical evidence for QIAstat-Dx Gastrointestinal Panel 2. The benefit-risk assessment based on systematic literature and database review, risk assessment activities (medical risk assessment, design, and system risk assessment), supported a favourable benefit-risk ratio for QIAstat-Dx Gastrointestinal Panel 2.

	The favourable benefit-risk ratio and the established clinical evidence of QIAstat-Dx Gastrointestinal Panel 2 demonstrates scientifically, by reference to the state of art, that the intended clinical benefit of the direct detection and identification of nucleic acids from the multiple viruses, bacteria, and parasites in stool specimens listed in the device intended use is achieved and the device is safe. The assay supports physicians in the diagnosis of specific agents of gastrointestinal infections, in conjunction with other clinical, laboratory, and epidemiological data.
6.6 Ongoing or planned post-market performance follow-up	Based on the collected evidence it was concluded that the QIAstat-Dx Gastrointestinal Panel 2 is safe and effective for its intended use and no unacceptable residual risks remain. However, an additional shelf life study will be performed to test the upper limit (25±3°C) of the intended room temperature storage claim (15–25°C) and to support the current shelf life claim of 9 months.
7. Metrological traceability of assigned values	
7.1 Explanation of the unit of measurement, if applicable	Not applicable
7.2 Identification of applied reference materials and/or reference measurement procedures of higher order used by the	Not applicable

manufacturer for the calibration of the device	
8. Suggested profile and training for users	
8.1 Suggested profile and training for users	The QIAstat-Dx Gastrointestinal Panel 2 is a multiplexed nucleic acid test intended for use with the QIAstat-Dx Analyzer 1.0, the QIAstat-Dx Analyzer 2.0, or the QIAstat-Dx Rise for the simultaneous qualitative detection and identification of nucleic acids from multiple viruses, bacteria, and parasites directly from stool samples in Cary-Blair or modified Cary-Blair transport media obtained from individuals with signs and/or symptoms of gastrointestinal infection. The QIAstat-Dx Gastrointestinal Panel 2 is intended for professional use only and is not intended for self-testing. The QIAstat-Dx Gastrointestinal Panel 2 is for in vitro diagnostic use. The product is to be used only by personnel specifically instructed and trained in molecular biology techniques and familiar with this technology.

Revision History

SSP Revision Number	Date issued	Change description	Revision validated by the Notified Body
01	October 2024	1st revision	☑ Yes Validation language: English □ No (only applicable for class C (IVDR, Article 48 (7)) for which the SSP is not yet validated by the NB)
02	December 2024	Included QIAstat-Dx Analyzer 2.0 as another instrument the panel can be used with. Alignment of Appendices with analytical and clinical performance sections of the handbook.	☑ Yes Validation language: English □ No (only applicable for class C (IVDR, Article 48 (7)) for which the SSP is not yet validated by the NB)

Appendix

Appendix 01 Analytical Performance

The analytical performance shown below was demonstrated using QIAstat-Dx Analyzer 1.0. The QIAstat-Dx Analyzer 2.0 uses the same Analytical Module as QIAstat-Dx Analyzer 1.0; therefore the performance is not impacted by QIAstat-Dx Analyzer 2.0.

With regards to QIAstat-Dx Rise, specific studies to demonstrate the carryover and the repeatability were executed. The rest of analytical performance parameters shown below were demonstrated using QIAstat-Dx Analyzer 1.0. The QIAstat-Dx Rise uses the same Analytical Module as QIAstat-Dx Analyzer 1.0 therefore the performance is not impacted by QIAstat-Dx Rise.

Limit of Detection

The Limit of Detection (LoD), is defined as the lowest concentration at which ≥95% of the tested samples generate a positive call.

The LoD for each of the QIAstat-Dx Gastrointestinal Panel 2 target pathogenic organisms was assessed, using in total 48 pathogen strains, by analyzing serial dilutions of analytical samples prepared from culture isolates from commercial suppliers (e.g., ZeptoMetrix® and ATCC®), confirmed clinical isolates, or artificial samples for target analytes commercially unavailable. Each sample tested was prepared in human stool matrix, which consists of a pool of previously tested negative clinical stool specimens resuspended in Cary-Blair transport medium.

Each of the 48 strains was tested in human stool matrix prepared following the manufacturer's instructions for the Para-Pak C&S® collection device. A matrix equivalency study between Para-Pak C&S and FecalSwab transport media was conducted to support the conclusions in the section.

Individual LoD values for each QIAstat-Dx Gastrointestinal Panel 2 target is shown in Table 1.

Table 1. LoD values obtained for the different gastrointestinal target strains tested with the QIAstat-Dx Gastrointestinal Panel 2

Pathogen	Strain	Source	Concentration (molecular units)* copies/mL	Concentration (microbiological units)	Detection rate
Campylobacter	*Campylobacter coli* 76-GA2 [LMG 21266]	ATCC 43478	5802	1.2 CFU/mL	20/20
	Campylobacter coli CIP 7080	ATCC 33559	8941	0.6 CFU/mL	20/20
	Campylobacter jejuni Z086	ZeptoMetrix 0801650	14491	1660 CFU/mL	20/20
	Campylobacter jejuni subsp. Jejuni RM3193	ATCC BAA-1234	7210	110 CFU/mL	19/20
	Campylobacter upsaliensis NCTC 11541	ZeptoMetrix 0801999	56165	2259.4 CFU/mL	20/20
	Campylobacter upsaliensis RM3195	ATCC BAA-1059	7631	35 CFU/mL	19/20
Clostridium difficile toxin A/B	(NAP1A) Toxinotype III A+ B+	ZeptoMetrix 0801619	11083	515 CFU/mL	19/20
	Toxinotype 0 A+ B+	ATCC 9689	101843	853.2 CFU/mL	20/20
Plesiomonas shigelloides	Z130	ZeptoMetrix 0801899	481	2291 CFU/mL	20/20
	Bader	ATCC 14029	116	2.7 CFU/mL	19/20
Salmonella	*Salmonella enterica* Serovar choleraseus	ATCC 13312	647	91.6 CFU/mL	20/20
	Salmonella enterica Serovar Typhimurium Z005	ZeptoMetrix 0801437	1441	4518.8 CFU/mL	20/20

Table 1. LoD values obtained for the different gastrointestinal target strains tested with the QIAstat-Dx Gastrointestinal Panel 2 (continued)

Pathogen	Strain	Source	Concentration (molecular units)* copies/mL	Concentration (microbiological units)	Detection rate
Vibrio cholerae	Z132; toxigenic	ZeptoMetrix 0801901	28298	13600 CFU/mL	20/20
	Z133; non-toxigenic	ZeptoMetrix 0801902	79749	54668 CFU/mL	20/20
Vibrio parahaemolyticus	EB 101	ATCC 17802	12862	1600 CFU/mL	20/20
	Z134	ZeptoMetrix 0801903	8904	143 CFU/mL	20/20
Vibrio vulnificus	329 [CDC B3547]	ATCC 33817	109131	260 CFU/mL	20/20
	324 [CDC B629]	ATCC 27562	2983	1905.1 CFU/mL	20/20
Yersinia enterocolitica	Z036	ZeptoMetrix 0801734	719	2070 CFU/mL	20/20
	subsp. *enterocolitica* NTCC 11175, Biotype 4, serotype 3	ATCC 700822	2496	120.1 CFU/mL	20/20
Enteroaggregative *E. coli* (EAEC)	*Escherichia coli* 92.0147, O77:HN	ZeptoMetrix 0801919	1075	634 CFU/mL	20/20
	Escherichia coli CDC3250-76, O111a, 111b: K58:H21	ATCC 29552	842	87 CFU/mL	19/20
Enteroinvasive *E. coli* (EIEC)/ *Shigella*	*Shigella sonnei* Z004	ZeptoMetrix 25931	488	0.2 CFU/mL	20/20
	Escherichia coli CDC EDL 1282, O29:NM	ATCC 43892	1431	41.3 CFU/mL	20/20

Table 1. LoD values obtained for the different gastrointestinal target strains tested with the QIAstat-Dx Gastrointestinal Panel 2 (continued)

Pathogen	Strain	Source	Concentration (molecular units)* copies/mL	Concentration (microbiological units)	Detection rate
Enteropathogenic *E. coli* (EPEC)	*Escherichia coli* O111:NM (EPEC)	ZeptoMetrix 0801747	1817	2581.7 CFU/mL	20/20
	Escherichia coli 7.1493; EPEC; O84:H28	Zeptometrix 0801938	29021	1190 CFU/mL	20/20
Enterotoxigenic *E. coli* (ETEC) *lt/st*	*Escherichia coli* H10407, O78:H11	ATCC 35401	367	10.1 CFU/mL	19/20
	Escherichia coli ETEC; ST+, LT+	ZeptoMetrix 0801624	855	567 CFU/mL	20/20
Shiga-like toxin-producing *E. coli* (STEC) *stx1/stx2*	*Escherichia coli* O26:H4	ZeptoMetrix 0801748	2012	726.8 CFU/mL	20/20
Shiga-like toxin-producing *E. coli* (STEC) *E. coli* O157	*Escherichia coli* O157:H7; EDL933	ZeptoMetrix 0801622	1217	2281.5 CFU/mL	STEC stx 1: 19/20 STEC stx2: 19/20 O157: 19/20
Cryptosporidium	*Cryptosporidium hominis*	Public Health Wales UKM 84	357	N/A	20/20
	Cryptosporidium parvum – Iowa isolate	Waterborne® P102C	661	N/A	20/20

Table 1. LoD values obtained for the different gastrointestinal target strains tested with the QIAstat-Dx Gastrointestinal Panel 2 (continued)

Pathogen	Strain	Source	Concentration (molecular units)* copies/mL	Concentration (microbiological units)	Detection rate
Cyclospora ayetanensis	N/A	LACNY-Clinical sample LAC2825	53	N/A	19/20
	N/A	LACNY Clinical sample LAC2827	137	N/A	20/20
Entamoeba histolytica	HM-1:IMSS (Mexico City 1967	ATCC 30459	7	0.2 cells/mL	20/20
	HK-9 (Korea)	ATCC 30015	1	0.13 cells/mL	19/20
Giardia lamblia	WB (Bethesda)	ATCC 30957	11850	790 cells/mL	19/20
	Portland-1	ATCC 30888	14500	635 cells/mL	20/20
Adenovirus F40/F41	Type 40 (Dugan)	ZeptoMetrix 0810084CF	11726	0.1 $TCID_{50}$/mL	20/20
	Type 41 (Tak)	ZeptoMetrix 0810085CF	979	0.05 $TCID_{50}$/mL	19/20
Astrovirus	ERE IID 2371 (type 8)	Zeptometrix 0810277CF	11586371	11.7 $TCID_{50}$/mL	20/20
	ERE IID 2868 (type 4)	Zeptometrix 0810276CF	52184	1.3 $TCID_{50}$/mL	19/20
Norovirus GI/GII	GI.1 (recombinant)	ZeptoMetrix 0810086CF	24629	891.1 $TCID_{50}$/mL	19/20
	GII.4 (recombinant)	ZeptoMetrix 0810087CF	8998	10.5 $TCID_{50}$/mL	20/20

Table 1. LoD values obtained for the different gastrointestinal target strains tested with the QIAstat-Dx Gastrointestinal Panel 2 (continued)

Pathogen	Strain	Source	Concentration (molecular units)* copies/mL	Concentration (microbiological units)	Detection rate
Rotavirus A	69M	ZeptoMetrix 0810280CF	5787	436.1 $TCID_{50}$/mL	19/20
	Wa	ZeptoMetrix 0810041CF	5201	14.1 $TCID_{50}$/mL	19/20
Sapovirus	Genogroup I, genotype 1	QIAGEN Barcelona -Clinical sample GI-88	187506	N/A	20/20
	Genogroup V	Universitat de Barcelona 160523351	3007	N/A	20/20

Exclusivity (Analytical Specificity)

The analytical specificity study was carried out by in vitro testing and in silico analysis to assess the potential cross-reactivity and exclusivity of the QIAstat-Dx Gastrointestinal Panel 2. On-panel organisms were tested to assess the potential for intra-panel cross-reactivity, and Off-panel organisms were tested to evaluate cross-reactivity with organisms not covered by the panel content. The On-panel and Off-panel organisms tested are shown in Table 2 and Table 3, respectively.

Samples were prepared by single spiking organisms into negative stool resuspended in Cary-Blair at the highest concentration possible based on the organism stock, preferably at 10^5 $TCID_{50}$/mL for viral, 10^5 cells/mL for parasite targets, and 10^6 CFU/mL for bacterial targets. The pathogens were tested in 3 replicates. There was no intra-panel or Off-panel cross-reactivity for all pathogens tested in vitro, except for two non-targeted *Campylobacter* species (*C. helveticus* and *C. lari*) that cross-reacted with the Campylobacter assay oligonucleotides included in the QIAstat-Dx Gastrointestinal Panel 2.

