510(k) SUBSTANTIAL EQUIVALENCE DETERMINATION
DECISION SUMMARY

A. 510(k) Number:

K181427

B. Purpose for Submission:

Clearance of the Enteric Viral Panel assay on the BD MAX System

C. Measurand:

Norovirus, Rotavirus, Adenovirus, Sapovirus, and Astrovirus.

D. Type of Test:

Qualitative real-time polymerase chain reaction

E. Applicant:

Becton, Dickinson and Company

F. Proprietary and Established Names:

BD MAX Enteric Viral Panel

G. Regulatory Information:

1. Regulation section:

   21 CFR 866.3990 - Gastrointestinal microorganism multiplex nucleic acid based assay

2. Classification:

   Class II

3. Product code:

   PCH, OOI

4. Panel:

Microbiology (83)

H. Intended Use:

1. Intended use(s):

   The BD MAX Enteric Viral Panel performed on the BD MAX System, is an automated in vitro diagnostic test for the direct qualitative detection and differentiation of enteric viral pathogens. The BD MAX Enteric Viral Panel detects nucleic acids from

   • Norovirus GI & GII
   • Rotavirus A
   • Adenovirus F40/41
   • Sapovirus (genogroups I, II, IV, V)
   • Human Astrovirus (hAstro)

   Testing is performed on unpreserved soft to diarrheal or Cary-Blair preserved stool specimens from symptomatic patients with suspected acute gastroenteritis, enteritis or colitis. The test is performed directly on the specimen, utilizing real-time polymerase chain reaction (PCR) for the amplification of relevant gene target DNA/RNA. The test utilizes fluorogenic gene-specific hybridization probes for the detection of the amplified DNA.

   This test is intended for use, in conjunction with clinical presentation, laboratory findings, and epidemiological information, as an aid in the differentialdiagnosis of Norovirus GI & GII, Rotavirus A, Adenovirus F40/41, Sapovirus (genogroups I, II, IV, V), and Astrovirus infections. Results of this test should not be used as the sole basis for diagnosis, treatment, or other patient management decisions. Positive results do not rule out co-infection with other organisms that are not detected by this test, and may not be the sole or definitive cause of patient illness. Negative results in the setting of clinical illness compatible with gastroenteritis may be due to infection by pathogens that are not detected by this test or non-infectious causes such as ulcerative colitis, irritable bowel syndrome, or Crohn's disease.

2. Indication(s) for use:

   Same as intended use.

3. Special conditions for use statement(s):

   For prescription use only.

   Limitations:
   - This product should only be used with the BD MAX System.
   - The Sample Buffer Tube has not been designed to support organism viability. If culture is necessary it must be performed from the original specimen.

- The performance of this test has not been evaluated for immunocompromised individuals or for patients without symptoms of gastrointestinal infection.
- BD MAX Enteric Viral Panel assay performance has not been evaluated in individuals who have received the Rotavirus A vaccine, which is known to react with this assay.
- Adenovirus Type 1 associated with infections in humans was shown to have the potential to cross-react with BD MAX Enteric Viral Panel.

Additional limitations are noted in the device labeling.

4. Special instrument requirements:

For use with the BD MAX System.

I. Device Description:

The BD MAX Enteric Viral Panel performed on the BD MAX System, is an automated *in vitro* diagnostic test for the direct qualitative detection and differentiation of enteric viral pathogens. The BD MAX Enteric Viral Panel detects nucleic acids from

• Norovirus GI & GII
• Rotavirus A
• Adenovirus F40/41
• Sapovirus (genogroups I, II, IV, V)
• Human Astrovirus (hAstro)

Testing is performed on unpreserved soft to diarrheal or Cary-Blair preserved stool specimens from symptomatic patients with suspected acute gastroenteritis, enteritis or colitis. The test is performed directly on the specimen, utilizing real-time polymerase chain reaction (PCR) for the amplification of relevant gene target DNA/RNA. The test utilizes fluorogenic gene-specific hybridization probes for the detection of the amplified DNA.

The BD MAX System and the BD MAX Enteric Viral Panel is run with the instrument, associated hardware and accessories, disposable microfluidic cartridges, master mixes, unitized reagent strips, extraction reagents, and sample buffer tubes. The instrument automates sample preparation including target lysis, DNA/RNA extraction and concentration, reagent rehydration, and target nucleic acid amplification and detection using real-time PCR. The assay includes a Sample Processing Control (SPC) that is present in the Extraction Tube. The SPC monitors DNA/RNA extraction steps, thermal cycling steps, reagent integrity and the presence of inhibitory substances. The BD MAX System software automatically interprets test results. A test result may be called as POS (Positive), NEG (Negative), or UNR (Unresolved) for each of the assay's targets, based on the amplification status of the target and of the Sample Processing Control. IND (Indeterminate) or INC (Incomplete) results are due to BD MAX System failure.

Materials provided in each BD MAX Enteric Viral Panel Kit:

Each kit contains sufficient reagents to test 24 samples (443985):

- BD MAX Enteric Viral Panel Master Mix (D6)
- BD MAX Enteric Viral Panel Master Mix (D5)
- BD MAX Enteric Viral Panel Unitized Reagent Strips
- BD MAX Enteric Viral Panel Extraction Tube (D4)
- BD MAX Enteric Viral Panel Ssample Buffer Tube
- BD MAX Disposable Inoculation Loops
- Septum Caps

Materials required but not provided:

- BD MAX PCR Cartridges
- VWR Multi-Tube Vortexer or equivalent
- Vortex Genie 2 or equivalent
- Nalgene Cryogenic Vial Holder
- Rack compatible with a multi-tube vortex mixer (e.g., Cryogenic Vial Holder or equivalent)
- Lab coat and disposable gloves, powderless
- Stopwatch or timer
- For "Unpreserved" stool specimen type:
  - Dry, clean containers for collection of liquid or soft stool specimens.
- For preserved stool specimen type:
  - Cary-Blair transport media (15 mL).

Interpretation of Results

Targets amplified by both mastermixes D6 and D5 are detected with hydrolysis probes (TaqMan probes) labelled at one end with a fluorescent reporter dye and at the other end with a quencher moiety. Six separate probes labelled with different reporter dyes are used to detect, in four different BD MAX System optical channels, the amplicons generated by their respective primers for MM D6 Enteric Viral Panel targets (Astrovirus, Sapovirus, and a sample processing control) and eight probes for MM D5 Enteric Viral Panel targets (Adenovirus, Norovirus, Rotavirus, and a sample processing control). The BD MAX System monitors several amplification curve metrics including: the fluorescence height at the end of the amplification curve (EP fluorescence), the location and value of the curve's first derivative, the location and value of the curve's second derivative, the threshold cycle value with an additional quality control applied to prevent false positives due to signal drift (Ct.Score), and measurements of system noise along the PCR amplification curve. Curve metrics are transformed into results via comparison of the metrics to cutoffs and the use of logic statements. Specifically, cutoffs are applied to the Ct.Score and EP values to determine amplification status with other metrics serving as quality controls.

Results are available on the "Results" tab in the "Results" window on the BD MAX System monitor. The BD MAX System software automatically interprets test results. Results are

reported for each of the analytes and for the Sample Processing Control. A test result may be called as NEG (negative), POS (positive) or UNR (unresolved) based on the amplification status of the target and of the Sample Processing Control. IND (Indeterminate) or INC (Incomplete) results are due to BD MAX System failure and require sample repeat testing. A sample can be re-tested directly from the already prepared Sample Buffer Tube or following the preparation of a new Sample Buffer Tube inoculation. In the case of a partial UNR, where one or more targets have a POS result and all other targets have a UNR result, the targets with a UNR result will not be called NEG. This will be reported on a per Master Mix basis.

Erroneous results may occur from improper specimen collection, handling, storage, technical error, specimen mix-up or because the number of organisms in the specimen is below the analytical sensitivity of the test.

The Sample Processing Control has been added to the test to aid in the identification of samples that contain inhibitors to PCR amplification and as a control for reagent integrity and of the assay system as a whole. The Sample Processing Control does not indicate if nucleic acid has been lost due to inadequate collection, transport or storage of samples, or whether viral capsids have been adequately lysed.

J. Substantial Equivalence Information:

1. Predicate device name(s):

   BioFire FilmArray Gastrointestinal (GI) Panel

2. Predicate 510(k) number(s):

   K143005

3. Comparison with predicate:

Similarities		
Item	**Device: BD MAX Enteric Viral Panel (K181427)**	**Predicate: FilmArray Gastrointestinal Pathogen Panel (K143005)**
Intended Use	The BD MAX Enteric Viral Panel performed on the BD MAX System, is an automated in vitro diagnostic test for the direct qualitative detection and differentiation of enteric viral pathogens. The BD MAX Enteric Viral Panel detects nucleic acids from • Norovirus GI & GII • Rotavirus A • Adenovirus F40/41 • Sapovirus (genogroups I, II, IV, V) • Human Astrovirus (hAstro) Testing is performed on unpreserved soft to diarrheal or Cary-Blair preserved stool specimens from symptomatic patients with suspected acute gastroenteritis, enteritis or colitis. The test is performed directly on the specimen, utilizing real-time polymerase chain reaction (PCR) for the amplification of relevant gene target DNA/RNA. The test utilizes fluorogenic gene-specific hybridization probes for the detection of the amplified DNA. This test is intended for use, in conjunction with clinical presentation, laboratory findings, and epidemiological information, as an aid in the differential diagnosis of Norovirus GI & GII, Rotavirus A, Adenovirus F40/41, Sapovirus (genogroups I, II, IV, V), and Astrovirus infections. Results of this test should not be used as the sole basis for diagnosis, treatment, or other patient management decisions. Positive results do not rule out co-infection with other organisms that are not detected by this test, and may not be the sole or definitive cause of patient illness. Negative results in the setting of clinical illness compatible with gastroenteritis may be due to infection by pathogens that are not detected by this test or non-infectious causes such as ulcerative colitis, irritable bowel syndrome, or Crohn's disease.	The FilmArray Gastrointestinal (GI) Panel is a qualitative multiplexed nucleic acid-based in vitro diagnostic test intended for use with FilmArray systems. The FilmArray GI Panel is capable of the simultaneous detection and identification of nucleic acids from multiple bacteria, viruses, and parasites directly from stool samples in Cary-Blair transport media obtained from individuals with signs and/or symptoms of gastrointestinal infection. The following bacteria (including several diarrheagenic *E. coli*/*Shigella* pathotypes), parasites, and viruses are identified using the FilmArray GI Panel: • *Campylobacter* (*C. jejuni*/*C. coli*/*C. upsaliensis*) • *Clostridium difficile* (*C. difficile*) toxin A/B • *Plesiomonas shigelloides* • *Salmonella* • *Vibrio* (*V. parahaemolyticus*/*V. vulnificus*/*V. cholerae*), including specific identification of *Vibrio cholerae* • *Yersinia enterocolitica* • Enteroaggregative *Escherichia coli* (EAEC) • Enteropathogenic *Escherichia coli* (EPEC) • Enterotoxigenic *Escherichia coli* (ETEC) lt/st • Shiga-like toxin-producing *Escherichia coli* (STEC) stx1/stx2 (including specific identification of the *E. coli* O157 serogroup within STEC) • *Shigella*/Enteroinvasive *Escherichia coli* (EIEC) • *Cryptosporidium* • *Cyclospora cayetanensis* • *Entamoeba histolytica* • *Giardia lamblia* (also known as *G. intestinalis* and *G. duodenalis*) • Adenovirus F 40/41 • Astrovirus • Norovirus GI/GII • Rotavirus A • Sapovirus (Genogroups I, II, IV, and V) The FilmArray GI Panel is indicated as an aid in the diagnosis of specific agents of gastrointestinal illness and results are meant to