Table 2. List of Analytical Specificity on-panel pathogens tested

Type	Pathogen	
Bacteria	*Campylobacter coli*	*Plesiomonas shigelloides*
	Campylobacter jejuni	*Salmonella enterica*
	Campylobacter upsaliensis	*Shigella sonnei*
	Clostridium difficile	*Vibrio cholerae*
	Escherichia coli (EAEC)	*Vibrio parahaemolyticus*
	Escherichia coli (EPEC)	*Vibrio vulnificus*
	Escherichia coli (ETEC)	*Yersinia enterocolitica*
	Escherichia coli (STEC)	
Parasites	*Cryptosporidium parvum*	*Entamoeba histolytica*
	Cyclospora cayetanensis	*Giardia lamblia*
Viruses	Adenovirus F41	Norovirus GII
	Astrovirus	Rotavirus A
	Norovirus GI	Sapovirus

Table 3. List of Analytical Specificity off-panel pathogens tested

Type	Pathogen (potential cross-reactant)	
Bacteria	*Abiotrophia defectiva*	*Enterobacter cloacae*
	Acinetobacter baumannii	*Enterococcus faecalis*
	Aeromonas hydrophila	*Enterococcus faecium*
	Arcobacter cryaerophilus	*Escherichia fergusonii*
	Bacillus subtilis	*Escherichia hermannii*
	Bifidobacterium bifidum	*Escherichia vulneris*
	Campylobacter fetus	*Faecalibacterium prausnitzii*
	Campylobacter gracilis	*Gardnerella vaginalis*
	Campylobacter helveticus	*Haemophilus influenzae*
	Campylobacter hominis	*Helicobacter pylori*
	Campylobacter lari	*Klebsiella pneumoniae*
	Campylobacter mucosalis	*Lactobacillus casei*
	Campylobacter rectus	*Listeria monocytogenes*
	Chamydia trachomatis	*Proteus mirabilis*
	Citrobacter freundii	*Proteus vulgaris*
	Clostridium difficile non-toxigenic	*Pseudomonas aeruginosa*
	Clostridium perfringens	*Staphylococcus aureus*
	Clostridium septicum	*Staphylococcus aureus* subsp. *Aureus*
	Clostridium tetani	*Staphylococcus epidermidis*
	Corynebacterium genitalium	*Streptococcus agalactiae*
	Enterobacter aerogenes	*Streptococcus pyogenes*
Fungi	*Aspergillus fumigatus*	*Saccharomyces boulardii*
	Candida albicans	*Saccharomyces cerevisiae*
Parasites	*Babesia microti*	*Toxoplasma gondii*
	Blastocystis hominis	*Trichomonas tenax*
	Giardia muris	

Table 3. List of Analytical Specificity off-panel pathogens tested (continued)

Type	Pathogen (potential cross-reactant)	
Viruses	Adenovirus C:2	Coronavirus 229E
	Adenovirus B:34	Coxsackievirus B3
	Adenovirus B3	Cytomegalovirus
	Adenovirus E:4a	Enterovirus 6 (*Echovirus*)
	Adenovirus serotype 1	Enterovirus 68
	Adenovirus serotype 5	Herpes Simplex Virus Type 2
	Adenovirus serotype 8	Rhinovirus 1A
	Bocavirus Type 1	

In silico predictions of potential cross-reactions showed that the following cross-reactions may occur when testing stool samples with the QIAstat-Dx Gastrointestinal Panel 2 (Table 4).

Table 1. Potential cross-reactions based on in silico analysis

QIAstat-Dx Gastrointestinal Panel 2 Target	Potential cross-reactive organisms
Enteropathogenic *E. coli* (EPEC)*	*Shigella boydii** †‡ *Escherichia albertii* *†
Campylobacter spp.	*Campylobacter lari* § *Campylobacter helveticus* §
Shiga-like toxin-producing *E. coli* (STEC) stx1	*Shigella sonnei* *‡ *Shigella dysenteriae** *Enterobacter cloacae**
Shiga-like toxin-producing *E. coli* (STEC) stx2	*Acinetobacter haemolyticus** ¶ *Citrobacter freundii** ¶ *Enterobacter cloacae** ¶ *Aeromonas caviae** ¶ *Escherichia albertii* *¶
E. coli O157	Non-STEC *E.coli* O157 strains**

* Note that these potential cross-reactions affect designs with target genes responsible of the pathogenicity of the corresponding QIAstat-Dx Gastrointestinal Panel 2 target pathogens which can be acquired within species in a known biological process in bacteria called horizontal gene transfer.

† Rare or less common *eae* intimin carrier organisms.

‡ On-panel target.

§ In vitro testing of *Campylobacter lari* and *Campylobacter helveticus* strains at high concentration confirmed potential cross-reaction of these *Campylobacter* species with the QIAstat- Gastrointestinal Panel 2 assay.

¶ Rare or less common Stx toxins producers.

**_E. coli_ O157 will only be reported by the QIAstat-Dx Gastrointestinal Panel 2 when there is a positive amplification for the _E. coli_ (STEC) design according to the calling algorithm. An infrequent case of an _E. coli_ (STEC) and an _E. coli_ O157 co-infection will not be differentiated from a single infection caused by an STEC O157:H7 strain.

Inclusivity (Analytical Reactivity)

Analytical Reactivity (Inclusivity) was evaluated with gastrointestinal pathogen isolates/strains that were selected based on clinical relevance and genetic, temporal and geographical diversity. Based on in vitro (wet) testing and in silico analysis, the QIAstat-Dx Gastrointestinal Panel 2 primers and probes are specific and inclusive for clinically prevalent and relevant strains for each pathogen tested.

In vitro (Wet) testing

QIAstat-Dx Gastrointestinal Panel 2 is inclusive for 100% (143 out of 143) of the pathogen strains tested in vitro. Most pathogen strains evaluated in wet testing (133/143) were detected at ≤ 3-fold of the corresponding LoD reference strain. (Table 5).

Table 5. Inclusivity test results for all the pathogens tested with the QIAstat-Dx Gastrointestinal Panel 2 Assay. LoD reference strain for every pathogen is written in bold

Table 5a. Inclusivity test results for *Campylobacter* strains

QIAstat-Dx target	Pathogen	Strain	Supplier	Catalog ID	Times LoD
Campylobacter	***Campylobacter coli***	**76-GA2 [LMG 21266]**	**ATCC**	**43478***	**1x LoD**
	Campylobacter coli	Z293	ZeptoMetrix	804272	1x LoD
	Campylobacter coli	CIP 7080 [1407, CIP 70.80]	ATCC	33559*	3x LoD
	Campylobacter jejuni	**Z086**	**ZeptoMetrix**	**0801650***	**1x LoD**
	Campylobacter jejuni	subsp. *jejuni* RM3193	ATCC	BAA-1234*	0.1x LoD
	Campylobacter jejuni subsp. jejuni	O:19 HL7; D3180	ATCC	BAA-218	0.1x LoD
	Campylobacter jejuni subsp. jejuni	AS-83-79	ATCC	33291	0.1x LoD
	Campylobacter jejuni subsp. doylei	NCTC 11951	ATCC	49349	0.1x LoD
	Campylobacter upsaliensis	**NCTC 11541**	**ZeptoMetrix**	**0801999***	**1x LoD**
	Campylobacter upsaliensis	RM 3195 (1994)	ATCC	BAA-1059*	0.3x LoD
	Campylobacter upsaliensis	NCTC 11541 [C231]	ATCC	43954	1x LoD

* Strain tested during LoD verification study.

Table 5b. Inclusivity test results for *Clostridium difficile* strains

QIAstat-Dx target	Pathogen	Strain	Supplier	Catalog ID	Times LoD
Clostridium difficile toxin A/B	*Clostridium difficile*	(90556-M6S) Toxinotype 0 A+ B+	ATCC	9689*	1x LoD
	Clostridium difficile	NAP1, toxinotype IIIb A+B+	ATCC	BAA-1805	1x LoD
	Clostridium difficile	5325, toxinotype V A+B+	ATCC	BAA-1875	1x LoD
	Clostridium difficile	1470, toxinotype VIII A-B+	ATCC	43598	1x LoD
	Clostridium difficile	toxinotype XII A+B+	ATCC	BAA-1812	1x LoD
	Clostridium difficile	toxinotype XXII A+B (unknown)	ATCC	BAA-1814	1x LoD
	Clostridium difficile	NAP1A, toxinotype III A+B+	ATCC	0801619*	0.1x LoD
	Clostridium difficile	NAP1, toxinotype III A+B+	ZeptoMetrix	0801620	3x LoD

*Strain tested during LoD verification study.

Table 5c. Inclusivity test results for *Plesiomonas shigelloides* strains

QIAstat-Dx target	Pathogen	Strain	Supplier	Catalog ID	Times LoD
Plesiomonas shigelloides	*Plesiomonas shigelloides*	Z130	ZeptoMetrix	0801899*	1x LoD
	Plesiomonas shigelloides	GNI 14	ATCC	51903	1x LoD
	Plesiomonas shigelloides	CDC 3085-55 [Bader M51, NCIB 9242, NCTC 10360, RH 798]	ATCC	14029*	0.3x LoD

*Strain tested during LoD verification study.

Table 5d. Inclusivity test results for *Salmonella* strains

QIAstat-Dx target	Pathogen	Strain	Supplier	Catalog ID	Times LoD
Salmonella	*Salmonella enterica*	Serovar Typhimurium Z005	ZeptoMetrix	0801437*	1x LoD
	Salmonella enterica	Subsp. Enterica, serovar Bareilly	–	NC05745	1x LoD
	Salmonella enterica	Subsp. Enterica, serovar typhi, Z152	ZeptoMetrix	0801933	0.1x LoD
	Salmonella enterica	Subsp. Enterica, serovar Enteridis, CDC K-1891 [ATCC 25928]	ATCC	13076	0.1x LoD
	Salmonella enterica	Subsp. Enterica, serovar Infantis, MZ1479 [SARB27]	ATCC	BAA-1675	0.1x LoD
	Salmonella enterica	Subsp. Enterica, serovar Montevideo, G4639	ATCC	BAA-710	0.1x LoD
	Salmonella enterica	Subsp. Enterica, serovar Javiana	–	NC06495	0.1x LoD
	Salmonella enterica	Subsp. Enterica, serovar Thompson	–	NC08496	0.1x LoD
	Salmonella enterica	Subsp. Enterica, serovar Saintpaul	–	9712	0.1x LoD
	Salmonella enterica	Subsp. Enterica, serovar Berta	–	NC05770	0.1x LoD
	Salmonella enterica	Subsp. Salame, II NCTC 10310 [JT945, SS140/61]	ATCC	700151	0.1x LoD
	Salmonella enterica	Subsp. diarizonae IIIb, 62	ATCC	29934	0.1x LoD
	Salmonella enterica	Subsp. houtenae IV, CIP 82.32 [264.66]	ATCC	43974	0.1x LoD
	Salmonella enterica	Subsp. Indica VI, CIP 102501 [F. Kauffmann 1240]	ATCC	43976	0.1x LoD

Table 5d. Inclusivity test results for *Salmonella* strains (continued)

QIAstat-Dx target	Pathogen	Strain	Supplier	Catalog ID	Times LoD
	Salmonella enterica	Subsp. Enterica, serovar Agona, CDC 873 [CDC 1111-61]	ATCC	51957	0.1x LoD
	Salmonella enterica	Subsp. Enterica, serovar Muenchen, 54	ATCC	8388	0.1x LoD
	Salmonella enterica	Subsp. Enterica, serovar Oranienburg, E1093	ATCC	9239	0.1x LoD
	Salmonella enterica	Subsp. Enterica, serovar Paratyphi B var. Java, CDC 5	ATCC	51962	0.1x LoD
	Salmonella enterica	CIP 82.33 [1224.72]	ATCC	43975	0.3x LoD
	Salmonella enterica	Subsp. Enterica, serovar Choleraesius, NCTC 5735 [1348, K.34]	ATCC	13312*	0.3x LoD
	Salmonella enterica	Subsp. Enterica, serovar Newport, C487-69	ATCC	27869	0.3x LoD
	Salmonella enterica	Subsp. Enterica, 4, 5, 12:7:-, serovar Typhimurium	–	NC13952	0.3x LoD
	Salmonella enterica	Subsp. Enterica, serovar Braenderup	–	700136	0.3x LoD
	Salmonella enterica	Subsp. Enterica, serovar Anatum	–	NC05779	0.3x LoD
	Salmonella enterica	Subps. arizonae IIIa, NCTC 7311 [CDAI 426]	ATCC	700156	0.3x LoD
	Salmonella enterica	Subsp. Enterica, serovar Heidelberg, [16]	ATCC	8326	0.3x LoD
	Salmonella enterica	Subsp. Enterica, serovar Mississippi, CDC 2012K-0487	ATCC	BAA-2739	0.3x LoD

* Strain tested during LoD verification study.