		be used in conjunction with other clinical, laboratory, and epidemiological data. Positive results do not rule out co-infection with organisms not included in the FilmArray GI Panel. The agent detected may not be the definite cause of the disease. Concomitant culture is necessary for organism recovery and further typing of bacterial agents. This device is not intended to monitor or guide treatment for *C. difficile* infection. Due to the small number of positive specimens collected for certain organisms during the prospective clinical study, performance characteristics for *E. coli* O157, *Plesiomonas shigelloides*, *Yersinia enterocolitica*, Astrovirus, and Rotavirus A were established primarily with retrospective clinical specimens. Performance characteristics for *Entamoeba histolytica*, and *Vibrio* (*V. parahaemolyticus*, *V. vulnificus*, and *Vibrio cholerae*) were established primarily using contrived clinical specimens. Negative FilmArray GI Panel results in the setting of clinical illness compatible with gastroenteritis may be due to infection by pathogens that are not detected by this test or non-infectious causes such as ulcerative colitis, irritable bowel syndrome, or Crohn's disease. A gastrointestinal microorganism multiplex nucleic acid-based assay also aids in the detection and identification of acute gastroenteritis in the context of outbreaks.
Assay Format	Amplification: Real-time PCR	Same
Organisms Detected	Norovoirus GI & GII Rotavirus A Adenovirus F40/41 Sapovirus (genogroups I, II, IV, V) Human Astrovirus (hAstro)	Same
Assay Results	Qualitative	Same
Analyte	DNA/RNA	Same
Extraction	Automated by instrument	Same
User Complexity	Moderate	Same

Differences		
Item	**Device: BD MAX Enteric Viral Panel (K181427)**	**Predicate: FilmArray Gastrointestinal Pathogen Panel (K143005)**
Assay Format	Detection: Fluorigenic target-specific oligo hybridization (TaqMan)	Detection: non-target-specific double stranded DNA fluorescent dye (LC Green Plus)
Assay Format	Single Real-time PCR reaction	Two-stage PCR amplification
Organisms Detected	See similarities above	Additional bacterial/parasitic analytes as listed in intended use statement above
Specimen Type	Cary-Blair preserved stool and unpreserved soft to diarrheal stool	Cary-Blair preserved stool only
Norovirus Target(s)	Junction RdRp and VP1 capsid gene	ORF1/2 junction
Adenovirus Target(s)	Hexon gene	Hexon Gene
Astrovirus Target(s)	RdRp gene	ORF1b
Rotavirus Target(s)	Non-coding sequence after non-structural protein 3 gene	VP1 and VP6
Sapovirus Target(s)	RdRp gene and Vp1 gene	ORF1 (RdRp)
Assay Controls	Sample Processing Control	Two controls in each pouch for sample processing and both stages of PCR and melt analysis
Time to result	Approximately 3 hours	Approximately 1 hour
Reagent Storage	2-25°C	15-25°C

K. Standard/Guidance Document Referenced (if applicable):

Guidance for the Content of Premarket Submissions for Software Contained in Medical Devices

Molecular Diagnostic Methods for Infectious Diseases; Clinical and Laboratory Standards Institute (CLSI) – Third Edition, MM03

User Protocol for Evaluation of Qualitative Test Performance; Approved Guideline, Clinical and Laboratory Standards Institute (CLSI) – Second Edition, EP12

Guidance for Industry and Food and Drug Administration Staff - Class II Special Controls Guidance Document: Gastrointestinal Microorganism Multiplex Nucleic Acid-Based Assays for Detection and Identification of Microorganisms and Toxin Genes from Human Stool Specimens (November 2, 2015)

L. Test Principle:

Stool specimens are collected from subjects and transported to the laboratory unpreserved in a clean container or preserved in Cary-Blair transport media. A loop is inserted to the depth of the loop into the specimen and expressed via swirling motion into a BD MAX Sample Buffer Tube included in the BD MAX Enteric Viral Panel kit. The Sample Buffer Tube is closed with a septum cap, vortexed and transferred to the BD MAX System. Once the work list is generated and the specimen is loaded on the BD MAX instrument, along with a BD

MAX Enteric Viral Panel Unitized Reagent Strip and PCR Cartridge, the run is started and no further operator intervention is required. The BD MAX System automates specimen preparation, including target organism lysis, DNA/RNA extraction and concentration, reagent rehydration, target nucleic acid sequence amplification and detection using real-time PCR. The interpretation of the signal is performed automatically by the BD MAX System. The assay also includes a Sample Processing Control that is provided in the Extraction Tube and subjected to extraction, concentration and amplification steps. The Sample Processing Control monitors for the presence of potential inhibitory substances as well as system or reagent failures. Following enzymatic viral lysis at an elevated temperature, the released nucleic acids are captured by magnetic affinity beads.

The beads, with the bound nucleic acids, are washed and the nucleic acids are eluted. Eluted DNA/RNA is neutralized and transferred to the Master Mix tubes to rehydrate the PCR reagents. After rehydration, the BD MAX System dispenses a fixed volume of PCR-ready solution into the BD MAX PCR Cartridge. Microvalves in the BD MAX PCR Cartridge are sealed by the system to prevent evaporation and amplicon contamination prior to the initiation of reverse transcriptase PCR to convert RNA to cDNA and subsequent real time PCR.

The amplified DNA targets are detected using hydrolysis (TaqMan) probes labeled at one end with a fluorescent reporter dye (fluorophore) and at the other end with a quencher moiety. Probes labeled with different fluorophores are used to detect the amplicons of the viral targets (Norovirus GI & GII, Rotavirus A, Adenovirus F40/41, Sapovirus (genogroups I, II, IV, V), and hAstro) and the Sample Processing Control amplicons in four different optical channels of the BD MAX System. When the probes are in their native state, the fluorescence of the fluorophore is quenched due to its proximity to the quencher. However, in the presence of target DNA, the probes hybridize to their complementary sequences and are hydrolyzed by the 5'–3' exonuclease activity of the DNA polymerase as it synthesizes the nascent strand along the cDNA template. As a result, the fluorophores are separated from the quencher molecules and fluorescence is emitted. The BD MAX System monitors these signals at each cycle and interprets the data at the end of the program to report the final results.

M. Performance Characteristics (if/when applicable):

1. <u>Analytical performance:</u>

   a. Precision/Reproducibility:

   The reproducibility panel utilized in all of the precision/reproducibility studies consisted of 18 individual members. Three members of the panel contained no analytes. Each of the 15 remaining panel members consisted of one viral pathogen at low positive levels (2x LoD) and one viral pathogen at moderate positive levels (3x LoD) with all other viral targets absent. In total, each individual viral target of the Enteric Viral Panel was represented with 3 low positive (LP), 3 moderate positive (MP) and 12 true negative (TN) samples. However, the combination of each analyte

per panel member is fixed. For example, the moderate positive Rotavirus specimens always contain low positive Norovirus. And the moderate positive Sapovirus samples always contain low positive Rotavirus. Proposed acceptance criteria included ≥95% agreement with expected results for all low positive specimens and 100% agreement with expected results for all moderate positive and true negative specimens. All study results met the acceptance criteria for all targets and all categories.

For the Site-to-Site Reproducibility study, a single lot of reagents was tested over the course of 5 days at three sites. Two users each completed a single run of 18 panel members each day for a total of 30 runs.

Table 1: Qualitative Site-to-Site Reproducibility Results

Target	Category	X LoD	Agreement with Expected Results (95% CI)			
			Site			Overall
			1	2	3	
Norovirus	TN	0	100% (97.0-100%)	100% (97.0-100%)	100% (97.0-100%)	100% (99.0-100)
	LP	2	100% (88.4-100)	100% (88.4-100)	100% (88.4-100)	100% (96.0-100)
	MP	3	100% (88.4-100)	100% (88.4-100)	100% (88.4-100)	100% (96.0-100)
Rotavirus	TN	0	100% (97.0-100%)	100% (97.0-100%)	100% (97.0-100%)	100% (99.0-100)
	LP	2	100% (88.4-100)	93.3% (77.9-99.2%)	100% (88.4-100)	97.8% (92.2-99.7)
	MP	3	100% (88.4-100)	100% (88.4-100)	100% (88.4-100)	100% (96.0-100)
Adenovirus	TN	0	100% (97.0-100%)	100% (97.0-100%)	100% (97.0-100%)	100% (99.0-100)
	LP	2	100% (88.4-100)	100% (88.4-100)	100% (88.4-100)	100% (96.0-100)
	MP	3	100% (88.4-100)	100% (88.4-100)	100% (88.4-100)	100% (96.0-100)
Sapovirus	TN	0	100% (97.0-100%)	100% (97.0-100%)	100% (97.0-100%)	100% (99.0-100)
	LP	2	100% (88.4-100)	100% (88.4-100)	100% (88.4-100)	100% (96.0-100)
	MP	3	100% (88.4-100)	90.0% (73.5-97.9%)	100% (88.4-100)	96.7% (90.6-99.3)
Astrovirus	TN	0	100% (97.0-100%)	100% (97.0-100%)	100% (97.0-100%)	100% (99.0-100)
	LP	2	100% (88.4-100)	96.7% (82.8-99.9%)	100% (88.4-100)	98.9% (94.0-100)
	MP	3	100% (88.4-100)	100% (88.4-100)	100% (88.4-100)	100% (96.0-100)

A quantitative analysis of site-to-site variance on the numerical outputs used by the BD MAX for sample classification (Ct.Score and Cycle EP) was also performed.

Table 2: Quantitative Site-to-Site Reproducibility Results

Target	Metric	Sample	N	Mean (ct)	Within Run		Between Run Within Day		Between Day Within Site		Between Site		Total	
					SD	%CV	SD	%CV	SD	%CV	SD	%CV	SD	%CV
Norovirus	Ct.Score	LP	90	30	0	1	0	0	0	0	0	0	0	1
		MP	90	30	0	1	0	0	0	0	0	0	0	1
	Cycle End Point	LP	90	4553	1215	27	368	8	0	0	0	0	1270	28
		MP	90	4129	1760	43	0	0	0	0	178	4	1769	43
Rotavirus	Ct.Score	LP	88	32	1	2	0	0	0	0	0	1	1	2
		MP	90	31	0	1	0	0	0	0	0	1	1	2
	Cycle End Point	LP	88	738	238	32	0	0	0	0	270	37	360	49
		MP	90	925	243	26	0	0	0	0	295	32	382	41
Adenovirus	Ct.Score	LP	90	29	1	2	0	0	0	1	0	1	1	2
		MP	90	29	1	2	0	0	0	0	0	1	1	2
	Cycle End Point	LP	90	1067	470	44	136	13	0	0	282	26	565	53
		MP	90	1097	411	38	146	13	0	0	241	22	498	46
Sapovirus	Ct.Score	LP	90	29	0	1	0	0	0	0	0	1	0	2
		MP	87	29	0	2	0	0	0	0	0	1	1	2
	Cycle End Point	LP	90	754	232	31	0	0	0	0	198	26	305	40
		MP	87	963	271	28	44	5	25	3	152	16	315	33
Astrovirus	Ct.Score	LP	89	29	0	2	0	0	0	0	0	0	0	2
		MP	90	28	0	1	0	0	0	0	0	0	0	1
	Cycle End Point	LP	89	3166	1110	35	71	2	343	11	0	0	1164	37
		MP	90	4786	1071	22	460	10	359	8	341	7	1266	27
SPC MM D6	Ct.Score	TN	90	27	0	1	0	0	0	0	0	1	0	1
	Cycle End Point	TN	90	8582	927	11	537	6	0	0	448	5	161	14
SPC MM D5	Ct.Score	TN	90	28	0	13	0	0	0	0	0	0	0	1
	Cycle End Point	TN	90	7668	1510	20	1010	13	0	0	707	9	1949	25

To evaluate lot-to-lot reproducibility, three lots of reagents were tested over five days at a single site. Two operators performed two runs per day for a total of 30 runs. Results from five days of the precision study were used as the final lot for analysis of lot-to-lot reproducibility. All lot-to-lot study results met the acceptance criteria for all targets and all categories.

The cycle end point fluorescence values typically have high standard deviations but also high absolute magnitudes (700-5,000) compared to the cut-off threshold for these values to make a positive call (70-200). A high degree of the observed variance is due to higher value outliers among a pool of relatively consistent datapoints that do not approach the threshold cutoff for these analytes.

Table 3: Qualitative Lot-to-Lot Reproducibility Results

Target	Category	X LoD	Agreement with Expected Results (95% CI)			
			Lot			Overall
			IUO3	IUO4	IUO5	
Norovirus	TN	0	100% (97.0-100)	100% (97.0-100)	100% (97.0-100)	100% (99.0-100)
	LP	2	100% (88.4-100)	100% (88.4-100)	100% (88.4-100)	100% (96.0-100)
	MP	3	100% (88.4-100)	100% (88.4-100)	100% (88.4-100)	100% (96.0-100)
Rotavirus	TN	0	99.2% (95.4-99.9)	100% (97.0-100)	100% (97.0-100)	99.7% (98.4-100)
	LP	2	100% (88.4-100)	93.3% (77.9-99.2%)	100% (88.4-100)	97.8% (92.2-99.7)
	MP	3	100% (88.4-100)	100% (88.4-100)	100% (88.4-100)	100% (96.0-100)
Adenovirus	TN	0	100% (97.0-100)	100% (97.0-100)	100% (97.0-100)	100% (99.0-100)
	LP	2	100% (88.4-100)	100% (88.4-100)	100% (88.4-100)	100% (96.0-100)
	MP	3	100% (88.4-100)	100% (88.4-100)	100% (88.4-100)	100% (96.0-100)
Sapovirus	TN	0	100% (97.0-100)	100% (97.0-100)	100% (97.0-100)	100% (99.0-100)
	LP	2	96.7% (83.3-99.4)	100% (88.4-100)	100% (88.4-100)	98.9% (94.0-99.8)
	MP	3	100% (88.4-100)	100% (88.4-100)	100% (88.4-100)	100% (96.0-100)
Astrovirus	TN	0	100% (97.0-100)	100% (97.0-100)	100% (97.0-100)	100% (99.0-100)
	LP	2	100% (88.4-100)	100% (88.4-100)	100% (88.4-100)	100% (96.0-100)
	MP	3	100% (88.4-100)	100% (88.4-100)	100% (88.4-100)	100% (96.0-100)

Table 4: Quantitative Lot-to-Lot Reproducibility Results

Target	Metric	Sample	N	Mean	Within Run		Between Run Within Day		Between Day Within Site		Between Site		Total	
					SD	%CV	SD	%CV	SD	%CV	SD	%CV	SD	%CV
Norovirus	Ct.Score	LP	90	30	0	1	0	1	0	0	0	0	0	1
		MP	90	30	0	1	0	1	0	0	0	0	0	1
	Cycle End Point	LP	90	4946	1188	24	1606	33	0	0	705	14	2118	43
		MP	90	4949	856	17	1702	34	0	0	1208	24	2256	46

Target	Metric	Sample	N	Mean	Within Run		Between Run Within Day		Between Day Within Site		Between Site		Total	
					SD	%CV	SD	%CV	SD	%CV	SD	%CV	SD	%CV
Rotavirus	Ct.Score	LP	90	32	0	1	0	0	0	0	0	0	0	2
		MP	90	31	0	1	0	0	0	0	0	0	0	1
	Cycle End Point	LP	90	1117	231	21	25	2	44	4	124	11	276	24
		MP	90	1346	165	12	104	8	59	4	85	6	221	16
Adenovirus	Ct.Score	LP	90	28	0	2	0	1	0	0	0	0	1	2
		MP	90	29	0	1	0	1	0	0	0	0	1	2
	Cycle End Point	LP	90	1191	360	30	515	43	0	0	392	28	710	60
		MP	90	1171	292	25	629	54	0	0	270	23	744	64
Sapovirus	Ct.Score	LP	89	29	0	1	0	0	0	0	0	0	0	1
		MP	90	29	1	3	0	0	0	0	0	0	1	3
	Cycle End Point	LP	89	1184	291	25	175	15	0	0	178	15	383	32
		MP	90	1311	382	29	0	0	0	0	138	11	406	31
Astrovirus	Ct.Score	LP	90	29	0	1	0	1	0	0	0	0	0	2
		MP	90	28	0	1	0	1	0	0	0	0	0	1
	Cycle End Point	LP	90	3278	575	18	579	18	0	0	500	14	932	28
		MP	90	4724	543	12	558	12	105	2	512	11	938	20
SPC MM D6	Ct.Score	TN	90	27	0	1	0	0	0	0	0	1	0	2
	Cycle End Point	TN	90	8994	651	7	667	7	0	0	259	3	967	11
SPC MM D5	Ct.Score	TN	90	27	0	1	0	0	0	0	0	1	0	2
	Cycle End Point	TN	90	8740	834	10	1198	14	0	0	565	7	1565	18

The precision study utilized only 12 of the 18 original reproducibility panel members. A single lot of reagents were tested over 12 days at a single site with two users completing a single run on each day of the study. The composition of the panel included true negative (TN), low positive (LP), and moderate positive (MP) reactivities for each analyte. A total of 24 runs were performed.

Table 5: Qualitative Precision Results

Category	Agreement with Expected Results				
	Norovirus	Rotavirus	Adenovirus	Sapovirus	Astrovirus
TN	100% (98-100)	99.5% (97.1-99.9)	100% (98.0-100)	100% (98.0-100)	100% (98.0-100)
LP	100% (92.6-100)	100% (92.6-100)	100% (92.6-100)	100% (92.6-100)	100% (92.6-100)
MP	100% (92.6-100)	100% (92.6-100)	100% (92.6-100)	100% (92.6-100)	100% (92.6-100)

Again, quantitative analysis was performed on numerical PCR metrics from the precision study (Table 6) and while the Cycle EP values do sometimes exhibit high variance, especially in low positive panel members, this is usually due to the presence of higher value outliers. No values are near the cutoff threshold for each analyte.

The largest Ct.Score variability observed during the quantitative Precision study segment (among TN, LP and MP) was obtained for the Adenovirus target, which obtained a 2.1% overall variability for the LP and MP. Overall variability values for Ct.Score obtained for the other targets ranged between 0.9% and 1.8%. In Cycle EP, variability for the LP and MP ranged from 15.5% to 64.7%.

Table 6: Quantitative Precision Results

Target	Metric	Sample	N	Mean	Within Run		Between Run Within Day		Between Day		Total	
					SD	%CV	SD	%CV	SD	%CV	SD	%CV
Norovirus	Ct.Score	LP	48	30	0	1	0	1	0	0	0	1
		MP	48	30	0	1	0	1	0	0	0	1
	Cycle End Point	LP	48	4416	911	21	1857	42	200	5	2078	47
		MP	48	4727	803	17	1470	31	1051	22	1978	42
Rotavirus	Ct.Score	LP	48	32	1	2	0	0	0	1	1	2
		MP	48	31	0	1	0	0	0	1	0	1
	Cycle End Point	LP	48	1050	242	23	97	9	80	8	273	26
		MP	48	1269	158	12	132	10	84	7	222	18
Adenovirus	Ct.Score	LP	48	28	0	2	0	1	0	0	1	2
		MP	48	29	0	1	0	2	0	0	1	2
	Cycle End Point	LP	48	1171	315	27	510	44	165	14	622	53
		MP	48	1119	335	30	641	57	0	0	724	65
Sapovirus	Ct.Score	LP	48	29	0	1	0	1	0	1	0	1
		MP	48	28	0	1	0	1	0	0	0	1
	Cycle End Point	LP	48	1205	170	14	199	17	0	0	262	22
		MP	48	1333	266	20	85	6	126	9	306	23
Astrovirus	Ct.Score	LP	48	29	0	2	0	1	0	0	1	2
		MP	48	28	0	1	0	0	0	0	0	1
	Cycle End Point	LP	48	3579	901	25	406	11	311	9	1036	29
		MP	48	5716	670	13	413	8	152	3	802	16
SPC MM D6	Ct.Score	TN	48	27	0	1	0	0	0	0	0	1
	Cycle End Point	TN	48	8666	754	9	853	10	0	0	1138	13
SPC MM D5	Ct.Score	TN	48	27	0	1	0	0	0	0	0	1
	Cycle End Point	TN	48	8421	1336	16	1261	15	0	0	1837	22

b. Linearity/assay reportable range:

Not applicable.

c. Traceability, Stability, Expected values (controls, calibrators, or methods):

Specimen Stability:

According to the package insert, specimens can be stored for up to 120 hours (5 days) at 2-8°C or for up to 48 hours at 2-25°C before testing. Similarly, prepared SBTs can be stored at 2-8°C for a maximum of 120 hours (5 days) OR at 2-25°C for a maximum of 48 hours. Studies to support this stability claim for both Cary-Blair preserved and unpreserved stool specimens followed the below scheme (**Tables 7 & 8**):

Table 7: Sample Stability Testing Scheme - Round 1

Test Point	**Neat**		**SBT**		**Minimum Total Hours**
	Storage Condition 1		***Storage Condition 2***		
1 (Baseline)	N/A				0
2	25°C	48 hrs	N/A		48
3			25°C	24 hrs	72
4			2-8°C	120 hrs	168
5	2-8°C	120 hrs	N/A		120
6			25°C	24 hrs	144
7			2-8°C	120 hrs	240

Table 8: Sample Stability Testing Scheme - Round 2

Test Point	**Neat**		**SBT**		**Minimum Total Hours**
	Storage Condition 1		***Storage Condition 2***		
1 (Baseline)	N/A				0
2	25°C	48 hrs	25°C	48 hrs	96
3	2-8°C	120 hrs	25°C	48 hrs	168

A minimum of twenty valid replicates for positives and four valid replicates for negatives were required for each condition tested. Baseline testing was required to yield 100% (20/20) positive replicates and 100% (4/4) negative replicates. Each subsequent test point was required to yield ≥ 95% (19/20) positive replicates and 100% (4/4) negative replicates. Additionally, a trend of the quantitative PCR curve metrics for each channel over time was modeled using simple linear regression analysis. The stability break point at which the specimen was no longer considered stable was reached when the one-sided 95% lower confidence interval of the linear regression crossed the acceptable drift limit ("ADL") in any channel. The ADL was determined for each target at baseline, which was derived from the mean Ct.Score endpoint thresholds.