Table 5e. Inclusivity test results for *Vibrio cholerae* strains

QIAstat-Dx target	Pathogen	Strain	Supplier	Catalog ID	Times LoD
Vibrio cholerae	*Vibrio cholerae*	Z133; non-toxigenic	ZeptoMetrix	801902*	1x LoD
	Vibrio cholerae	Pacini 1854; NCTC 8021, O:1 Ogawa	CECT	514	1x LoD
	Vibrio cholerae	Z132; toxigenic	ZeptoMetrix	0801901*	0.3x LoD

* Strain tested during LoD verification study.

Table 5f. Inclusivity test results for *Vibrio parahaemolyticus* strains

QIAstat-Dx target	Pathogen	Strain	Supplier	Catalog ID	Times LoD
Vibrio parahaemolyticus	*Vibrio para-haemolyticus*	EB101 [P. Baumann 113] (Japan)	ATCC	17802*	1x LoD
	Vibrio para-haemolyticus	VP250,O1:KUT	ATCC	BAA-242	1x LoD
	Vibrio para-haemolyticus	205 [9302]	ATCC	33846	3x LoD
	Vibrio para-haemolyticus	Z134	ZeptoMetrix	0801903*	0.3x LoD

* Strain tested during LoD verification study.

Table 5g. Inclusivity test results for *Vibrio vulnificus* strains

QIAstat-Dx target	Pathogen	Strain	Supplier	Catalog ID	Times LoD
Vibrio vulnificus	*Vibrio vulnificus*	324 [CDC B9629]	ATCC	27562	1x LoD
	Vibrio vulnificus	329 [CDC B3547],Biotype 2	ATCC	33817*	1x LoD
	Vibrio vulnificus	Z473	ZeptoMetrix	804349	3x LoD

* Strain tested during LoD verification study.

Table 5h. Inclusivity test results for *Yersinia enterocolitica* strains

QIAstat-Dx target	Pathogen	Strain	Supplier	Catalog ID	Times LoD
Yersinia enterocolitica	*Yersinia enterocolitica*	Z036	ZeptoMetrix	0801734*	1x LoD
	Yersinia enterocolitica	NTCC 11175, Biotype 4, serotype 3 (O:3)	ATCC	700822*	1x LoD
	Yersinia enterocolitica	33114 [CCUG 11291, CCUG 12369, CIP 80.27, DSM 4780, LMG 7899, NCTC 12982], Biovar 1, O:8	ATCC	9610	1x LoD
	Yersinia enterocolitica	0:9	ATCC	55075	3x LoD

* Strain tested during LoD verification study.

Table 5i. Inclusivity test results for Enteroaggregative *E. coli* (EAEC) strains

QIAstat-Dx target	Pathogen	Strain	Supplier	Catalog ID	Times LoD
Enteroaggregative *E. coli* (EAEC)	Enteroaggregative *E. coli* (EAEC)	92.0147	ZeptoMetrix	0801919*	1x LoD
	Enteroaggregative *E. coli* (EAEC)	CDC3250-76, O111a, 111b: K58:H21, CVD432+, aggR+, stx1-, stx2-, eae-	ATCC	29552*	1x LoD
	Enteroaggregative *E. coli* (EAEC)	–	Vall d'Hebrón	Clinical sample; VH 529140369015	3x LoD

* Strain tested during LoD verification study.

Table 5j. Inclusivity test results for Enteropathogenic *E. coli* (EPEC) strains

QIAstat-Dx target	Pathogen	Strain	Supplier	Catalog ID	Times LoD
Enteropathogenic *E. coli* (EPEC)	Enteropathogenic *E. coli* (EPEC)	O111:NM	ZeptoMetrix	0801747*	1x LoD
	Enteropathogenic *E. coli* (EPEC)	7.1493,O84:H28	ZeptoMetrix	0801938*	1x LoD
	Enteropathogenic *E. coli* (EPEC)	Stoke W,O111:K58 (B4):H-	ATCC	33780	1x LoD

* Strain tested during LoD verification study.

Table 5k. Inclusivity test results for Enterotoxigenic *E. coli* (ETEC) strains

QIAstat-Dx target	Pathogen	Strain	Supplier	Catalog ID	Times LoD
Enterotoxigenic *E. coli* (ETEC) lt/st	Enterotoxigenic *E. coli* (ETEC) lt/st	ST+, LT+	ZeptoMetrix	0801624*	1x LoD
	Enterotoxigenic *E. coli* (ETEC) lt/st	H10407,O78:H11,LT (+)/ctx A11(+)	ATCC	35401*	0.3x LoD
	Enterotoxigenic *E. coli* (ETEC) lt/st	O27:H7,ST (+)/ LT (-)	SSI Diagnostica	82173	0.1x LoD
	Enterotoxigenic *E. coli* (ETEC) lt/st	O115:H15,ST (+)/ LT (-)	SSI Diagnostica	82174	3x LoD
	Enterotoxigenic *E. coli* (ETEC) lt/st	O169:H-,ST (-)/LT (+)	SSI Diagnostica	82172	10x LoD†

* Strain tested during LoD verification study.

Table 5l. Inclusivity test results for Enteroinvasive *E. coli* (EIEC)/*Shigella* strains

QIAstat-Dx target	Pathogen	Strain	Supplier	Catalog ID	Times LoD
Enteroinvasive *E. coli* (EIEC)/ *Shigella*	**Enteroinvasive *E. coli* (EIEC)**	**CDC EDL 1282, O29:NM**	**ATCC**	**43892***	**1x LoD**
	Enteroinvasive *E. coli* (EIEC)	O172:H-	SSI Diagnostica	82171	3x LoD
	Shigella sonnei	**NCDC 1120-66**	**ATCC**	**25931***	**1x LoD**
	Shigella boydii (Serogroup C)	Z131	ZeptoMetrix	0801900	1x LoD
	Shigella flexneri (Serogroup B)	AMC 43-G-68 [EVL 82, M134]	ATCC	9199	1x LoD
	Shigella flexneri (Serogroup B)	Z046	ZeptoMetrix	0801757	1x LoD
	Shigella sonnei (Serogroup D)	WRAIR I virulent	ATCC	29930	1x LoD
	Shigella sonnei (Serogroup D)	Z004	ZeptoMetrix	0801627	3x LoD
	Shigella boydii (Serogroup C)	AMC 43-G-58 [M44 (Type 170)]	ATCC	9207	10x LoD

* Strain tested during LoD verification study

Table 5m. Inclusivity test results for Shiga-like toxin-producing *E. coli* (STEC) (stx1-carrier strains)

QIAstat-Dx target	Pathogen	Strain	Supplier	Catalog ID	Times LoD
Shiga-like toxin producing *E. coli* (STEC) - stx1	Shiga-like toxin producing *E. coli* (STEC) - stx1	O157:H7; EDL933	ZeptoMetrix	0801622*	1x LoD
	Shiga-like toxin producing *E. coli* (STEC) - stx1	O26:H4,stx1 (+)	ZeptoMetrix	0801748*	1x LoD
	Shiga-like toxin producing *E. coli* (STEC) - stx1	O22:H8,stx1c (+), stx2b (+)	SSI Diagnostica	91350	1x LoD
	Shiga-like toxin producing *E. coli* (STEC) - stx1	O8 ,stx1d (+)	SSI Diagnostica	91349	1x LoD
	Shiga-like toxin producing *E. coli* (STEC) - stx1	Reference ATCC 35150 (EDL 931),O157:H7,stx1 (+), stx2 (+)	Microbiologics	617	1x LoD
	Shiga-like toxin producing *E. coli* (STEC) - stx1	Reference CDC 00-3039,O45:H2,unknown	Microbiologics	1098	1x LoD
	Shiga-like toxin producing *E. coli* (STEC) - stx1	O103:H2,stx1 (+)	SSI Diagnostica	82170	3x LoD
	Shiga-like toxin producing *E. coli* (STEC) - stx1	O128ac:H-,stx2f (+)	SSI Diagnostica	91355	10x LoD

* Strain tested during LoD verification study

Table 5n. Inclusivity test results for Shiga-like toxin-producing *E. coli* (STEC) (stx2-carrier strains)

QIAstat-Dx target	Pathogen	Strain	Supplier	Catalog ID	Times LoD
Shiga-like toxin producing *E. coli* (STEC) - stx2	Shiga-like toxin producing *E. coli* (STEC) - stx2	O157:H7; EDL933	ZeptoMetrix	0801622*	1x LoD
	Shiga-like toxin producing *E. coli* (STEC) - stx2	O22:H8,stx1c (+), stx2b (+)	SSI Diagnostica	91350	1x LoD
	Shiga-like toxin producing *E. coli* (STEC) - stx2	O26:H11,stx2a (+)	SSI Diagnostica	95211	1x LoD
	Shiga-like toxin producing *E. coli* (STEC) - stx2	O101:K32:H-,stx2e (+)	SSI Diagnostica	91354	0.3x LoD
	Shiga-like toxin producing *E. coli* (STEC) - stx2	Reference ATCC 35150 (EDL 931),O157:H7,stx1 (+), stx2 (+)	Microbiologics	617	3x LoD
	Shiga-like toxin producing *E. coli* (STEC) - stx2	O92,O107:K+:H48, stx2d (+)	SSI Diagnostica	91352	10x LoD
	Shiga-like toxin producing *E. coli* (STEC) - stx2	O128ac:H-,stx2f (+)	SSI Diagnostica	91355	10x LoD

* Strain tested during LoD verification study

Table 5o. Inclusivity test results for Shiga-like toxin producing *E. coli* (STEC) *stx1/stx2* O157 strains

QIAstat-Dx target	Pathogen	Strain	Supplier	Catalogue ID	Times LoD
Shiga-like toxin producing *E. coli* (STEC) O157	Shiga-like toxin producing *E. coli* (STEC) - O157	O157:H7; EDL933	ZeptoMetrix	0801622*	1x LoD
	Shiga-like toxin producing *E. coli* (STEC) O157	O128ac:H-,stx2f (+)	SSI Diagnostica	91355†	1x LoD
	Shiga-like toxin producing *E. coli* (STEC) O157	Reference ATCC 35150 (EDL 931), O157:H7, stx1 (+), stx2 (+)	Microbiologics	617	1x LoD

* Strain tested during LoD verification study.

†The *E. coli* strain 91355 from SSI Diagnostica is reported as following in its catalog: vtx2f+, eae+. However, it was found to amplify for *E. coli* O157 in both QIAstat-Dx and FilmArray devices.

Table 5p. Inclusivity test results for *Cryptosporidium* strains

QIAstat-Dx target	Pathogen	Strain	Supplier	Catalog ID	Times LoD
Cryptosporidium	*Cryptosporidium parvum*	Iowa isolate	Waterborne	P102C*	1x LoD
	Cryptosporidium hominis	n/a	Public Health Wales	Clinical sample; UKM 84*	0.01x LoD
	Cryptosporidium parvum	–	ATCC	PRA-67DQ (isolated genomic DNA)	<0.01 LoD
	Cryptosporidium meleagridis	–	Public Health Wales	Clinical sample; UKMEL 14	<0.01 LoD

* Strain tested during LoD verification study.

Table 5q. Inclusivity test results for *Cyclospora cayetanensis* strains

QIAstat-Dx target	Pathogen	Strain	Supplier	Catalogue ID	Times LoD
Cyclospora cayetanensis	*Cyclospora cayetanensis*	n/a	Clinical sample	LAC2825*	1x LoD
	Cyclospora cayetanensis	n/a	Clinical sample	LAC2827*	1x LoD
	Cyclospora cayetanensis	–	ATCC	PRA-3000SD	1x LoD

* Strain tested during LoD verification study.

Table 5r. Inclusivity test results for *Entamoeba histolytica* strains

QIAstat-Dx target	Pathogen	Strain	Supplier	Catalogue ID	Times LoD
Entamoeba histolytica	*Entamoeba histolytica*	HM-1:IMSS (Mexico City 1967)	ATCC	30459*	1x LoD
	Entamoeba histolytica	HK-9 (Korea)	ATCC	30015*	1x LoD
	Entamoeba histolytica	–	Vall d'Hebrón	Clinical sample; 1	1x LoD

* Strain tested during LoD verification study.

Table 5s. Inclusivity test results for *Giardia lamblia* strains

QIAstat-Dx target	Pathogen	Strain	Supplier	Catalogue ID	Times LoD
Giardia lamblia	*Giardia lamblia*	Portland-1 (Portland, OR, 1971)	ATCC	30888*	1x LoD
	Giardia lamblia	WB (Bethesda, MD, 1979)	ATCC	30957*	1x LoD
	Giardia intestinalis	H3 isolate	Waterborne	P101	1x LoD

* Strain tested during LoD verification study.