Data from the specimen stability study supports claims in the package insert, with no observed change in sample status (**Table 9** and **Table 10**) or significant loss of cycle EP . One run of test point 4 for unpreserved stool samples included several samples with unexpected negative results. The run was repeated to exclude sample stability issues and this data is presented in **Table 10**. Regression lines of quantitative PCR parameters were plotted with the 95% confidence interval and the

slope of the regression analysis determined for each sample and condition. In no instance did the lower 95% confidence bound intersect the lower specification (EP min) within the duration of the study period.

Table 9: Cary-Blair Preserved Stool Sample Stability

Test Point	Neat		SBT		Min. Total Hrs	Positive Results					Negative Results	UNR/ IND/ INC Results
	Storage Condition 1		Storage Condition 2			AdV F41	AdV Type 4	NoV GII	RoV Va70	SaV GI		
1	Baseline				0	20/20	20/20	20/20	20/20	20/20	4/4	0
2	25°C	48 h	N/A		48	20/20	20/20	20/20	20/20	20/20	4/4	0
3			25°C	24 h	72	20/20	20/20	20/20	19/20	20/20	4/4	0
1[a]	Baseline				0	19/20	19/20	19/20	19/20	19/20	4/4	5
1[b]	Baseline				0	1/1	1/1	1/1	1/1	1/1	1/1	0
4	25°C	48 h	2-8°C	120h	168	19/20	19/20	19/20	19/20	19/20	4/4	5
4[c]						1/1	1/1	1/1	1/1	1/1	N/A	0
5	2-8°C	120	N/A		120	20/20	20/20	20/20	20/20	20/20	4/4	0
6			25°C	24 h	144	20/20	20/20	20/20	19/20	20/20	4/4	0
7			2-8°C	120 h	240	20/20	20/20	20/20	19/20	20/20	4/4	0

[a]Baseline repeated due to instrument malfunction
[b]Sample retested to obtain valid result
[c]Sample repeated due to IND result

Table 10: Unpreserved Stool Sample Stability

Test Point	Neat		SBT		Min. Total Hrs	Positive Results					Negative Results	UNR/ IND/ INC Results
	Storage Condition 1		Storage Condition 2			AdV F41	AdV Type 4	NoV GII	RoV Va70	SaV GI		
1	Baseline				0	20/20	20/20	20/20	20/20	20/20	4/4	0
2[a]	25°C	48 h	N/A		48	38/40	40/40	38/40	38/40	40/40	8/8	0
3			25°C	24 h	72	20/20	20/20	20/20	20/20	20/20	4/4	0
4[b]	25°C	48 h	2-8°C	120h	168	20/20	20/20	20/20	20/20	20/20	4/4	0
4[b]						10/10	10/10	10/10	10/10	10/10	2/2	0
5	2-8°C	120	N/A		120	20/20	20/20	20/20	20/20	20/20	4/4	0
6			25°C	24 h	144	20/20	20/20	20/20	20/20	20/20	4/4	0
7			2-8°C	120 h	240	20/20	19/20	20/20	20/20	19/20	4/4	0

[a]Instrument/reagent error caused repeat testing
[b]Retest to ensure original results were due to instrument error

A fresh vs. frozen study was performed to demonstrate no difference in assay performance upon repeated freeze-thaw cycles and validate the use of frozen retrospective samples in the clinical studies. A total of 60 replicates for each analyte present at 1.99x LoD (N = 30), 4x LoD (N = 15), and 10x LoD (N = 15) were analyzed at baseline and after 1, 2, or 3 freeze-thaw cycles. All data agreed with the expected results (**Table 11**) and the data demonstrated no significant drift in Ct cycle values.

Table 11: Freeze-Thaw Study

Condition		Proportion Positive (%)[a]				
Matrix	**Freeze-Thaw Cycles**	**Norovirus GII**	**Rotavirus Va70**	**Adenovirus F41**	**Astrovirus Type 4**	**Sapovirus GI**
Unpreserved	**0**	60/60 (100)	60/60 (100)	60/60 (100)	60/60 (100)	60/60 (100)
	1	60/60 (100)	60/60 (100)	60/60 (100)	60/60 (100)	60/60 (100)
	2	60/60 (100)	60/60 (100)	60/60 (100)	60/60 (100)	60/60 (100)
	3	60/60 (100)	60/60 (100)	60/60 (100)	60/60 (100)	60/60 (100)
Preserved	**0**	60/60 (100)	60/60 (100)	60/60 (100)	60/60 (100)	60/60 (100)
	1	60/60 (100)	60/60 (100)	60/60 (100)	60/60 (100)	60/60 (100)
	2	60/60 (100)	60/60 (100)	60/60 (100)	60/60 (100)	60/60 (100)
	3	60/60 (100)	60/60 (100)	60/60 (100)	60/60 (100)	60/60 (100)

[a]Proportion positive rates were calculated based on sample number after exclusion of IND/UNR results

Internal Control Effectiveness

The sample processing control is designed to flag the user to potentially disruptive errors in either sample extraction and nucleic acid purification or inhibition of the PCR reaction. Samples that are reactive in the absence of a positive SPC control signal will still be called positive; however, negative samples will be labeled unresolved and necessitate repeat testing. To validate proper performance of the SPC control, the sponsor performed 20 runs of the assay under normal conditions (control), improper extraction (I), and absence of a mastermix tube (II). These conditions were evaluated for each mastermix in the assay. All test runs agreed with expected results except for one improper extraction sample that actually exhibited unexpected SPC amplification (**Table 12**).

Table 12: SPC Effectiveness Testing

Condition	# Tested	Expected Result	Results					% Agreement
			IND	INC	UNR	POS	NEG	
Control	20	Negative	0	0	0	0	20	100%
I MM D6	20	Unresolved	0	0	19	0	1	95%
I MM D5	20	Unresolved	0	0	20	0	0	100%
II MM D6	20	Indeterminate	20	0	0	0	0	100%
II MM D5	20	Indeterminate	20	0	0	0	0	100%

d. Detection limit:

Individual sample buffer tubes were spiked with the viral pathogens detected by the BD MAX Enteric Viral Panel assay in the presence of either unpreserved or Cary-Blair preserved stool matrix. A putative LoD was determined by testing 4 replicates across a range of 5 analyte levels using 3 lots of assay reagents. Further confirmation of LoD was determined by additional testing of 20 replicates near the putative LoD levels to achieve 95% detection. The final LoD determination for each analyte in either Unpreserved and Cary-Blair preserved stool matrix is displayed in **Table 13** and **Table 14**, respectively.

Table 13: BD MAX Enteric Viral Panel LoD Results in Unpreserved Stool Matrix

Organism	Strain	LoD (cp/mL)	Positivity	95% Confidence Interval
Adenovirus	F40	6.89E+04	95% (19/20)	76.4% - 99.1%
	F41	8.16E+04	100% (20/20)	83.9% - 100%
Astrovirus	Type 4	1.75E+07	100% (20/20)	83.9% - 100%
	Type 8	5.23E+06	100% (20/20)	83.9% - 100%
Rotavirus	WA	6.46E+03	95% (19/20)	76.4% - 99.1%
	Va70	1.16E+04	100% (20/20)	83.9% - 100%
Norovirus	GI	6.28E+06	95% (19/20)	76.4% - 99.1%
	GII	2.49E+05	95% (19/20)	76.4% - 99.1%
Sapovirus	GI	6.51E+07	95% (19/20)	76.4% - 99.1%
	GII	1.94E+06	100% (20/20)	83.9% - 100%

Table 14: BD MAX Enteric Viral Panel LoD Results in Preserved Stool Matrix

Organism	Strain	LoD (cp/mL)	Positivity	95% Confidence Interval
Adenovirus	F40	2.75E+05	100% (20/20)	83.9% - 100%
	F41	1.22E+05	100% (20/20)	83.9% - 100%
Astrovirus	Type 4	3.49E+07	100% (20/20)	83.9% - 100%
	Type 8	2.09E+07	95% (19/20)	76.4% - 99.1%
Rotavirus	WA	1.29E+04	95% (19/20)	76.4% - 99.1%
	Va70	5.82E+03	100% (20/20)	83.9% - 100%
Norovirus	GI	4.71E+06	95% (19/20)	76.4% - 99.1%
	GII	2.49E+05	100% (20/20)	83.9% - 100%
Sapovirus	GI	6.51E+07	100% (20/20)	83.9% - 100%
	GII	1.94E+06	95% (19/20)	76.4% - 99.1%

e. Analytical specificity:

Cross reactivity:

Other off-panel phylogenetically related microorganisms that may be present in human stool were evaluated for potential Enteric Viral Panel reactivity. Specifically, 94 bacteria. ten viruses, and eight parasites were tested in three replicates using three reagent lots and twelve BD MAX instruments (**Table 15**). The concentrations of bacteria/parasites were confirmed by colony/cell count while parasites were enumerated by the respective suppliers. Viruses were quantitated by their respective vendor(s) and the concentrations were documented in the Certificates of Analysis. Samples that exhibited initial reactivity or had INC or UNR results were subsequently retested (**Table 16** and **Table 17**). Adenovirus Type 1 was the only pathogen to exhibit cross-reactivity, being consistently detected by the Enteric Viral Panel adenovirus test and thus included as a cross-reactant in the package insert. This reactivity disappeared at a tenfold lower dilution of virus.

Cross-reactivity with organisms other than those listed in the table below has not been evaluated.

Table 15: Testing of Potentially Cross-Reactive Organisms

Microorganism	Concentration (CFU/mL)	Collection Number	Test Result (Positive/Total)	Initial Result Details
Abiotrophia defectiva	1.1E+08	ATCC 49176	0/3	All NEG
Acinetobacter baumannii	2.0E+08	ATCC 19606	0/3	All NEG
Acinetobacter iwoffii	2.0E+08	ATCC 15309	0/3	All NEG
Aeromonas caviae	1.7E+08	ATCC 15468	0/0[b]	3 INC
Aeromonas hydrophila	1.7E+08	ATCC 7966	0/3	All NEG
Aeromonas schubertii	1.7E+08	ATCC 43700	0/3	All NEG
Aeromonas sobria	1.7E+08	ATCC BAA-237	0/3	All NEG

Microorganism	Concentration (CFU/mL)	Collection Number	Test Result (Positive/Total)	Initial Result Details
Aeromonas veronii	1.7E+08	ATCC 35623	0/3	All NEG
Alcaligenes faecalis subsp. faecalis	3.4E+08	ATCC 15554	1/3[b]	1 NoV POS 2 NEG
Anaerococcus tetradius	1.2E+08	ATCC 35098	0/3	All NEG
Arcobacter butzleri	2.0E+08	ATCC 49616	0/3	All NEG
Bacillus cereus	8.2E+07	ATCC 13472	0/3	All NEG
Bacteroides caccae	6.8E+08	ATCC 43185	0/3	All NEG
Bacteroides stercoris	6.8E+08	ATCC 43183	0/2[b]	2 NEG 1 UNR
Bifidobacterium adolescentis	9.2E+08	ATCC 15703	0/3	All NEG
Bifidobacterium bifidum	9.2E+08	ATCC 29521	0/3	All NEG
Campylobacter coli	1.0 McF[a]	ATCC 43134	0/3	All NEG
Campylobacter jejuni	6.4E+07	NH 411	0/3	All NEG
Candida albicans	1.8E+07	ATCC 24433	0/2[b]	2 NEG 1 INC
Cedecea davisae	2.4E+08	ATCC 33431	0/3	All NEG
Citrobacter freundii	2.4E+08	ATCC 8090	0/3	All NEG
Citrobacter koseri	2.4E+08	ATCC 27028	0/3	All NEG
Chlamydia trachomatis serovar D	6.84E+08 EBs/mL[a]	RD013117-01	0/3	All NEG
Clostridium difficile	6.1E+06	ATCC 43598	0/3	All NEG
Clostridium histolyticum	6.1E+06	ATCC 19401	0/3	All NEG
Clostridium perfringens	6.1E+06	ATCC 13124	0/3	All NEG
Clostridium sordellii	6.1E+06	ATCC 9714	0/3	All NEG
Clostridium tetani	6.1E+06	ATCC 19406	0/3	All NEG
Collinsella aerofaciens	2.2E+08	ATCC 33031	0/3	All NEG
Corynebacterium genitalium	2.8E+08	ATCC 33031	0/3	All NEG
Desulfovibrio piger	7.5E+07	ATCC 29098	0/3	All NEG
Edwardsiella tarda	3.3E+08	ATCC 15947	0/3	All NEG
Eggerthella lenta	4.7E+08	CCRI-9926	0/2[b]	2 NEG 1 UNR
Enterobacter cloacae	2.6E+08	ATCC 35030	0/3	All NEG
Enterococcus faecalis	2.5E+08	ATCC 29212	0/3	All NEG
Enterococcus faecium	2.5E+08	ATCC 700221	0/3	All NEG
Escherichia coli	4.4E+08	ENF 10513	0/3	All NEG
Escherichia coli O157: H7 EHEC	4.1E+08	ATCC 43889	0/3	All NEG
Escherichia coli ETEC H10405 O78:H11 (Lt/St)	1.6E+08	ATCC 35401	0/3	All NEG
Escherichia fergusonii	2.5E+08	ATCC 35469	0/3	All NEG
Escherichia hermannii	2.5E+08	ATCC 33650	1/3	1 NoV POS 2 NEG
Escherichia vulneris	2.5E+08	ATCC 33821	0/3	All NEG
Fusobacterium varium	3.4E+08	ATCC 8501	0/3	All NEG
Gardnerella vaginalis	2.1E+08	ATCC 14019	0/2[b]	2 NEG 1 INC
Gemella morbillorum	1.3E+08	ATCC 27824	0/3	All NEG

Microorganism	Concentration (CFU/mL)	Collection Number	Test Result (Positive/Total)	Initial Result Details
Hafnia alvei	3.5E+08	ATCC 13337	0/3	All NEG
Helicobacter pylori	2.4E+08	ATCC 43504	0/2[b]	2 NEG 1 INC
Klebsiella aerogenes	2.6E+08	ATCC 13048	0/3	All NEG
Klebsiella oxytoca	1.8E+08	ATCC 33496	0/3	All NEG
Klebsiella pneumoniae	1.8E+08	ATCC 700603	0/3	All NEG
Lactobacillus acidophilus	9.2E+07	ATCC 4356	0/2[b]	2 NEG 1 INC
Lactococcus lactis	1.9E+08	ATCC 11454	0/3	All NEG
Leminorella grimontii	6.5E+08	ATCC 33999	0/3	All NEG
Listeria monocytogenes	6.3E+08	ATCC 15313	0/3	All NEG
Megamonas hypermegale	2.5E+07	ATCC 25560	0/3	All NEG
Megasphaeara elsdenii	3.5E+07	ATCC 25940	0/3	All NEG
Morganella morganii	2.8E+08	ATCC 25830	0/3	All NEG
Parabacteroides merdae	5.5E+08	ATCC 43184	0/3	All NEG
Peptoniphilus asaccharolyticus	2.7E+08	ATCC 14963	0/3	All NEG
Peptostreptococcus anaerobius	2.1E+08	ATCC 27337	0/3	All NEG
Photobacterium damselae subsp. damselae	1.1E+08	ATCC 33539	0/3	All NEG
Plesiomonas shigelloides	1.6E+08	ATCC 14029	0/3	All NEG
Porphyromonas asaccharolytica	3.4E+07	ATCC 25260	0/3	All NEG
Prevotella melaninogenica	1.2E+09	ATCC 25845	0/2[b]	2 NEG 1 INC
Proteus mirabilis	4.8E+08	ATCC 25933	0/3	All NEG
Proteus vulgaris	4.8E+08	ENF 12392	0/3	All NEG
Providencia alcalifaciens	3.1E+08	ATCC 9886	0/3	All NEG
Ruminococcus bromii	2.1E+08	ATCC 27255	1/2[b]	1 hAstV POS 1 NEG 1 INC
Saccharomyces cerevisiae	2.6E+07	ATCC 76527	0/2[b]	2 NEG 1 INC
Salmonella bongori	2.3E+08	ATCC 43975	0/3	All NEG
Salmonella enterica subsp. arizonae	2.3E+08	7379	0/3	All NEG
Salmonella enterica subsp. Enterica serovar enteriditis	2.3E+08	ATCC 13076	0/3	All NEG
Salmonella typhimurium	4.0E+08	ATCC 14028	0/3	All NEG
Serratia liquefaciens	1.5E+08	ATCC 27592	0/3	All NEG
Serratia marcescens	1.5E+08	ATCC 13880	0/3	All NEG
Shigella boydii	1.9E+08	ATCC 9207	0/3	All NEG
Shigella dysenteriae	1.9E+08	2933	0/3	All NEG
Shigella flexneri	1.9E+08	ATCC 700930	0/3	All NEG
Shigella sonnei	1.9E+08	ENF 7142	0/3	All NEG
Staphylococcus aureus	4.0E+08	ATCC 43300	0/3	All NEG

Microorganism	Concentration (CFU/mL)	Collection Number	Test Result (Positive/Total)	Initial Result Details
Staphylococcus epidermidis	4.0E+08	ATCC 14990	0/3	All NEG
Stenotrophomonas maltphilia	7.0E+07	ATCC 13637	0/3	All NEG
Streptococcus agalactiae	4.6E+08	ATCC 13813	0/3	All NEG
Streptococcus intermedius	4.6E+08	ATCC 27335	0/3	All NEG
Trabulsiella guamensis	4.3E+08	ATCC 49490	0/3	All NEG
Veillonella parvula	1.8E+08	CCUG 59474	0/3	All NEG
Vibrio cholerae	3.0E+08	ATCC 14033	0/3	All NEG
Vibrio mimicus	2.2E+08	ATCC 33653	0/3	All NEG
Vibrio parahaemolyticus	2.5E+08	ATCC 17802	0/3	All NEG
Vibrio vulnificus	2.6E+08	ATCC 27562	0/3	All NEG
Yersinia bercovieri	2.8E+08	ATCC 43970	0/3	All NEG
Yersinia enterocolitica	6.0E+07	CCUG 4588	0/3	All NEG
Yersinia enterocolitica subsp. enterocolitica	4.7E+07	ATCC 9610	0/3	All NEG
Yersinia rohdei	2.8E+08	ATCC 43380	0/3	All NEG
Blastocystic hominis	1.0E+07	ATCC 50608	0/2[b]	2 NEG 1 INC
Cryptosporidium hominis	1.5E+07	IDI-P-22	0/2[b]	2 NEG 1 INC
Cryptosporidium parvum	6.3E+06	Waterborne P102 (lot 131219)	0/2[b]	2 NEG 1 INC
Encephalitozoon intestinalis	2.08E+08 cells/mL	ATCC 50651	0/2[b]	2 NEG 1 INC
Entamoeba histolytica	6.0E+05 cells/mL	ATCC 30458	0/3	All NEG
Giardia lamblia	6.3E+06	Waterborne P101	0/3	All NEG
Giardia muris	5.6E+05	Waterborne P105 (lot: 130904)	0/3	All NEG
Pentatrichomonas hominis	8.5E+06	ATCC 30098	0/3	All NEG
Adenovirus Type 1	1.0E+6.58 TCID50 units/mL	Zeptometrix 0810050CF	3/3[b]	3 AdV POS
Adenovirus Type 18	1.0E+7.25 TCID50 units/mL	ATCC VR-19	1/3[b]	1 hAstV POS 2 NEG
Adenovirus Type 3	1.0E+5.23 TCID50 units/mL	Zeptometrix 0810062CF	0/3	All NEG
Adenovirus Type 4	1.0E+5.86 TCID50 units/mL	Zeptometrix 0810070CF	0/3	All NEG
Adenovirus Type 8	1.0E+5.15 TCID50 units/mL	Zeptometrix 0810069CF	0/3	All NEG
Coxsackie A9	1.0E+4.5 TCID50 units/ 0.2 mL	ATCC VR-186	0/3	All NEG
Coxsackie B1	1.0E+7.5 TCID50 units/ 0.2 mL	ATCC VR-28	0/3	All NEG
Echovirus 19	1.2E+06 TCID50 units/mL	CCRI-15850	0/3	All NEG
Enterovirus type 68	1.0E+5.3 TCID50 units/ 0.1 mL	ATCC VR-561	0/3	All NEG

Microorganism	Concentration (CFU/mL)	Collection Number	Test Result (Positive/Total)	Initial Result Details
Herpes Simplex Virus 1	1.0E+4.25 TCID50 units/ 0.2 mL	ATCC VR-735	0/3	All NEG

[a]Concentration in CFU/mL was unavailable for certain panels. Evaluation of the concentration of *Campylobacter coli* was estimated in McFarland units. Evaluation of the concentration of *Chlamydia trachomatis* was estimated in elementary bodies per mL.
[b]UNR, INC, POS, results were subject to supplemental testing.