Table 5t. Inclusivity test results for Adenovirus F40/F41 targets

QIAstat-Dx target	Pathogen	Strain	Supplier	Catalog ID	Times LoD
Adenovirus F40/F41	Human Adenovirus F41	Tak	ZeptoMetrix	0810085CF*	1x LoD
	Human Adenovirus F41	Tak (73-3544)	ATCC	VR-930	10x LoD
	Human Adenovirus F40	Dugan [79-18025]	ATCC	VR-931	10x LoD
	Human Adenovirus Type 40	Dugan	ZeptoMetrix	0810084CF*	3x LoD

* Strain tested during LoD verification study.

Table 5u. Inclusivity test results for Astrovirus strains

QIAstat-Dx target	Pathogen	Strain	Supplier	Catalog ID	Times LoD
Astrovirus	Human Astrovirus	ERE IID 2371 (type 8)	ZeptoMetrix	0810277CF*	1x LoD
	Human Astrovirus	HAstV-1	Universitat de Barcelona	Clinical sample; 160521599	1x LoD
	Human Astrovirus	ERE IID 2868 (type 4)	ZeptoMetrix	0810276CF*	1x LoD
	Human Astrovirus	HAstV-3	Universitat de Barcelona	Clinical sample; 151601306	1x LoD

* Strain tested during LoD verification study.

Table 5v. Inclusivity test results for Norovirus GI/GII strains

QIAstat-Dx target	Pathogen	Strain	Supplier	Catalog ID	Times LoD
Norovirus GI/GII	**Human Norovirus Genogroup 1**	**Recombinant GI.1**	**ZeptoMetrix**	**0810086CF***	**1x LoD**
	Human Norovirus Genogroup 1	–	Indiana University Health	Clinical sample; IU3156	1x LoD
	Human Norovirus Genogroup 1	–	Indiana University Health	Clinical sample; IU3220	1x LoD
	Human Norovirus Genogroup 1	–	TriCore Reference Laboratories	Clinical sample; TC4274	3x LoD
	Human Norovirus Genogroup 2	**Recombinant GII.4**	**ZeptoMetrix**	**0810087CF***	**1x LoD**
	Human Norovirus Genogroup 2	GII.2	Vall d'Hebrón	Clinical sample; 198058327	1x LoD
	Human Norovirus Genogroup 2	GII.4	Universitat de Barcelona	Clinical sample; N26.2TA	1x LoD
	Human Norovirus Genogroup 2	–	Lacny Hospital	Clinical sample; LAC2019	1x LoD
	Human Norovirus Genogroup 2	–	Nationwide Children's Hospital	Clinical sample; NWC6063	1x LoD
	Human Norovirus Genogroup 2	GII.6	QIAGEN Barcelona (STAT-Dx)	Clinical sample; GI 12	3x LoD
	Human Norovirus Genogroup 2	–	Lacny Hospital	Clinical sample; LAC2133	10x LoD
	Human Norovirus Genogroup 2	–	Lacny Hospital	Clinical sample; LAC2074	10x LoD

* Strain tested during LoD verification study.

Table 5w. Inclusivity test results for Rotavirus A strains

QIAstat-Dx target	Pathogen	Strain	Supplier	Catalog ID	Times LoD
Rotavirus A	Human Rotavirus A	69M	ZeptoMetrix	0810280CF*	1x LoD
	Human Rotavirus A	Wa, G1P1A[8]	ZeptoMetrix	0810041CF*	1x LoD
	Human Rotavirus A	DS-1, G2P1B[4]	ATCC	VR-2550	1x LoD
	Human Rotavirus A	Va70	ZeptoMetrix	0810281CF	1x LoD
	Human Rotavirus A	RRV	ZeptoMetrix	0810530CF	10x LoD

* Strain tested during LoD verification study.

Table 5x. Inclusivity test results for Sapovirus strains

QIAstat-Dx target	Pathogen	Strain	Supplier	Catalog ID	Times LoD
Sapovirus	Human Sapovirus Genogroup I	–	QIAGEN Barcelona	Clinical sample; GI-88*	1x LoD
	Human Sapovirus Genogroup V	n/a	Universitat Barcelona	Clinical sample; 160523351*	1x LoD
	Human Sapovirus Genogroup I	GI.1	Universitat Barcelona	Clinical sample; 171016324	1x LoD
	Human Sapovirus Genogroup II	GII.3	Universitat Barcelona	Clinical sample; 215512	1x LoD

* Strain tested during LoD verification study.

In silico analysis

In silico analysis of potential reactivity showed that the following organisms (including species, subspecies, subtypes, serotypes or serovars) are predicted to be detected with the QIAstat-Dx Gastrointestinal Panel 2 (Table 6).

Table 6. Organisms with predicted reactivity based on in silico analysis

QIAstat-Dx GI Panel 2	Organisms with predicted reactivity (species, subspecies, subtypes, serotypes or serovars)
Bacteria	
Campylobacter	*Campylobacter coli**, *Campylobacter jejuni*, *Campylobacter jejuni* subsp. *jejuni*, *Campylobacter jejuni* subsp. doylei, *Campylobacter upsaliensis*
Clostridium difficile	Clostridium *difficile* (including ribotypes 01 and 17 and strains BI1, BI9, NAP1, SD1, SD2, M68, M120)
Salmonella	*Salmonella bongori**, *Salmonella enterica* subsp. salamae II (e.g. serovar 55:k:z39), *Salmonella enterica* subsp. arizonae IIIa (e.g. serovar 63:g:z51), *Salmonella enterica* subsp. diarizonae IIIb (e.g. serovar 47:l,v:z), *Salmonella enterica* subsp. houtenae IV (e.g. serovar 43:z4), *Salmonella enterica* subsp. indica VI. *Salmonella enterica* subsp. enterica (up to 92 different serovars including Agona, Anatum, Bareilly, Choleraesuis, Enteritidis, Heidelberg, Infantis, Kentucky, Montevideo, Newport, Paratyphi A*, Senftenberg, Tennessee, Thompson, Typhi, Typhimurium, Weltevreden*)
Plesiomonas shigelloides	*Plesiomonas shigelloides* (e.g. strains NCTC10360, ATCC 14029T, R4605035)
Vibrio cholerae	*Vibrio cholerae* (including biovars El Tor and Bengal)
Vibrio parahaemolyticus	*Vibrio parahaemolyticus*
Vibrio vulnificus	*Vibrio vulnificus*
Yersinia enterocolitica	*Yersinia enterocolitica*, *Yersinia enterocolitica* subsp. palearctica, *Yersinia enterocolitica* subsp. *enterocolitica*
Enteroaggregative *E. coli* (EAEC)	Enteroaggregative *E. coli* (EAEC) (including serotypes O104:H4, O111:HND, O126:HND, O25:H4, O86:H2, O86:HND, OUT:H4, OUT:HND)

Table 6. Organisms with predicted reactivity based on in silico analysis (continued)

QIAstat-Dx GI Panel 2	Organisms with predicted reactivity (species, subspecies, subtypes, serotypes or serovars)
Enteroinvasive *E. coli* (EIEC)/*Shigella*	Enteroinvasive *E. coli* (EIEC), *Escherichia coli* sp., *Shigella flexneri, Shigella dysenteriae, Shigella boydii, Shigella sonnei.*
Enteropathogenic *E. coli* (EPEC)	Enteropathogenic *E. coli* (EPEC) (e.g. including serotypes OUT: HND, OUT:H6, OUT:H34, OUT:H21, O55:H7, O119:HNM, O117) Other eae-carriers bacteria: some Shiga-like toxin-producing *E. coli* (STEC), STEC O157:H7 and few *Shigella boydii* strains
Enterotoxigenic *E. coli* (ETEC)†	Enterotoxigenic *E. coli* (ETEC) (including H10407 and E24377A strains and serotypes O169:H41, O25:H42, O148:H28, O6:H16) carrier of: Heat-labile enterotoxin gene subtype LT-I and Heat-stable enterotoxin gene variant Sta, subtypes STp and STh
Shiga-like toxin-producing *E. coli* (STEC) - stx1	Shiga-like toxin-producing *E. coli* (STEC) (including non-O157 serotypes O111:NM, O111:H-, O26:H11, O145:NM, O145:H28, O45:H2, O26:H11, ONT:NM, and including STEC O157 serotypes O157:H7) Stx1 toxin subtypes predicted to be detected include stx1a, stx1c and stx1d Other stx-carriers bacteria: *Shigella sonnei, Shigella dysenteriae*
Shiga-like toxin-producing *E. coli* (STEC) - stx2	Shiga-like toxin-producing *E. coli* (STEC) (including non-O157 serotypes O111:NM, O104:H4, O111:H-, O26:H11, O121:H19, O145:H34, O113:H21, ONT:H-, O128:H2, OUT:HNM, O124:HNM and including STEC O157 serotypes O157:H7, O157:NM) Stx2 toxin subtypes predicted to be detected include stx2a, stx2b, stx2c, stx2d, stx2e, stx2f, stx2g, stx2h*, stx2i, stx2j, stx2k and stx2l
Shiga-like toxin-producing *E. coli* (STEC) O157	*Escherichia coli* O157 including: STEC O157:H7 strains (e.g. EDL933) and *E. coli* O157: non-H7 groups including Non-Shiga-toxigenic *E. coli* O157 bacteria (e.g. serotype O157:H45) Other bacteria with O157 O-antigen: *Escherichia fergusonii* O157

Table 6. Organisms with predicted reactivity based on in silico analysis (continued)

QIAstat-Dx GI Panel 2	Organisms with predicted reactivity (species, subspecies, subtypes, serotypes or serovars)
Parasites	
Cryptosporidium‡	Common *Cryptosporidium* species involved in human disease: *C. parvum, C. hominis.* Less common *Cryptosporidium* species involved in human infections: *C. meleagridis, C. felis , C. bovis, C. viatorum, C. ubiquitum, C. tyzzeri, C. cuniculus, Cryptosporidium sp. Chipmunk genotype I, C. canis*.* Rare or non-human species: *Cryptosporidium wrairi*
Cyclospora cayetanensis	*Cyclospora cayetanensis* (including strains LG, CY9, NP20, and NP21) *
Entamoeba histolytica	*Entamoeba histolytica* (e.g. strains HM-1: IMSS, EHMfas1, and HK-9)*
Giardia lamblia	*Giardia lamblia* (a.k.a. *Giardia duodenalis, Giardia intestinalis*)*
Viruses	
Adenovirus	Human Adenovirus F40/41
Astrovirus§	Human Astrovirus (including types 1, 2, 3, 4, 5, 6, 7, 8)
Norovirus GI/GII	Norovirus genogroup II genotypes: GII.1, GII.2, GII.3*, GII.4*, GII.5, GII.6, GII.7, GII.8, GII.9, GII.10, GII.12, GII.13, GII.14, GII.16, GII.17, GII.20, GII.21, GII.22, GII.23, GII.24*, GII.25, GII.26, GII.27, GII.NA1, and GII.NA2* Norovirus genogroup I genotypes: GI.1, GI2, GI.3*, GI.4*, GI.5, GI.6*, GI.7*, GI.8, and GI.9
Rotavirus	Rotavirus A including genotypes: G1P[8]*, G2P[4]*, G3P[8]*, G4P[8]*, G9P[6], G9P[8]*, G12P[6]* and G12P[8]*

Table 6. Organisms with predicted reactivity based on in silico analysis (continued)

QIAstat-Dx GI Panel 2	Organisms with predicted reactivity (species, subspecies, subtypes, serotypes or serovars)
Sapovirus	Genogroups: GI (including genotypes GI.1*, GI.2*, GI.3*, GI.4, GI.5, GI.6* and GI.7), GII (including genotypes GII.1*, GII.2, GII.3, GII.4*, GII.5, GII.6, GII7, GII.8*), GIV (including genotype GIV.1), and GV (including genotypes GV.1* and GV.2*)

* Certain sequences are predicted to be detected with reduced sensitivity due to the presence of a reduced number of mismatches at critical positions of the primer-probe design.
[&] The assay is not predicted to detect bacteria carrier of Heat-labile enterotoxin gene subtype LT-II and/or of Heat-stable enterotoxin gene variant Stb.
[#] The assay is not predicted to detect other *Cryptosporidium spp.* less involved in human disease: *C. andersoni* and *C. muris*.
[$] The assay is not predicted to detect Human Astrovirus types MLB1-3 and VA1-5.