Table 16: Retesting of Analytes with Positive Initial Results from the Exclusivity Study

Microorganism	Dilution	Concentration (CFU/mL)	NoV Result	RoV Result	AdV Result	SaV Result	hAstV Result
Adenovirus Type 1	1:10	1 x $10^{5.58}$ $TCID_{50}$/mL	20/20 NEG	20/20 NEG	9/20 POS	20/20 NEG	20/20 NEG
	1:00	1 x $10^{4.58}$ $TCID_{50}$/mL	20/20 NEG	20/20 NEG	20/20 NEG	20/20 NEG	20/20 NEG
Adenovirus Type 18	NA	1 x $10^{7.25}$ $TCID_{50}$/mL	20/20 NEG	20/20 NEG	20/20 NEG	20/20 NEG	20/20 NEG
	1:10	1 x $10^{6.25}$ $TCID_{50}$/mL	20/20 NEG	20/20 NEG	20/20 NEG	20/20 NEG	20/20 NEG
Alcaligenes faecalis subsp. faecalis	NA	3.4E+08	20/20 NEG	20/20 NEG	20/20 NEG	20/20 NEG	20/20 NEG
	1:10	3.4E+07	20/20 NEG	20/20 NEG	20/20 NEG	20/20 NEG	20/20 NEG
Collinsella aerofaciens	NA	2.2E+08	20/20 NEG	20/20 NEG	20/20 NEG	20/20 NEG	20/20 NEG
	1:10	2.2E+07	20/20 NEG	20/20 NEG	20/20 NEG	20/20 NEG	20/20 NEG
Escherichia hermannii	NA	2.5E+08	20/20 NEG	20/20 NEG	20/20 NEG	20/20 NEG	20/20 NEG
	1:10	2.5E+07	19/19[a] NEG	19/19[a] NEG	19/19[a] NEG	19/19[a] NEG	19/19[a] NEG
Ruminococcus bromii	NA	2.1E+08	20/20 NEG	20/20 NEG	20/20 NEG	20/20 NEG	20/20 NEG
	1:10	2.1E+07	20/20 NEG	20/20 NEG	20/20 NEG	20/20 NEG	20/20 NEG

[a]1/20 replicates yielded an IND result and was excluded from analysis

Table 17: Retesting of Analytes with INC/UNR Results from the Exclusivity Study

Microorganism	Concentration (CFU/mL)	Collection Number	Initial Result	Repeated Test Result (Positive/Total)	Repeated Result Details
Aeromonas caviae	1.7E+08	ATCC 15468	INC	0/3	NEG
Bacteroides stercoris	6.8E+08	ATCC 43183	UNR	0/1	NEG
Candida albicans	1.8E+07	ATCC 24433	INC	0/1	NEG
Eggerthella lenta	4.7E+08	CCRI-9926	UNR	0/1	NEG
Gardnerella vaginalis	2.1E+08	ATCC 14019	INC	0/1	NEG
Helicobacter pylori	2.4E+08	ATCC 43504	INC	0/1	NEG

Microorganism	Concentration (CFU/mL)	Collection Number	Initial Result	Repeated Test Result (Positive/Total)	Repeated Result Details
Lactobacillus acidophilus	9.2E+07	ATCC 4356	INC	0/1	NEG
Prevotella melaninogenica	1.2E+09	ATCC 25845	INC	0/1	NEG
Ruminococcus bromii	2.1E+08	ATCC 27255	INC	0/1	NEG
Saccharomyces cerevisiae	2.6E+07	ATCC 76527	INC	0/1	NEG
Blastocystis hominis	1.0E+07	ATCC 50608	INC	0/1	NEG
Cryptosporidium hominis	1.5E+07	IDI-P-22	INC	0/1	NEG
Cryptosporidium parvum	6.3E+06	Waterborne P102 (lot:131219)	INC	0/1	NEG
Encephalitozoon intestinalis	2.08E+08 cells/mL	ATCC 50651	INC	0/1	NEG

Interference

Exogenous and endogenous interfering substances were evaluated for potential interference by spiking into unpreserved stool or Cary-Blair preserved stool matrix containing 2x LoD concentrations of Adenovirus, Astrovirus, Rotavirus, Norovirus, and Sapovirus. A total of 3 replicates were tested and compared to expected results with an acceptance criteria of 100% of spiked samples showing reactivity and 100% of organism-free samples being negative.

Hydrocortisone cream at concentrations of 50% v/v was shown to reduce sample reactivity and was labeled as an interferant. However, repeat testing with Hydrocortisone present at 25% v/v demonstrated 100% agreement with expected results (**Table 18**). The RotaTeq live Rotavirus vaccine was also picked up by the assay, as expected.

Potential interference has not been evaluated for substances other than those described in the table below. Interference by substances other than those described in the table below could lead to erroneous results.

Table 18: Interfering Substances Study Percent Agreement with Expected Results

Pool/Individual	Substance	Test Concentration	RoV	AdV	hAstV	SaV	NoV	No Org.
Individually Tested	Hydrocortisone Cream	50% v/v	100%	100%	100%	67%	100%	100%
		25% v/v	-	-	-	100%	-	-
	Benzalkonium Chloride	50% v/v	100%	100%	100%	100%	100%	100%
	Enema/Mineral Oil	50% v/v	100%	100%	100%	100%	100%	100%
	Hemorrhoidal gel	50% v/v	100%	100%	100%	100%	100%	100%
	Anti-fungal/itch vaginal;	50% v/v	100%	100%	100%	100%	100%	100%

Pool/Individual	Substance	Test Concentration	RoV	AdV	hAstV	SaV	NoV	No Org.
	Nystatin							
	Vagisil	50% v/v	100%	100%	100%	100%	100%	100%
	Polymixin B sulfate, bacitracin zinc, Neomycin Sulfate	50% v/v	100%	100%	100%	100%	100%	100%
	Nonoxynol-9	50% v/v	100%	100%	100%	100%	100%	100%
Individually Tested	Fecal Fats, Triglycerides	14% v/v	100%	100%	100%	100%	100%	100%
	Mucus	3.5% v/v	100%	100%	100%	100%	100%	100%
	Human Whole Blood	50% v/v	100%	100%	100%	100%	100%	100%
	Suppository	50% v/v	100%[a]	100%[a]	100%	100%	100%[a]	100%
	RoV Vaccine (ATCC VR-2195 and VR-2415)	2-116 x 10^6 IU	100%	100%	100%	100%	100%	100%
	Cary-Blair: Remel	75%	100%	100%	100%	100%	100%	100%
	Cary-Blair: Meridian: Para-Pack Enteric Plus	75%	100%	100%	100%	100%	100%	100%
	Cary-Blair: Meridian Para-Pack C&S	75%	100%	100%	100%	100%	100%	100%
Antibiotic Pool	Naproxen sodium	81 mg/ml	100%	100%	100%	100%	100%	100%
	Ceftriaxone disodium	16.0 mg/ml						
	Erythromycin	14.0 mg/ml						
	Metronidazole	60.8 mg/ml						
	Sulfamethoxazole	80.0 mg/ml						
	Tetracycline hydrochloride	16.0 mg/ml						
	Trimethoprim	16.0 mg/ml						
Other stool organisms Pool	*Enterococcus faecalis*	1 x 10^6 cells/mL each	100%	100%	100%	100%	100%	100%
	Escgerichia coli							
	Peptostreptococcus anaerobius							
	Proteus vulgaris							
	Salmonella typhimurium							
OTC Pool	Laxatives (Sennosides)	47 mg/ml	100%	100%	100%	100%	100%	100%
	Anti-diarrheal (Bismuth subsalicylate)	8.75 mg/ml						
	Anti-diarrheal (Loperamide hydrochloride)	3.75 mg/ml						
	Antacids (Calcium Carbonate)	32 mg/ml						

[a]One replicate resulted in partial UNR result but repeat testing resolved the issue

Mixed infection studies were carried out for each mastermix reaction with one viral pathogen being represented at 2x LoD concentration and the other pathogens in the same mastermix occurring at the 95th percentile concentration observed in the clinical study. The acceptance criteria were 100% reactivity for high concentration analytes and ≥95% reactivity for samples present at 2x LoD concentrations. All test conditions met acceptance criteria (**Table 19**).

Table 19: Mixed Infection Study Results

Test Condition	Organism	Concentration	Replicates	Negatives
1	Rotavirus	High	20	0
	Adenovirus	High	20	0
	Norovirus	2x LoD	20	1

Test Condition	Organism	Concentration	Replicates	Negatives
2	Rotavirus	High	20	0
	Adenovirus	2x LoD	20	0
	Norovirus	High	20	0
3	Rotavirus	2x LoD	20	0
	Adenovirus	High	20	0
	Norovirus	High	20	0
4	Sapovirus	2x LoD	20	0
	Astrovirus	High	20	0
5	Sapovirus	High	20	0
	Astrovirus	2x LoD	20	0

Cross-contamination (Carry-Over) Study

The sponsor analyzed a panel of alternating negative and high positive specimens to demonstrate the absence of significant carry-over effects in the BD MAX instrument during processing. Specifically, twelve high reactivity replicates of both Astrovirus and Adenovirus were tested with negative samples lacking any analyte. Three runs were performed on three instruments for a total of 108 negative and 108 high positive samples. The final analysis determined that 2/108 expected negative samples were reactive demonstrating a false-reactivity rate of 1.85% due to cross-contamination effects.

Guardrail Family D and Workflow Compatibility Study

A Guardrail Family describes the list of assays that can be run together on the BD MAX Instrument within one sample rack. Guardrail Family D follows the basic extraction workflow for an IVD assay established in Guardrail Family A with two major differences: it utilizes a 4-snap Unitized Reagent Strip (URS) and can accommodate assays of either one or two Master Mix tubes.

The purpose of this challenge testing was to ensure the Enteric Viral Panel assay can be simultaneously run with other assays utilizing the same Guardrail Family D software parameters. Two BD MAX instruments each ran 18 Enteric Viral Panel tests (9 positive and 9 negative) and 6 guardrail challenge tests. An additional instrument completed a single run of 4 Enteric Viral Panel tests (2 positive and 2 negative) and 2 guardrail challenge tests. In total, 54 samples were analyzed. All data conformed to acceptance guidelines and Enteric Viral Panel results as expected demonstrating no interference from the Guardrail challenge tests.

Analytical Reactivity/Inclusivity Study

Inclusivity testing of the BD MAX Enteric Viral Panel included the strains listed in **Table 20**. Three strains did not confirm at ≥ 95% at 3x LoD. Sapovirus GI clinical strain BA0145AP required titration to 6x LoD before results were ≥ 95%. Sapovirus GI clinical strain BA0141AP and Rotavirus A isolate WISC2 VR-2517 required

titration to 20x LoD before results were ≥ 95%.

Four strains of Norovirus (GI.3, GII.P16_GII.2, GII.P16_GII.4, GII.Pe_GII.4) were unavailable for wet laboratory testing and were thus evaluated *in silico* for potential sequence amplification by the Enteric Viral Panel. From gene sequences available in the NCBI database, no significant primer or probe mismatches were identified that would theoretically limit the detection capability of the Enteric Viral Panel for these strains.

Table 20: Inclusivity Testing Results

Virus	Isolate ID	Type/Strain	Spike Level (xLoD)	Percent Positive (%)
Adenovirus	MG10973	F40/41	3	100
	MG08756	F40/41	3	100
	BA0034AP	F40/41	3	100
	BA0042AP	F40/41	3	100
	BA0066AP	F40/41	3	100
Adenovirus	BA0313AP	F40/41	3	100
	DLS14-07148	F40/41	3	100
	DLS14-07137	F40/41	3	100
	BA0002AP	F40/41	3	100
	BA0221AP	F40/41	3	100
Astrovirus	Guix HastV-1	1	3	100
	Guix HastV-2	2	3	100
	Guix HastV-3	3	3	100
	Guix HastV-4	4	3	100
	ZeptoMetrix	4	3	100
	Guix HastV-5	5	3	100
	Guix HastV-6	6	3	100
	Guix HastV-7	7	3	100
	Guix HastV-8	8	3	100
	NYB488277	UNKNOWN	3	100
Rotavirus	DS-1 VR-2550	A	3	100
	W161 VR-2551	A	3	100
	WISC 2 VR02517	A	3	33
			6	67
			9	33
			20	100
	W179-4.9	A	3	100
	DLS14-07384	A	3	100
Sapovirus	BA0355AP	GI	3	100
	NS10653	GI	3	100
	BA0141AP	GI	3	33
			6	67
			9	67

Virus	Isolate ID	Type/Strain	Spike Level (xLoD)	Percent Positive (%)
			20	100
	BA0130AP	GI	3	100
	BA0145AP	GI	3	67
			6	100
	NYB470159	GII	3	100
	BA0260AP	GIV	3	100
	MG10206	GIV	3	100
	NYB488186	GIV	3	100
	NYB470205	GV	3	100
Norovirus	Guix M21.2	GI.4	3	100
	Guix D20171A	GI.6	3	100
	Guix V15	GII.1	3	100
	UNP262	GII.1	3	100
	NYB 488093	GII.2	3	100
	NYB 470206	GII.3	3	100
	UNP062	GII.3	3	100
	Guix N23.1 2009	GII.4	3	100
	(2008) N23.1	GII.4	3	100
	NYB 470009	GII.4	3	100
	UNP088	GII.4	3	100
	UNP178	GII.4	3	100
	UNP193	GII.4	3	100
	UNP297	GII.4	3	100
	UNP300	GII.4	3	100
	NYB470011	GII.6	3	100
	NYB 470169	GII.6	3	100
	UNP082	GII.6	3	100
	Guix FII.3	GII.12	3	100
	J95.10	GII.12	3	100
	NYB 470155	GII.17	3	100
	MG10737	Unknown	3	100

In silico analysis predicted that most strains of all genotypes would be detected, though some variant strains may be detected with reduced sensitivity or may not be detected due to inefficient amplification or exclusion by melt analysis. For Norovirus in silico analysis, three sequences showed more than one mismatch, two GI.3 variants and one GI.7 variant. Some Norovirus sequences showed more than two mismatches, one GII.3 variant, one GII.4 variant, one GII.6 variant and one GII.12 variant. These mutations could affect the detection of these variants. For Rotavirus A in silico analysis, there were five variants that had more than three mismatches. There were ten Rotavirus A sequences that were truncated by four nucleotides. These mutations could affect the detection of these variants. For Sapovirus GI in silico analysis, one GI.2 variant showed more than one mismatch, this mutation could affect the detection

of this variant. One Sapovirus GV sequence showed two mismatches, these mutations could affect the detection of this variant.

f. Assay cut-off:

The clinical trial data used in this analysis included testing results collected from 2148 patients (1786 prospective specimens and 362 retrospective specimes) and seven testing sites. There were 1010 Cary-Blair preserved samples and 776 unpreserved samples collected prospectively and 136 Cary-Blair preserved samples and 226 unpreserved samples collected as part of a retrospective study. For each specimen, the BD MAX Enteric Viral Panel result and a reference method result were determined. The reference method result is determined from a composite reference method and the validation of the BD MAX cutoffs is performed against the reference method.

Table 21: Cutoff Threshold Values for BD MAX Enteric Viral Panel

Cut-off Enteric Viral Panel	RoV	NoV	AdV	AstV	SaV	SPC
Ct.Score threshold	50	100	50	40	32	100
Ct.Score Min	6	6	6	6	6	6
Ct.Score Max	40	38	39	37	38	40
EP Min.	201	202	70	190	130	100
PCR Noise Max.	10	10	0	10	10	0
PCR Noise Min.	3.8	3.8	0	3.8	3.8	0

2. Comparison studies:

a. Method comparison with predicate device:

Not applicable.

b. Matrix comparison:

Not applicable.

3. Clinical studies:

a. Clinical Sensitivity:

Prospective Study

Six clinical sites enrolled prospective specimens and performed BD MAX testing. Five were located in the U.S. and one was located in Canada. One additional internal BD site was used as a testing site only. One internal BD site performed reference method testing (alternate PCR and bi-directional sequencing). Sites were selected

based on several criteria, such as investigator and site personnel availability, number of specimens eligible, historical prevalence rate for each target, familiarity with reference methods and/or PCR methodologies, and characteristics of their respective served patient populations.

All six geographically diverse clinical sites enrolled prospective specimens that were being collected as part of routine patient care. The collection period for Enteric Viral Panel Prospective specimens ranged from November 2015 to April 2017. The study included 1873 Prospective specimens (818 unpreserved and 1055 Cary-Blair preserved). These specimens were tested within the stability period established for the BD MAX Enteric Viral Panel Assay and reference method.

Retrospective Study

Due to the low prevalence of the assay targets, archived (retrospective) specimens collected from November 2011 to March 2017 were utilized to support the number of positive specimens for all five targets. Retrospective specimens were collected from the USA, Canada, and Uganda. The retrospective specimens were obtained from various sources, including the participating clinical centers and commercial sources. A total of 366 retrospective specimens were enrolled in the study (230 unpreserved and 136 Cary-Blair preserved). Historical results were used as the first portion of the composite reference method for the retrospective specimens.

Reference Method (RM)

The sponsor employed a composite reference method consisting of two validated alternate PCRs followed by bi-directional sequencing analysis for one of the primer sets. Confirmatory PCR primers were designed to target different regions of gene sequence than those targeted by the BD MAX Enteric Viral Panel assay. Importantly, while all prospective samples tested on the BD MAX Enteric Viral Panel assay were evaluated fresh, they were frozen before being tested by the reference method.

Only specimens with positive or negative RM results and positive, negative, UNR or IND MAX results were analyzed for each virus, which resulted in 1881 results for Norovirus, 1909 results for Rotavirus, 1871 results for Adenovirus, 1827 results for Sapovirus and 1847 results for Astrovirus. The primary reason for specimen exclusion was the lack of data for the RM, but other reasons included specimens that were too old, duplicate specimens that were collected from the same patient, and samples that were enrolled before IRB renewal.

The sponsor submitted results from extensive testing of analytical LoD determination and inclusivity testing for the reference PCR methods that utilized analytes prepared from stock viral culture as well as characterized clinical stool specimens. The LoD was determined for each of the 21 reference method assays. Testing was then performed on ten representative assays, covering all five viral targets, in twenty sample replicates at 1x LoD to validate viral DNA/RNA extraction from stool

samples, RT-PCR amplification and subsequent sequencing of viral genomic targets. Samples with amplification above the cutoff values were called positive; any concentration below these values was deemed negative. Non-sequencing master mixes usually used cutoffs for YmaxEP conditions. Sequencing master mix positives were based on melt temperature. However, the mixes were required to be sequenced prior to calling a positive result.

To demonstrate analytical reactivity (inclusivity) for the reference method 61 strains were tested by the non-sequencing PCR, with 41 confirmed ≥95% positive at 3x LoD. Seven more were confirmed at 30x LoD, five more were confirmed at 300x LoD, and four more required titration to 3000x LoD. The four isolates not detected were: ID Sapovirus NYB 470159, Guix NoV GI.7 10.31750, NoV MG10737, and Guix NoV GII.12 FII.3.

The sequencing PCR method detected 39/60 tested strains at 3x LoD. The remaining samples were then titrated up to 30x LoD where seven more samples were confirmed. Nine samples confirmed at 300x LoD, and finally two were confirmed at 3000x LoD. The remaining three samples were not detected. The three strains not detected were: Astrovirus Guix HAstV-7, Sapovirus BA0141AP, and Sapovirus NYB 470159.

Acceptance Criteria

Performance of ≥90% positive agreement of a NAAT test and NAAT reference method was considered acceptable for Norovirus, Rotavirus, Adenovirus and Astrovirus compared to current clinical practice. The acceptable performance of Sapovirus was adjusted by the sponsor to a point estimate of ≥80% on the rationale that the infection has a reduced severity compared to the other assay targets.

Study Demographics

The clinical study analyzed a total of 1146 Cary-Blair Preserved stool samples and 1002 Unpreserved stool samples across in-patient, out-patient, emergency, and long-term care facility patient groups. The sponsor provided the following demographic breakdown for the samples from the combined Retrospective and Prospective clinical studies.

Table 22: Combined Prospective and Retrospective Study Demographics

Age Group	Cary-Blair Preserved	Unpreserved	Combined
0-1 month	4	0	4
1 month – 2 y/o	188	112	300
2-12 y/o	228	153	381
13-18 y/o	117	66	183
19-21 y/o	20	21	41
>21 y/o	568	640	1208
Unknown	21	10	31
Total	1146	1002	2148

Norovirus Detection

Among prospectively collected fresh specimens, the BD MAX Enteric Viral Panel assay achieved a PPA of 92.5% (95% CI: 84.6-96.5%) for Cary-Blair preserved stool samples and a PPA of 90.7% (95% CI: 78.4-96.3%) for unpreserved stool samples.

Table 23: Norovirus Clinical Performance Stratified by Fresh/Frozen Sample Status

Specimen Type	Specimen Origin	BD MAX	RM		Total
			P	N	
Cary-Blair Preserved	**Prospective (fresh)**	**P**	74	7	81
		N	6	835	841
		Total	80	842	922
PPA (95% CI): 92.5% (84.6-96.5%)					
NPA (95% CI): 99.2% (98.3-99.6%)					
Cary-Blair Preserved	**Retrospective (frozen)**	**P**	6	1	7
		N	0	105	105
		Total	6	106	112
PPA (95% CI): 100% (61-100%)					
NPA (95% CI): 99.1% (94.8-99.9%)					
Unpreserved	**Prospective (fresh)**	**P**	39	3	42
		N	4	694	698
		Total	43	697	740
PPA (95% CI): 90.7% (78.4-96.3%)					
NPA (95% CI): 99.6% (98.7-99.9%)					
Unpreserved	**Retrospective (frozen)**	**P**	35	0	35
		N	2	58	60
		Total	37	58	95
PPA (95% CI): 94.6% (82.3-98.5%)					
NPA (95% CI): 100% (93.8-100%)					

Table 24: Norovirus Clinical Performance Stratified by Stool Type Only

Specimen Type	BD MAX	RM		Total
		P	N	
Cary-Blair Preserved	P	80	8	88
	N	6	940	946
	Total	86	948	1034
PPA (95% CI): 93% (85.6-96.8%)				
NPA (95% CI): 99.2% (98.3-99.6%)				
Unpreserved	P	74	3	77
	N	6	752	758
	Total	80	755	835
PPA (95% CI): 92.5% (84.6-96.5%)				
NPA (95% CI): 99.6% (98.8-99.9%)				

Historical data for 2 of BD MAX Enteric Viral Panel false negative samples indicate positive FilmArray GI Panel status. Another 6 Enteric Viral Panel false negative Cary-Blair preserved samples tested by FilmArray GI panel were negative. One other false negative sample displayed an alert code for LLS Failure. Seven false positive preserved samples available for discrepant resolution were also positive by FilmArray GI panel.