Interfering Substances

The effect of potentially interfering substances on the detectability of the QIAstat-Dx Gastrointestinal Panel 2 organisms was evaluated. Forty-three (43) potentially interfering substances were spiked into the sample mixes at a level predicted to be above the concentration of the substance likely to be found in stool specimens. Each organism was tested at 3x LoD and testing was performed in triplicates. Endogenous substances such as human whole blood, human genomic DNA and several pathogens were tested alongside exogenous substances like antibiotics, other gastrointestinal-related medications, and different technique-specific substances.

For the vast majority of substances tested, no inhibition was observed, with the exceptions of mucin from bovine submaxillary, bisacodyl, calcium carbonate, nonoxynol-9 and Rotavirus reassortants, that may cause inhibition at high concentration.

Mucin from bovine submaxillary was found to interfere with the detection of EAEC at concentrations above 25.0 mg/mL.

Bisacodyl was found to interfere with the detection of EAEC at concentrations above 1.5 mg/mL.

Calcium carbonate was found to interfere with the detection of all the QIAstat-Dx Gastrointestinal Panel 2 targets at concentrations above 10.7 mg/mL.

Nonoxynol-9 was found to interfere with the detection of Entamoeba at concentrations above 0.2 µL/mL.

Rotavirus reassortants WC3:2-5, R574(9), and WI79-4,9 used in Rotavirus A vaccines were predicted to be reactive with Rotavirus A in the QIAstat-Dx Gastrointestinal Panel 2. Final concentrations without observable interfering effects on the detection of targets at 3x LoD concentration for WC3:2-5, R574(9) and WI79-4,9 were 8.89×10^{-5} $TCID_{50}$/mL and 1.10 PFU/mL, respectively (see Table 7) for other concentrations tested.

Competitive interference was tested in a subset of pathogens. No interference was observed when evaluating competitive interference by target pathogens when two QIAstat-Dx Gastrointestinal Panel target pathogens were tested by spiking samples with one pathogen target at 3x LoD and one at 50x LoD. Results from the pathogen targets tested are provided in Table 8.

Results from the 43 interfering substances that could be present or introduced in a stool specimen are provided in Table 7.

Table 7. Final highest concentration without observable inhibitory effect

Substance tested	Concentration tested	Result
Endogenous substances		
Bovine and ovine bile	120.0 mg/mL	No Interference
Cholesterol	15.0 mg/mL	No Interference
Fatty acids (palmitic acid)	2.0 mg/mL	No Interference
Fatty acids (stearic acid)	4.0 mg/mL	No Interference
Human genomic DNA	20 µg/mL	No Interference
Human stool (overfill of Cary Blair vial)	300 mg/mL	No Interference
Human urine	0.5 mg/mL	No Interference
Human whole blood with Na Citrate	0.4 mg/mL	No Interference
Mucin from bovine submaxillary	50.0 mg/mL 25.0 mg/mL	Interference No Interference
Triglycerides	50 mg/mL	No Interference
Non-target microorganisms		
Aeromonas hydrophila	1 x 10^6 units/mL	No Interference
Bacteroides vulgatus	1 x 10^6 units/mL	No Interference
Bifidobacterium bifidum	1 x 10^6 units/mL	No Interference
Enterovirus Species D, Serotype EV-D68	1 x 10^5 units/mL	No Interference
Non-pathogenic *E. coli*	1 x 10^6 units/mL	No Interference
Helicobacter pylori	1 x 10^6 units/mL	No Interference
Saccharomyces cerevisiae (deposited as *S. boul-ardii*)	1 x 10^5 units/mL	No Interference
Exogenous substances		
Bacitracin	250.0 U/mL	No Interference

Table 7. Final highest concentration without observable inhibitory effect (continued)

Substance tested	Concentration tested	Result
Bisacodyl	3.0 mg/mL 1.5 mg/mL	Interference No Interference
Bismuth subsalicylate	3.5 mg/mL	No Interference
Calcium carbonate (TUMS® Extra Strength 750)	100 mg/mL 10 mg/mL	Interference No Interference
Docusate sodium	25 mg/mL	No Interference
Doxycycline hydrochloride	0.50 mg/mL	No Interference
Glycerin	0.50 mL	No Interference
Hydrocortisone	5.0 mg/mL	No Interference
Loperamide hydrochloride	0.78 mg/mL	No Interference
Magnesium hydroxide	1.0 mg/mL	No Interference
Metronidazole	15.0 mg/mL	No Interference
Mineral oil	0.50 mL	No Interference
Naproxen sodium	7 mg/mL	No Interference
Nonoxynol-9	12.0 µL/mL 6.0 µL/mL 3.0 µL/mL 1.5 µL/mL 0.75 µL/mL 0.20 µL/mL	Interference Interference Interference Interference Interference No Interference
Nystatin	10,000.0 USP units/mL	No Interference
Phenylephrine hydrochloride	0.75 mg/mL	No Interference
Sodium phosphate	50.0 mg/mL	No Interference
Vaccine components		

Table 7. Final highest concentration without observable inhibitory effect (continued)

Substance tested	Concentration tested	Result
Rotavirus reassortant WC3:2-5, R574(9) - VR 2195	8.89 x 10−3 $TCID_{50}$/mL	Interference
	8.89 x 10−4 $TCID_{50}$/mL	Interference
	8.89 x 10−5 $TCID_{50}$/mL	No Interference
Rotavirus reassortant WI79-4,9 - VR 2415	1.10 x 10^2 pfu/mL	Interference
	1.10 x 10 pfu/mL	Interference
	1.10 pfu/mL	No Interference
Technique-specific Substances		
Bleach	5.0 µL/mL	No Interference
Ethanol	2.0 µL/mL	No Interference
Fecal swab Cary-Blair Medium	100%	No Interference
Fecal Opti-Swab Cary-Blair Medium	100%	No Interference
PurSafe® DNA/RNA Preservative	100%	No Interference
Para-Pak C&S spoon	1 swab/2mL Cary Blair	No Interference
Sigma transwab	1 swab/2mL Cary Blair	No Interference

Table 8. QIAstat-Dx Gastrointestinal Panel 2 results for competitive interference

Sample Mix	Target	Final concentration tested x LoD	Co-infection detected
Norovirus 50x - Rotavirus 3x	Norovirus GI/GII	50x	Yes
	Rotavirus A	3x	
Norovirus 3x - Rotavirus 50x	Norovirus GI/GII	3x	Yes
	Rotavirus A	50x	
Giardia 50x - Adenovirus 3x	*Giardia lamblia*	50x	Yes
	Adenovirus F40/F41	3x	

Table 8. QIAstat-Dx Gastrointestinal Panel 2 results for competitive interference (continued)

Sample Mix	Target	Final concentration tested x LoD	Co-infection detected
Adenovirus 50x - *Giardia* 3x	*Giardia lamblia*	3x	Yes
	Adenovirus F40/F41	50x	
Norovirus 50x - *C.diff* 3x	Norovirus GII	50x	Yes
	Clostridium difficile toxin A/B	3x	
Norovirus 3x - *C.diff* 50x	Norovirus GII	3x	Yes
	Clostridium difficile toxin A/B	50x	
EPEC 50x - EAEC 3x	EPEC	50x	Yes
	EAEC	3x	
EPEC 3x - EAEC 50x	EPEC	3x	Yes
	EAEC	50x	
EPEC 50x - *C.diff* 3x	EPEC	50x	Yes
	Clostridium difficile toxin A/B	3x	
EPEC 3x - *C.diff* 50x	EPEC	3x	Yes
	Clostridium difficile toxin A/B	50x	
EPEC 50x - ETEC 3x	EPEC	50x	Yes
	ETEC	3x	
EPEC 3x - ETEC 50x	EPEC	3x	Yes
	ETEC	50x	
ETEC 50x - EIEC 3x	ETEC	50x	Yes
	EIEC/ *Shigella*	3x	
ETEC 3x - EIEC 50x	ETEC	3x	Yes
	EIEC/ *Shigella*	50x	

Carryover

A carryover study was performed to evaluate the potential occurrence of cross-contamination between consecutive runs when using the QIAstat-Dx Gastrointestinal Panel 2 on the QIAstat-Dx Analyzer 1.0.

Pathogen samples of stool sample matrix, with alternating high-positive (10^5–10^6 organism/mL) and negative samples, were conducted on two QIAstat-Dx Analyzer 1.0 instruments.

No carryover between samples was observed in the QIAstat-Dx Gastrointestinal Panel 2, demonstrating that the system design and recommended sample handling and testing practices are effective in preventing false-positive results due to carryover or cross-contamination between samples.

Reproducibility

Reproducibility testing of contrived samples was performed at three test sites including one internal site (Site A) and two external sites (Site B and Site C). The study incorporated a range of potential variation introduced by sites, days, replicates, cartridge lots, operators, and QIAstat-Dx analyzers. For each site, testing was performed across 5 non-consecutive days with 6 replicates per day (leading to a total of 30 replicates per target, concentration and site), 4 QIAstat-Dx Analyzers (2 analyzers per operator and per site), and at least 2 operators on each testing day. A total of 5 sample mixes (two combined samples at 1x LoD and 3x LoD plus one negative sample) were prepared. For each mix, 6 replicates were tested and evaluated.

Table 9 shows the detection rate per target and concentration for each site of the Reproducibility study. In addition, data obtained at all three sites have been compiled to calculate the exact 2-sided 95% Confidence Interval by target and concentration.

During the reproducibility study, potential variation introduced by sites, days, replicates, cartridge lots, operators, and QIAstat-Dx analyzers was analyzed showing no significant contribution to variability (Standard Deviation and Coefficient of Variation values below 1 and 5%, respectively) caused by any of the assessed variables.

Table 9. Detection rate per target and concentration for each site of the Reproducibility study and exact 2-sided 95% Confidence Interval by target and concentration

			% Agreement with Expected Result			
Pathogen Tested	**Concentration Tested**	**Expected Result**	**Site A**	**Site B**	**Site C**	**All Sites (95% Confidence Interval)**
Adenovirus F41 ZeptoMetrix 0810085CF	3x LoD	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
	1x LoD	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
	None	Not Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)

Table 9. Detection rate per target and concentration for each site of the Reproducibility study and exact 2-sided 95% Confidence Interval by target and concentration (continued)

			% Agreement with Expected Result			
Pathogen Tested	**Concentration Tested**	**Expected Result**	**Site A**	**Site B**	**Site C**	**All Sites (95% Confidence Interval)**
Clostridium difficile ZeptoMetrix 0801619	3x LoD	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
	1x LoD	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
	None	Not Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
Campylobacter ZeptoMetrix 801650	3x LoD	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
	1x LoD	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
	None	Not Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)

Table 9. Detection rate per target and concentration for each site of the Reproducibility study and exact 2-sided 95% Confidence Interval by target and concentration (continued)

			% Agreement with Expected Result			
Pathogen Tested	**Concentration Tested**	**Expected Result**	**Site A**	**Site B**	**Site C**	**All Sites (95% Confidence Interval)**
Escherichia coli **(EPEC)** ZeptoMetrix 801747	3x LoD	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
	1x LoD	Detected	30/30 100%	29/30 96.67%	30/30 100%	89/90 98.89% (93.96 – 99.97%)
	None	Not Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98– 100.00%)
Entamoeba histolytica ATCC 30459	3x LoD	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
	1x LoD	Detected	30/30 100%	30/30 100%	29/30 96.67%	89/90 98.89% (93.96 – 99.97%)
	None	Not Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)

Table 9. Detection rate per target and concentration for each site of the Reproducibility study and exact 2-sided 95% Confidence Interval by target and concentration (continued)

			% Agreement with Expected Result			
Pathogen Tested	**Concentration Tested**	**Expected Result**	**Site A**	**Site B**	**Site C**	**All Sites (95% Confidence Interval)**
Giardia lamblia ATCC 30888	3x LoD	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
	1x LoD	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
	None	Not Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
Norovirus GII ZeptoMetrix 0810087CF	3x LoD	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
	1x LoD	Detected	29/30 96.67%	30/30 100%	30/30 100%	89/90 98.89% (93.96 – 99.97%)
	None	Not Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)

Table 9. Detection rate per target and concentration for each site of the Reproducibility study and exact 2-sided 95% Confidence Interval by target and concentration (continued)

			% Agreement with Expected Result			
Pathogen Tested	**Concentration Tested**	**Expected Result**	**Site A**	**Site B**	**Site C**	**All Sites (95% Confidence Interval)**
Rotavirus A ZeptoMetrix 0810280CF	3x LoD	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
	1x LoD	Detected	30/30 100%	29/30 96.67%	30/30 100%	89/90 98.89% (93.96 – 99.97%)
	None	Not Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
***Escherichia coli* (STEC) O157:H7** ZeptoMetrix 0801622	3x LoD	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
	1x LoD	Detected	30/30 100%	30/30 100%	29/30 96.67%	89/90 98.89% (93.96 – 99.97%)
	None	Not Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)

Table 9. Detection rate per target and concentration for each site of the Reproducibility study and exact 2-sided 95% Confidence Interval by target and concentration (continued)

			% Agreement with Expected Result			
Pathogen Tested	**Concentration Tested**	**Expected Result**	**Site A**	**Site B**	**Site C**	**All Sites (95% Confidence Interval)**
***Escherichia coli* (STEC) stx1** ZeptoMetrix 0801622	3x LoD	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
	1x LoD	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
	None	Not Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
***Escherichia coli* (STEC) stx2** ZeptoMetrix 0801622	3x LoD	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
	1x LoD	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
	None	Not Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)

Table 9. Detection rate per target and concentration for each site of the Reproducibility study and exact 2-sided 95% Confidence Interval by target and concentration (continued)

			% Agreement with Expected Result			
Pathogen Tested	**Concentration Tested**	**Expected Result**	**Site A**	**Site B**	**Site C**	**All Sites (95% Confidence Interval)**
Salmonella enterica ZeptoMetrix 0801437	3x LoD	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
	1x LoD	Detected	30/30 100%	29/30 96.67%	29/30 96.67%	88/90 97.78% (92.20 – 99.73%)
	None	Not Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
Vibrio parahaemolyticus ATCC 17802	3x LoD	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
	1x LoD	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
	None	Not Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)

Table 9. Detection rate per target and concentration for each site of the Reproducibility study and exact 2-sided 95% Confidence Interval by target and concentration (continued)

			% Agreement with Expected Result			
Pathogen Tested	Concentration Tested	Expected Result	Site A	Site B	Site C	All Sites (95% Confidence Interval)
Yersinia enterocolitica Zeptometrix 0801734	3x LoD	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
	1x LoD	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)
	None	Not Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (95.98 – 100.00%)

Repeatability

A repeatability study was conducted on the QIAstat-Dx Analyzer 1.0 instruments using a set of samples composed of low-concentrated analytes spiked into stool matrix (3x LoD and 1x LoD) and negative stool samples. Pathogens included in the positive samples were Adenovirus, *Clostridium difficile*, *Campylobacter*, Enteropathogenic *E. coli* (EPEC), *Entamoeba histolytica*, *Giardia lamblia*, Norovirus GII, Rotavirus, *E. coli* O157, STEC stx1, STEC stx2, *Salmonella enterica*, *Vibrio parahaemolyticus*, and *Yersinia enterocolitica*. Each sample was tested with the same instrument over 12 days. In total, 60 replicates of 1x LoD and 60 replicates of 3x LoD per each of the tested targets and 60 replicates of negative samples were run. Overall results showed a 93.33–100.00% and 95.00–100.00% detection rate for 1x LoD and 3x LoD samples, respectively. Negative samples showed 100% of negative calls for all panel analytes.

Repeatability in the QIAstat-Dx Rise instrument was also evaluated in comparison with QIAstat-Dx Analyzers. A study was conducted on two QIAstat-Dx Rise instruments using a representative set of samples composed of low-concentrated analytes (3x LoD and 1x LoD) spiked

into stool matrix and negative stool samples. Pathogens included in the positive samples were Norovirus GII, *Entamoeba histolytica*, *Clostridium difficile*, *Yersinia enterocolitica*, *Salmonella enterica*, Adenovirus F 40, and Rotavirus A. Samples were tested in replicates using two lots of cartridges. In total, 128 replicates of 1x LoD positive samples, 128 replicates of 3x LoD positive samples, and 64 replicates of negative samples were run on the QIAstat-Dx Rise instrument. Overall results showed a 99.22–100.00% detection rate for both 1x LoD and 3x LoD samples. Negative samples showed 100% of negative calls for all panel analytes. Testing with two QIAstat-Dx Analyzers (each with four Analytical Modules) was included in the study for results comparison. QIAstat-Dx Rise performance was shown to be equivalent to QIAstat-Dx Analyzer 1.0.

Appendix 02 Clinical Performance

The clinical performance shown below was demonstrated using QIAstat-Dx Analyzer 1.0. The QIAstat-Dx Rise and the QIAstat-Dx Analyzer 2.0 use the same Analytical Modules as QIAstat-Dx Analyzer 1.0; therefore, the performance is not impacted by QIAstat-Dx Rise or the QIAstat-Dx Analyzer 2.0. The equivalency on performance between QIAstat-Dx Rise and QIAstat-Dx Analyzer 1.0 was confirmed through a repeatability study

Prevalence of Detected Analytes with QIAstat-Dx Gastrointestinal Panel 2

The number and percentage of positive results as determined by the QIAstat- Dx Gastrointestinal Panel 2 in the prospective clinical evaluation, stratified by age group, are presented in Table 10. Overall, the QIAstat-Dx Gastrointestinal Panel 2 detected at least 1 organism in 34.3% (665/1939) of the prospectively collected specimens.

Table 10. Prevalence Summary by Age Group for the Prospective Clinical study as determined by the QIAstat-Dx Gastrointestinal Panel 2

Analyte	Overall	0-6 years	6-21 years	22-49 years	50+ years	Not Reported
Viruses						
Adenovirus F40/F41	7 (0.4%)	4 (1.9%)	2 (1.3%)	0 (0.0%)	1 (0.1%)	0 (0.0%)
Astrovirus	9 (0.5%)	5 (2.3%)	0 (0.0%)	3 (0.6%)	1 (0.1%)	0 (0.0%)
Norovirus GI/GII	59 (3.1%)	25 (11.7%)	2 (1.3%)	17 (3.4%)	15 (1.4%)	0 (0.0%)
Rotavirus A	27 (1.4%)	15 (7.0%)	2 (1.3%)	7 (1.4%)	3 (0.3%)	0 (0.0%)
Sapovirus	15 (0.8%)	9 (4.2%)	3 (1.9%)	3 (0.6%)	0 (0.0%)	0 (0.0%)
Bacteria						
Campylobacter	101 (5.2%)	27 (12.7%)	7 (4.5%)	27 (5.3%)	40 (3.8%)	0 (0.0%)
Clostridium difficile	200 (10.3%)	20 (9.4%)	14 (8.9%)	44 (8.7%)	119 (11.3%)	3 (42.9%)
Plesiomonas shigelloides	9 (0.5%)	1 (0.5%)	0 (0.0%)	6 (1.2%)	2 (0.2%)	0 (0.0%)

Salmonella	33 (1.7%)	9 (4.2%)	6 (3.8%)	6 (1.2%)	12 (1.1%)	0 (0.0%)
Vibrio cholerae	2 (0.1%)	0 (0.0%)	0 (0.0%)	1 (0.2%)	1 (0.1%)	0 (0.0%)
Vibrio parahaemolyticus	3 (0.3%)	0 (0.0%)	0 (0.0%)	2 (0.7%)	1 (0.2%)	0 (0.0%)
Vibrio vulnificus	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)

Table 10. Prevalence Summary by Age Group for the Prospective Clinical study as determined by the QIAstat-Dx Gastrointestinal Panel 2 (continued)

Analyte	Overall	0-6 years	6-21 years	22-49 years	50+ years	Not Reported
Yersinia enterocolitica	30 (1.6%)	3 (1.4%)	2 (1.3%)	13 (2.6%)	12 (1.1%)	0 (0.0%)
Diarrheagenic *E. coli*/*Shigella*						
Enteroaggregative *E. coli* (EAEC)	53 (2.7%)	11 (5.2%)	1 (0.6%)	24 (4.8%)	17 (1.6%)	0 (0.0%)
Enteropathogenic *E. coli* (EPEC)	192 (9.9%)	57 (26.6%)	14 (8.9%)	52 (10.3%)	69 (6.6%)	0 (0.0%)
Enterotoxigenic *E. coli* (ETEC) *lt/st*	36 (1.9%)	4 (1.9%)	2 (1.3%)	18 (3.6%)	12 (1.1%)	0 (0.0%)
Shiga-like toxin *E. coli* (STEC) *stx1/stx2*	24 (1.2%)	9 (4.2%)	1 (0.6%)	8 (1.6%)	6 (0.6%)	0 (0.0%)
E. coli O157	3 (0.2%)	3 (1.4%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Shigella/ EnteroinvasiveE. *coli* (EIEC)	13 (0.7%)	1 (0.5%)	0 (0.0%)	7 (1.4%)	5 (0.5%)	0 (0.0%)
Parasites						
Cryptosporidium	9 (0.5%)	0 (0.0%)	2 (1.3%)	5 (1.0%)	2 (0.2%)	0 (0.0%)
Cyclospora cayetanensis	21 (1.1%)	0 (0.0%)	1 (0.6%)	8 (1.6%)	12 (1.1%)	0 (0.0%)
Giardia lamblia	16 (0.8%)	4 (1.9%)	1 (0.6%)	7 (1.4%)	4 (0.4%)	0 (0.0%)

The clinical performance of QIAstat-Dx Gastrointestinal Panel 2 was established during a multi-center international prospective study conducted at thirteen clinical settings representatives of different geographical areas within USA and Europe (9 sites in USA and 4 sites in Europe) between May and July 2021. All study sites were hospital-associated or independent clinical diagnostics laboratories that perform routine diagnostics of gastrointestinal infections. A total of 1939 prospectively collected stool specimens (stool in Cary-Blair transport medium using Para-Pak C&S (Meridian Bioscience) or FecalSwab (COPAN) were obtained from patients with clinical indications of diarrhea caused by gastrointestinal infection. Table 11 provides a summary of the specimen's distribution across all study sites.

Table 11. Prospective Specimen Distribution Across Study Sites

Site/Country	Prospective (Fresh)
Germany	339
Denmark	293
Spain	247
France	63
USA site 1	186
USA site 2	43
USA site 3	282
USA site 4	177
USA site 5	44
USA site 6	39
USA site 7	0*
USA site 8	131
USA site 9	95
Total	**1939**

* The specimens from this site were excluded from the analysis because they were collected with another device different to Para-Pak C&S or FecalSwab.

The demographic information for the 1,939 specimens evaluated in the prospective study is summarized in Table 12.

Table 12. Demographic Data For Prospective Evaluated Specimens

Demographic data	N	%
Gender		
Female	1070	55.2
Male	869	44.8
Age Group		
0–5 years	213	11.0
6–21 years	159	8.2
22–49 years	505	26.0
50+ years	1055	54.4
Not Reported	7	0.4
Patient population		
Emergency room	75	3.9
Hospitalized	485	25.0
Immunocompromised	3	0.2
Outpatient	816	42.1
No information available	560	28.9
Number of Days between Symptom Onset and QIAstat-Dx Testing		
> 7 days	89	4.6
≤ 7 days	162	8.3
Not Reported	1688	87.1

The performance of the QIAstat-Dx Gastrointestinal Panel 2 was evaluated for each panel test result using one FDA-cleared/CE-marked test as comparator or using a composite comparator of three independent FDA-cleared/CE-marked test methods or two independent FDA-cleared/CE-marked tests methods and validated PCR assays followed by bi-directional sequencing (Table 13). The composite comparator method result was determined as the majority of the three individual test results.

Table 13. Comparator Methods for the Clinical Evaluation of QIAstat-Dx Gastrointestinal Panel 2

QIAstat-Dx GI Panel 2 Test Result	Comparator Method
Astrovirus	One FDA-cleared/CE-marked test method
Rotavirus A	
Sapovirus	
Campylobacter	
Clostridium difficile	
Plesiomonas shigelloides	
Salmonella	
Yersinia enterocolitica	
Shigella/Enteroinvasive *E. Coli* (EIEC)	
Enteroaggregative *Escherichia coli* (EAEC)	
Enteropathogenic *E. coli* (EPEC)	
E. coli O157	
Cryptosporidium	
Cyclospora cayetanensis	
Entamoeba histolytica	
Vibrio parahaemolyticus	One FDA-cleared/CE-marked test method and one validated PCR test followed by bidirectional sequencing*†
Vibrio vulnificus	
Adenovirus F40/F41	Composite of three FDA-cleared/CE-marked test methods *‡
Norovirus GI/GII	
Vibrio cholerae	
Enterotoxigenic *E. coli* (ETEC) *lt/st*	
Shiga-like toxin- *E. coli* (STEC) *stx1/stx2*	

Table 13. Comparator Methods for the Clinical Evaluation of QIAstat-Dx Gastrointestinal Panel 2 (continued)

QIAstat-Dx GI Panel 2 Test Result	Comparator Method
Giardia lamblia	Composite of two FDA-cleared/CE-marked test methods and two validated PCR tests followed by bi-directional sequencing*

*Each PCR assay used was a well-characterized and validated nucleic acid amplification tests (NAAT) followed by bi-directional sequencing analysis. Each assay was designed to amplify different sequences than those targeted by the QIAstat-Dx Gastrointestinal Panel 2. Positive results required to generate sequences from bi-directional sequencing with at least 200 bases of adequate quality that by BLAST analyses matched a sequence of the expected organism or gene from NCBI GenBank database with at least 95% query coverage and at least 95% identity compared to the reference.

†The FDA-cleared/CE-marked test method used did not differentiate between *V. parahaemolyticus* and *V. vulnificus* species, therefore additional testing was conducted on the positive specimens using validated PCR assays followed by bidirectional sequencing to identify the corresponding *Vibrio* species.

‡One of the FDA-cleared/CE-marked test methods used in the composite comparator did not differentiate *V. cholerae* species, additional testing was conducted on the positive specimens using a validated PCR test followed by bidirectional sequencing for *V. cholerae* identification.

In addition, to supplement the results of the prospective clinical study, a total of 750 preselected archived frozen specimens known to be positive for at least one of the QIAstat-Dx Gastrointestinal Panel 2 targets were also evaluated (retrospective study). These specimens served to increase the sample size for analytes that showed lower prevalence in the clinical prospective study or that were less represented in a particular sample type (Para-Pak C&S or FecalSwab). The same Comparator Methods detailed in Table 12 was used as confirmatory testing for the presence of the nucleic acids from the expected analytes.

In total, 2689 specimens (1939 prospectively collected and 750 preselected archived specimens) were evaluated in the clinical study. These specimens were collected using Para-Pak C&S (1150) or FecalSwab (1539).

The positive percentage agreement (PPA) and the negative percentage agreement (NPA) were calculated for the prospective and retrospective clinical studies combined.

The PPA was calculated as 100% x (TP / (TP + FN)). True positive (TP) indicates that both the QIAstat-Dx Gastrointestinal Panel 2 and comparator method showed a positive result for this specific target, and false negative (FN) indicates that the QIAstat-Dx Gastrointestinal Panel 2 result was negative while the comparator method result was positive. The NPA was calculated as 100% x (TN / (TN + FP)). True negative (TN) indicates that both the QIAstat-Dx Gastrointestinal Panel 2 and the comparator method showed negative results, and a false positive (FP) indicates that the QIAstat-Dx Gastrointestinal Panel 2 result was positive, but the comparator method result was negative. The PPA and NPA exact binomial two-sided 95% confidence interval was calculated.

Additionally, since several analytes, such as *Entamoeba histolytica* or *Vibrio* species are so rare that both prospective and retrospective testing efforts were insufficient to demonstrate system performance. To supplement the prospective and archived specimens' test results, an evaluation of contrived specimens was performed for several pathogens (Adenovirus F40/F41, Astrovirus, Rotavirus, Sapovirus, *Campylobacter*, ETEC, EIEC/*Shigella*, STEC *stx1/stx2*, *E. coli* O157, *Plesiomonas shigelloides*, *Salmonella*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificus*, *Yersinia enterocolitica*, *Cryptosporidium*, *Cyclospora cayetanensis*, *Entamoeba histolytica* and *Giardia lamblia*). Contrived specimens were prepared using negative residual specimens that had previously tested negative by QIAstat-Dx Gastrointestinal Panel 2 and comparator methods. At least, 50% of these specimens were spiked at concentrations slightly above the Limit of Detection (2x LoD) and the rest at 5x and 10x LoD, using quantified strains for each pathogen. A minimum of 50 contrived specimens were tested for each evaluated analyte. The analyte status of each contrived specimen was blinded to the users analyzing the specimens. The PPA was established for the mentioned targets on contrived specimens as well.

The clinical performance results are summarized in individual performance tables for each target that include clinical specimens (prospective and archived) and contrived specimens test results (Table 14 to Table 36).

Discrepancies between the QIAstat-Dx Gastrointestinal Panel 2 and the comparator methods were investigated for the analytes that the QIAstat-Dx Gastrointestinal Panel 2 test result was compared to one FDA-cleared/CE-marked method. Discrepancies analyses are footnoted on each individual clinical performance Table below and data is presented before and after discordances analysis resolution, except for the 6 targets where a composite of three separate methods was used as comparator (Adenovirus F40/41, Norovirus GI/GII, *V. cholerae*, ETEC, STEC and *Giardia lamblia*) and for the two *Vibrio* species (*V. parahaemolyticus* and *V. vulnificus*) where the comparator method included one FDA-cleared/CE-marked method and PCR assays followed bidirectional sequencing for specific *Vibrio* species identification.

Viruses

Table 14. Adenovirus F40/41

	Positive Percent Agreement			Negative Percent Agreement		
Sample group	**TP/TP+FN**	**%**	**95% CI**	**TN/TN+FP**	**%**	**95% CI**
Clinical	51 / 52	98.1	89.7–100.0	1049 / 1050	99.9	99.5–100.0
Contrived	68 / 70	97.1	90.1–99.7	N/A	N/A	N/A

Table 15. Astrovirus

		Positive Percent Agreement			Negative Percent Agreement		
Sample group	**Analyses**	**TP/TP+FN**	**%**	**95% CI**	**TN/TN+FP**	**%**	**95% CI**
Clinical	Pre-discordant	11 / 12	91.7	61.5–99.8	2124 / 2124	100.0	99.8–100.0
	Post-discordant	11/12*	91.7	61.5–99.8	2124 / 2124	100.0	99.8–100.0
Contrived	N/A	67 / 68	98.5	92.1–100.0	N/A	N/A	N/A

*Astrovirus was detected in the single false negative specimen (1/1) using a different FDA-cleared/CE-marked test method.

Table 16. Norovirus GI/GII

	Positive Percent Agreement			Negative Percent Agreement		
Sample group	TP/TP+FN	%	95% CI	TN/TN+FP	%	95% CI
Clinical	100 / 111	90.1	83.0–95.0	1052 / 1055	99.7	99.2–99.9

Table 17. Rotavirus A

		Positive Percent Agreement			Negative Percent Agreement		
Sample group	Analyses	TP/TP+FN	%	95% CI	TN/TN+FP	%	95% CI
Clinical	Pre-discordant	34 / 37	91.9	78.1–98.3	2096 / 2099	99.9	99.6–100.0
	Post-discordant	34 / 36*	94.4	81.3–99.3	2097 / 2100*	99.9	99.6–100.0
Contrived	N/A	69 / 70	98.6	92.3–100.0	N/A	N/A	N/A

*Rotavirus A was detected in two of three false negative specimens (2/3) and was not detected in the three false positive specimens (0/3) using a different FDA-cleared/CE-marked test method.

Table 18. Sapovirus

		Positive Percent Agreement			Negative Percent Agreement		
Sample group	Analyses	TP/TP+FN	%	95% CI	TN/TN+FP	%	95% CI
Clinical	Pre-discordant	56 / 67	83.6	72.5–91.5	2213 / 2216	99.9	99.6–100.0
	Post-discordant	53 / 54*	98.2	90.1–100.0	2223 / 2229*	99.7	99.4–99.9
Contrived	N/A	69/ 69	100.0	94.8–100.0	N/A	N/A	N/A

*Sapovirus was detected in one of the eleven false negative specimens (1/11) and was detected in one of the three false positive specimens (1/3) using a different FDA-cleared/CE-marked test method.

Bacteria

Table 19. Campylobacter

		Positive Percent Agreement			Negative Percent Agreement		
Sample group	Analyses	TP/TP+FN	%	95% CI	TN/TN+FP	%	95% CI
Clinical	Pre-discordant	129 / 132	97.7	93.5–99.5	1998 / 2006	99.6	99.2–99.8
	Post-discordant	134 / 134*	100.0	97.3–100.0	2001 / 2004*	99.9	99.6–100.0
Contrived	N/A	45/ 46†	97.8	88.5–99.9	N/A	N/A	N/A

**Campylobacter* was not detected in the three false negative specimens (0/3) and was detected in five of the eight false positive specimens (5/8) using a different FDA-cleared/CE-marked test method.

† Less than 50 contrived were tested for *Campylobacter* because the testing was discontinued due to the higher prevalence observed during clinical prospective and retrospective studies.

Table 20. *Clostridium difficile* toxin A/B

		Positive Percent Agreement			Negative Percent Agreement		
Sample group	Analyses	TP/TP+FN	%	95% CI	TN/TN+FP	%	95% CI
Clinical	Pre-discordant	213 / 239	89.1	84.5–92.8	1899 / 1902	99.8	99.5–100.0
	Post-discordant	213 / 224*	95.1	91.4–97.5	1914 / 1917*	99.8	99.5–100.0

**Clostridium difficile* toxin A/B was detected on eleven of the twenty-seven false negative (11/27) and was not detected in any of the three false positive specimens (0/3) using PCR followed by bi-directional sequence analysis.

Table 21. ***Plesiomonas shigelloides***

		Positive Percent Agreement			Negative Percent Agreement		
Sample group	**Analyses**	**TP/TP+FN**	**%**	**95% CI**	**TN/TN+FP**	**%**	**95% CI**
Clinical	Pre-discordant	40 / 44	90.9	78.3–97.5	2227 / 2231	99.8	99.5–100.0
	Post-discordant	40/41*	97.6	87.1–99.9	2230 / 2234*	99.8	99.5–100.0
Contrived	N/A	67 / 68	98.5	92.1–100.0	N/A	N/A	N/A

**Plesiomonas shigelloides* was detected in one of the four false negative specimens (1/4) and was not detected in the four false positive specimens using a different FDA-cleared/CE-marked test method.

Table 22. ***Salmonella***

		Positive Percent Agreement			Negative Percent Agreement		
Sample group	**Analyses**	**TP/TP+FN**	**%**	**95% CI**	**TN/TN+FP**	**%**	**95% CI**
Clinical	Pre-discordant	64 / 68	94.1	85.6–98.4	2068 / 2070	99.9	99.7–100.0
	Post-discordant	64 / 64*	100.0	94.4–100.0	2072 / 2074*	99.9	99.7–100.0
Contrived	N/A	33 / 33†	100.0	89.4–100.0	N/A	N/A	N/A

**Salmonella* was not detected in the four false negative specimen (0/4) and was not detected in the two false positive specimens (0/2) using a different FDA-cleared/CE-marked test method.

†Less than 50 contrived were tested for *Salmonella* because the testing was discontinued due to the higher prevalence observed during clinical prospective and retrospective studies.

Table 23. ***Vibrio cholerae***

	Positive Percent Agreement			Negative Percent Agreement		
Sample group	**TP/TP+FN**	**%**	**95% CI**	**TN/TN+FP**	**%**	**95% CI**
Clinical	1 /1	100.0	2.5–100.0	987 / 989	99.8	99.3–100.0
Contrived	67 / 70	95.7	88.0–99.1	N/A	N/A	N/A

Table 24. ***Vibrio parahaemolyticus***

	Positive Percent Agreement			Negative Percent Agreement		
Sample group	**TP/TP+FN**	**%**	**95% CI**	**TN/TN+FP**	**%**	**95% CI**
Clinical	1 /2*	50.0	9.5–90.6	2133 / 2134*	99.9	99.7–100.0
Contrived	70 / 70	100.0	94.9–100.0	N/A	N/A	N/A

**Vibrio parahaemolyticus* was detected in one additional sample with the QIAstat-Dx Gastrointestinal Panel 2 which was also detected with the FDA-cleared/CE-marked comparator method as *Vibrio* but the specific *Vibrio* species could not be determined with the PCR assays followed by bidirectional sequencing, and therefore was not considered as true positive on the data analyses.

Table 25. ***Vibrio vulnificus***

	Positive Percent Agreement			Negative Percent Agreement		
Sample group	**TP/TP+FN**	**%**	**95% CI**	**TN/TN+FP**	**%**	**95% CI**
Clinical	0 / 0	N/A	N/A	2136 / 2136	100.0	99.8–100.0
Contrived	69 / 69	100.0	94.8–100.0	N/A	N/A	N/A

Table 26. ***Yersinia enterocolitica***

		Positive Percent Agreement			Negative Percent Agreement		
Sample group	**Analyses**	**TP/TP+FN**	**%**	**95% CI**	**TN/TN+FP**	**%**	**95% CI**
Clinical	Pre-discordant	51 / 54	94.4	84.6–98.8	2071 / 2083	99.4	99.0–99.7
	Post-discordant	51 / 51*	100.0	93.0–100.0	2074 / 2086*	99.4	99.0–99.7
Contrived	N/A	68 / 69	98.6	92.2–100.0	N/A	N/A	N/A

**Yersinia enterocolitica* was not detected in the three false negative specimens (0/3) and was not detected in the twelve false positive specimens (0/12) using a different FDA-cleared/CE-marked test method.

Diarrheagenic E. coli/Shigella

Table 27. Enteroaggregative *E. coli* (EAEC)

		Positive Percent Agreement			Negative Percent Agreement		
Sample group	Analyses	TP/TP+FN	%	95% CI	TN/TN+FP	%	95% CI
Clinical	Pre-discordant	82 / 97	84.5	75.8–91.1	2035 / 2040	99.8	99.4–99.9
	Post-discordant	82 / 93*	88.2	79.8–94.0	2039 / 2044*	99.8	99.4–99.9

*Enteroaggregative *E. coli* (EAEC) was detected on thirteen of the seventeen false negatives (13/17) and none of the five false positive specimens were detected (0/5) using PCR followed by bi-directional sequence analysis.

Table 28. Enteropathogenic *E. coli* (EPEC)

		Positive Percent Agreement			Negative Percent Agreement		
Sample group	Analyses	TP/TP+FN	%	95% CI	TN/TN+FP	%	95% CI
Clinical	Pre-discordant	289 / 318	90.9	87.2–93.8	1897 / 1901	99.8	99.5–99.9
	Post-discordant	295 / 316*	93.4	90.0–95.8	1914 / 1917*	99.8	99.5–100.0

*Enteropathogenic *E. coli* (EPEC) was detected in thirteen out of twenty-one false negative specimens (13/21) and was detected in one of the two false positive specimens (1/2) using PCR followed by bi-directional sequence analysis. There were eight (8) other false negative specimens and two (2) false positive specimens that were not further investigated by discrepant analyse.

Table 29. Enterotoxigenic *E.coli* (ETEC) *lt/st*

	Positive Percent Agreement			Negative Percent Agreement		
Sample group	TP/TP+FN	%	95% CI	TN/TN+FP	%	95% CI
Clinical	63 / 67	94.0	85.4–98.4	963 / 975	98.8	97.9–99.4
Contrived	43 / 43	100.0	91.8–100.0	N/A	N/A	N/A

Table 30. Shiga-like toxin *E. coli* (STEC) *stx1/stx2*

	Positive Percent Agreement			Negative Percent Agreement		
Sample group	**TP/TP+FN**	**%**	**95% CI**	**TN/TN+FP**	**%**	**95% CI**
Clinical	70 / 75	93.3	85.1–97.8	937 / 945	99.2	98.3–99.6
Contrived	200 / 200*	100.0	98.2–100.0	N/A	N/A	N/A

*A higher number of test results are shown for STEC *stx1/stx2* target on contrived specimens because they come from non-O157 STEC strains as well as STEC strains with serogroup O157.

Table 31. *E. coli* O157

		Positive Percent Agreement			Negative Percent Agreement		
Sample group	**Analyses**	**TP/TP+FN**	**%**	**95% CI**	**TN/TN+FP**	**%**	**95% CI**
Clinical	Pre-discordant	39 / 41	95.1	83.5–99.4	26 / 26	100.0	86.8–100.0
	Post-discordant	39 / 39*	100.0	91.0–100.0	28 / 28	100.0	87.7–100.0
Contrived	N/A	67 / 69	97.1	89.9–99.7	N/A	N/A	N/A

**E. coli* O157 was not detected in the two false negative specimens (0/2) using a different FDA-cleared/CE-marked test method.

Table 32. *Shigella*/Enteroinvasive *E. coli* (EIEC)

		Positive Percent Agreement			Negative Percent Agreement		
Sample group	**Analyses**	**TP/TP+FN**	**%**	**95% CI**	**TN/TN+FP**	**%**	**95% CI**
Clinical	Pre-discordant	34 / 36	94.4	81.3–99.3	2099 / 2100	99.9	99.7–100.0
	Post-discordant	36 / 37*	97.3	85.8–99.9	2100 / 2100*	100.0	99.8–100.0
Contrived	N/A	69 / 69	100.0	94.8–100.0	N/A	N/A	N/A

**Shigella*/Enteroinvasive *E. coli* (EIEC) was detected in one of the two false negative specimens (1/2) and was detected in the single false positive specimen (1/1) using a FDA-cleared/CE-marked test.

Parasites

Table 33. *Cryptosporidium*

		Positive Percent Agreement			Negative Percent Agreement		
Sample group	Analyses	TP/TP+FN	%	95% CI	TN/TN+FP	%	95% CI
Clinical	Pre-discordant	40 / 42	95.2	83.8–99.4	2220 / 2223	99.9	99.6–100.0
	Post-discordant	40 / 40*	100.0	91.2–100.0	2223 / 2226*	99.9	99.6–100.0
Contrived	N/A	58 / 58	100.0	93.8–100.0	N/A	N/A	N/A

**Cryptosporidium* was not detected in the two false negative specimens (0/2) and was not detected in the three false positive specimens using PCR followed by bi-directional sequence analysis.

Table 34. *Cyclospora cayetanensis*

		Positive Percent Agreement			Negative Percent Agreement		
Sample group	Analyses	TP/TP+FN	%	95% CI	TN/TN+FP	%	95% CI
Clinical	Pre-discordant	23 / 24	95.8	78.9–99.9	2112 / 2112	100.0	99.8–100.0
	Post-discordant	23 / 24*	95.8	78.9–99.9	2112 / 2112	100.0	99.8–100.0
Contrived	N/A	56 / 56	100.0	93.6–100.0	N/A	N/A	N/A

**Cyclospora cayetanensis*, there was one (1) false negative specimen that was not further investigated by discrepant analyses.

Table 35. *Entamoeba histolytica*

		Positive Percent Agreement			Negative Percent Agreement		
Sample group	Analyses	TP/TP+FN	%	95% CI	TN/TN+FP	%	95% CI
Clinical	Pre-discordant	0 / 0	N/A	N/A	2136 / 2136	100.0	99.8–100.0
	Post-discordant	0 / 0	N/A	N/A	2136 / 2136	100.0	99.8–100.0
Contrived	N/A	69 / 70	98.6	92.3–100.0	N/A	N/A	N/A

Table 36. *Giardia lamblia*

	Positive Percent Agreement			Negative Percent Agreement		
Sample group	TP/TP+FN	%	95% CI	TN/TN+FP	%	95% CI
Clinical	63 / 63	100.0	94.3–100.0	983 / 993	99.0	98.2–99.5
Contrived	56 / 56	100.0	93.6–100.0	N/A	N/A	N/A

Clinical Performance Summary

The results for all target pathogens obtained during clinical specimens testing in the prospective and retrospective studies is summarized in Table 37. For the targets that discordances were analyzed, the data is presented after resolution.

Table 37. Clinical Performance Summary in the Prospective and Retrospective studies

Analyte	Positive Percent Agreement			Negative Percent Agreement		
	TP/TP+FN	%	95% CI	TN/TN+FP	%	95% CI
Viruses						
Adenovirus F40/F41	51 / 52	98.1	89.7–100.0	1049 / 1050 *	99.9	99.5–100.0
Astrovirus	11 / 12	91.7	61.5–99.8	2124 / 2124	100.0	99.8–100.0
Norovirus GI/GII	100 / 111	90.1	83.0–94.9	1052 / 1055 *	99.7	99.2–99.9
Rotavirus A	34 / 36	94.4	81.3–99.3	2097 / 2100	99.9	99.6–100.0
Sapovirus	53 / 54	98.2	90.1–100.0	2223 / 2229	99.7	99.4–99.9
Bacteria						
Campylobacter	134 / 134	100.0	97.3–100.0	2001 / 2004	99.9	99.6–100.0
Clostridium difficile	213 / 224	95.1	91.4–97.5	1914 / 1917	99.8	99.5–100.0
Plesiomonas shigelloides	40 / 41	97.6	87.1–99.9	2230 / 2234	99.8	99.5–100.0
Salmonella	64 / 64	100.0	94.4–100.0	2072 / 2074	99.9	99.7–100.0
Vibrio cholerae	1 / 1	100.0	2.5–100.0	987 / 989 *	99.8	99.3–100.0
Vibrio parahaemolyticus	1 / 2	50.0	9.5–90.6	2133 / 2134	99.9	99.7–100.0
Vibrio vulnificus	0 / 0	N/A	N/A	2136 / 2136	100.0	99.8–100.0
Yersinia enterocolitica	51 / 51	100.0	93.0–100.0	2074 / 2086	99.4	99.0–99.7

Table 37. Clinical Performance Summary in the Prospective and Retrospective studies (continued)

Analyte	Positive Percent Agreement			Negative Percent Agreement		
	TP/TP+FN	%	95% CI	TN/TN+FP	%	95% CI
Diarrheagenic *E. coli*/*Shigella*						
Enteroaggregative *E. coli* (EAEC)	82 / 93	88.2	79.8–94.0	2039 / 2044	99.8	99.4–99.9
Enteropathogenic *E. coli* (EPEC)	295 / 316	93.4	90.0–95.8	1914 / 1917	99.8	99.5–100.0
Enterotoxigenic *E. coli* (ETEC) *lt/st*	63 / 67	94.0	85.4–98.4	963 / 975*	98.8	97.9–99.4
Shiga-like toxin *E. coli* (STEC) *stx1/stx2*	70 / 75	93.3	85.1–97.8	937 / 945*	99.2	98.3–99.6
E. coli O157	39 / 39	100.0	91.0–100.0	28 / 28	100.0	87.7–100.0
Shigella/ Enteroinvasive *E. coli* (EIEC)	36 / 37	97.3	85.8–99.9	2100 / 2100	100.0	99.8–100.0
Parasites						
Cryptosporidium	40 / 40	100.0	91.2–100.0	2223 / 2226	99.9	99.6–100.0
Cyclospora cayetanensis	23 / 24	95.8	78.9–99.9	2112 / 2112	100.0	99.8–100.0
Entamoeba histolytica	0 / 0	N/A	N/A	2136 / 2136	100.0	99.8–100.0
Giardia lamblia	63 / 63	100.0	94.3– 100.0	983 / 993*	99.0	98.2–99.5
Overall Panel Performance						
All Analytes	**1464 / 1536**	**95.3**	**94.1–96.3**	**39527/ 39608**	**99.8**	**99.8–99.8**

*The sample size for clinical specificity (NPA) is smaller for the pathogens evaluated with a composite reference (Adenovirus F40/41, Norovirus GI/GII, *Vibrio cholerae*, ETEC, STEC, *Giardia lamblia*) due to a portion of all true negative samples (> 33%) being tested with the full composite comparator method (39.03–43.59 %).

Co-infections

The QIAstat-Dx Gastrointestinal Panel 2 reported multiple organism detections (i.e., mixed infections) for a total of 142 prospectively collected specimens. This represents 21.3% of positive specimens (142/665). Most multiple detections contained two organisms (107/142; 75.4%), while 17.6% (25/142) contained three organisms, 4.2% (6/142) contained four organisms, and 2.8% (4/142) contained five organisms. The most common multiple infections are shown in Table 38 below.

Table 38. Most Prevalent Multiple Detection Combinations (≥5 instances) as Determined by the QIAstat-Dx Gastrointestinal Panel 2

Multiple Detection Combination	Number of Specimens
Enteropathogenic *E. coli* (EPEC) + Enterotoxigenic *E. coli* (ETEC) lt/st	5
Enteroaggregative *E. coli* (EAEC) + Enterotoxigenic *E. coli* (ETEC) lt/st	6
Enteroaggregative *E. coli* (EAEC) + Enteropathogenic *E. coli* (EPEC)	7
Enteropathogenic *E. coli* (EPEC) + Norovirus GI/GII	10
Campylobacter + Enteropathogenic *E. coli* (EPEC)	13
Clostridium difficile toxin A/B + Enteropathogenic *E. coli* (EPEC)	16

As shown in Table 39, the analytes most commonly found (≥10 instances) in mixed infections were EPEC (88), *Clostridium difficile* toxin A/B (44), *Campylobacter* (34), EAEC (33), Norovirus GI/GII (30), ETEC (23) and STEC (12).

Table 39. Prevalence of Analytes in Mixed Infections as determined by the QIAstat-Dx Gastrointestinal Panel 2

Analyte	N	%
Adenovirus F40/F41	5	1.5
Astrovirus	3	0.9
Campylobacter	34	10.2
Clostridium difficile toxin A/B	44	13.2
Cryptosporidium	2	0.6
Cyclospora cayetanensis	4	1.2
E. coli O157	3	0.9
Enteroaggregative *E. coli* (EAEC)	33	9.9
Enteropathogenic *E. coli* (EPEC)	88	26.4
Enterotoxigenic *E. coli* (ETEC) lt/st	23	6.9
Giardia lamblia	6	1.8
Norovirus GI/GII	30	9.0
Plesiomonas shigelloides	8	2.4
Rotavirus A	8	2.4
Salmonella	7	2.1
Sapovirus	8	2.4
Shiga-like toxin *E. coli* (STEC) *stx1/stx2*	12	3.6
Shigella/Enteroinvasive *E. coli* (EIEC)	6	1.8
Vibrio cholerae	2	0.6
Vibrio parahaemolyticus	1	0.3
Yersinia enterocolitica	6	1.8