Rotavirus Detection

Among prospectively collected fresh specimens, the BD MAX Enteric Viral Panel assay achieved a PPA of 100% (95% CI: 89-100%) for Cary-Blair preserved stool samples and a PPA of 100% (95% CI: 74.1-100%) for unpreserved stool samples.

Table 25: Rotavirus Clinical Performance Stratified by Fresh/Frozen Sample Status

Specimen Type	Specimen Origin	BD MAX	RM		Total
			P	N	
Cary-Blair Preserved	Prospective (fresh)	P	31	7	38
		N	0	888	888
		Total	31	895	926
PPA (95% CI): 100% (89.0-100%)					
NPA (95% CI): 99.2% (98.4-99.6%)					
Cary-Blair Preserved	Retrospective (frozen)	P	38	1	39
		N	0	76	76
		Total	38	77	115
PPA (95% CI): 100% (90.8-100%)					
NPA (95% CI): 98.7% (93-99.8%)					
Unpreserved	Prospective (fresh)	P	11	1	12
		N	0	735	735
		Total	11	736	747
PPA (95% CI): 100% (74.1-100%)					
NPA (95% CI): 99.9% (99.2-100%)					

Specimen Type	Specimen Origin	BD MAX	RM		Total
			P	N	
Unpreserved	Retrospective (frozen)	P	56	1	57
		N	0	47	47
		Total	56	48	104
PPA (95% CI): 100% (93.6-100%)					
NPA (95% CI): 97.9% (89.1-99.6%)					

Table 26: Rotavirus Clinical Performance Stratified by Stool Type Only

Specimen Type	BD MAX	RM		Total
		P	N	
Cary-Blair Preserved	P	69	8	77
	N	0	964	964
	Total	69	972	1041
PPA (95% CI): 100% (94.7-100%)				
NPA (95% CI): 99.2% (98.4-99.6%)				
Unpreserved	P	67	2	69
	N	0	782	782
	Total	67	784	851
PPA (95% CI): 100% (94.6-100%)				
NPA (95% CI): 99.7% (99.1-99.9%)				

Seven false positive Cary-Blair preserved results available for discrepant analysis were tested with the FilmArray GI panel. 4/7 of these samples were positive. Two other preserved false positive specimens had historical negative results on either the FilmArray GI panel or Luminex xTAG GPP assays.

Adenovirus Detection

Among prospectively collected fresh specimens, the BD MAX Enteric Viral Panel assay achieved a PPA of 93.8% (95% CI: 71.7-98.9%) for Cary-Blair preserved stool samples and a PPA of 80% (95% CI: 37.6-96.4%) for unpreserved stool samples.

Clinical performance of the BD MAX Enteric Viral Panel Adenovirus assay failed to meet specific acceptance criteria for PPA due to a low number of positive samples detected in the patient cohort. To supplement their prospective study results, the sponsor performed additional contrived testing.

Table 27: Adenovirus Clinical Performance Stratified by Fresh/Frozen Sample Status

Specimen Type	Specimen Origin	BD MAX	RM		Total
			P	N	
Cary-Blair Preserved	Prospective (fresh)	P	15	0	15
		N	1	914	915
		Total	16	914	930
PPA (95% CI): 93.8% (71.7-98.9%)					
NPA (95% CI): 100% (99.6-100%)					
Cary-Blair Preserved	Retrospective (frozen)	P	18	0	18
		N	0	84	84
		Total	18	84	102
PPA (95% CI): 100% (82.4-100%)					
NPA (95% CI): 100% (95.6-100%)					
Unpreserved	Prospective (fresh)	P	4	1	5
		N	1	747	748
		Total	5	748	753
PPA (95% CI): 80% (37.6-96.4%)					
NPA (95% CI): 99.9% (99.2-100%)					
Unpreserved	Retrospective (frozen)	P	6	0	6
		N	0	68	68
		Total	6	68	74
PPA (95% CI): 100% (61-100%)					
NPA (95% CI): 100% (94.7-99.6%)					

Table 28: Adenovirus Clinical Performance Stratified by Stool Type Only

Specimen Type	BD MAX	RM		Total
		P	N	
Cary-Blair Preserved	P	33	0	33
	N	1	998	999
	Total	34	998	1032
PPA (95% CI): 97.1% (85.1-99.5%)				
NPA (95% CI): 100% (99.6-100%)				
Unpreserved	P	10	1	11
	N	1	815	816
	Total	11	816	827
PPA (95% CI): 90.9% (62.3-98.4%)				
NPA (95% CI): 99.9% (99.3-100%)				

Since the minimum number of RM positives required as per the protocol was not reached for Adenovirus among unpreserved specimens, contrived samples were also tested. Contrived samples were prepared by spiking stock Adenovirus into BD MAX SBT and adding unpreserved clinical stool matrix. A total of 48 samples were tested at two external sites for a total of 96 samples. 50% of contrived specimens were made at 1.99x LoD while the other 50% of specimens spanned the expected clinical range of pathogen concentrations. Negative controls were prepared from the same clinical

matrix unspiked with virus. These results conformed to expected result with high PPA and NPA values.

Table 29: Adenovirus Contrived Clinical Sample Performance

BD MAX	Expected Result		Total
	Positive	Negative	
Positive	48	0	48
Negative	0	48	48
Total	48	48	96
PPA (95% CI): 100% (92.6-100%)			
NPA (95% CI): 100% (92.6-100%)			

Sapovirus Detection

Among prospectively collected fresh specimens, the BD MAX Enteric Viral Panel assay achieved a PPA of 87.8% (95% CI: 75.8-94.3%) for Cary-Blair preserved stool samples and a PPA of 80% (95% CI: 62.7-90.5%) for unpreserved stool samples.

BD MAX Enteric Viral Panel Sapovirus detection met the sponsor's indicated lower acceptance criteria (a PPA ≥80% as opposed to 90% for other analytes).

Table 30: Sapovirus Clinical Performance Stratified by Fresh/Frozen Sample Status

Specimen Type	Specimen Origin	BD MAX	RM		Total
			P	N	
Cary-Blair Preserved	**Prospective (fresh)**	**P**	43	9	52
		N	6	863	869
		Total	49	872	921
PPA (95% CI): 87.8% (75.8-94.3%)					
NPA (95% CI): 99.0% (98.1-99.5%)					
Cary-Blair Preserved	**Retrospective (frozen)**	**P**	2	0	2
		N	1	98	99
		Total	3	98	101
PPA (95% CI): 66.7% (20.8-93.9%)					
NPA (95% CI): 100% (96.2-100%)					
Unpreserved	**Prospective (fresh)**	**P**	24	1	25
		N	6	720	726
		Total	30	721	751
PPA (95% CI): 80% (62.7-90.5%)					
NPA (95% CI): 99.9% (99.2-100%)					
Unpreserved	**Retrospective (frozen)**	**P**	4	1	5
		N	0	39	39
		Total	4	40	44
PPA (95% CI): 100% (51-100%)					
NPA (95% CI): 97.5% (87.1-99.6%)					

Table 31: Sapovirus Clinical Performance Stratified by Stool Type Only

Specimen Type	BD MAX	RM		Total
		P	N	
Cary-Blair Preserved	P	45	9	54
	N	7	961	968
	Total	52	970	1022
PPA (95% CI): 86.5% (74.7-93.3%)				
NPA (95% CI): 99.1% (98.2-99.5%)				
Unpreserved	P	28	2	30
	N	6	759	765
	Total	34	761	795
PPA (95% CI): 82.4% (66.5-91.7%)				
NPA (95% CI): 99.7% (99-99.9%)				

Nine false positive Cary-Blair preserved specimens were available for discrepant testing by FilmArray GI Panel. Four out of nine of these samples tested positive on the predicate device. One other false positive specimen had a negative historical result by an unknown "other molecular method".

Six false negative preserved samples were similarly tested by the FilmArray GI panel with four specimens testing negative for Sapovirus.

Despite meeting a less stringent acceptance criterion, the observed lower PPA between the BD MAX Enteric Viral Panel and the reference method for Sapovirus among unpreserved stool samples raised potential performance concerns. These concerns were mitigated by additional discrepant testing performed by the sponsor. Briefly, discordant unpreserved stool samples were mixed with Cary-Blair transport medium and evaluated on the BioFire FilmArray GI panel. 5/6 unpreserved false negative samples were also negative on the FilmArray GI panel. The one unpreserved BD MAX Enteric Viral Panel false positive specimen, however, was negative by BioFire FilmArray GI panel. These results support similar Sapovirus performance characteristics between the BD MAX Enteric Viral Panel assay and the predicate device.

Astrovirus Detection

Among prospectively collected fresh specimens, the BD MAX Enteric Viral Panel assay achieved a PPA of 93.5% (95% CI: 79.3-98.2%) for Cary-Blair preserved stool samples and a PPA of 93.3% (95% CI: 78.7-98.2%) for unpreserved stool samples.

Table 32: Astrovirus Clinical Performance Stratified by Fresh/Frozen Sample Status

Specimen Type	Specimen Origin	BD MAX	RM		Total
			P	N	
Cary-Blair Preserved	Prospective (fresh)	P	29	1	30
		N	2	899	901
		Total	31	900	931
PPA (95% CI): 93.5% (79.3-98.2%)					
NPA (95% CI): 99.9% (99.4-100%)					
Cary-Blair Preserved	Retrospective (frozen)	P	20	1	2
		N	2	80	82
		Total	22	81	103
PPA (95% CI): 90.9% (72.2-97.5%)					
NPA (95% CI): 98.8% (93.3-99.8%)					
Unpreserved	Prospective (fresh)	P	28	2	30
		N	2	722	724
		Total	30	724	754
PPA (95% CI): 93.3% (78.7-98.2%)					
NPA (95% CI): 99.7% (99-99.9%)					
Unpreserved	Retrospective (frozen)	P	3	1	4
		N	0	45	45
		Total	3	46	49
PPA (95% CI): 100% (43.9-100%)					
NPA (95% CI): 97.8% (88.7-99.6%)					

Table 33: Astrovirus Clinical Performance Stratified by Stool Type Only

Specimen Type	BD MAX	RM		Total
		P	N	
Cary-Blair Preserved	P	49	2	51
	N	4	979	983
	Total	53	981	1034
PPA (95% CI): 92.5% (82.1-97%)				
NPA (95% CI): 99.8% (99.3-99.9%)				
Unpreserved	P	31	3	34
	N	2	767	769
	Total	33	770	803
PPA (95% CI): 93.9% (80.4-98.3%)				
NPA (95% CI): 99.6% (98.9-99.9%)				

One false positive Cary-Blair preserved result was tested by FilmArray GI panel with negative results. Two other false positive specimens had historical negative Astrovirus results by "other molecular methods."

Two false negative preserved samples tested by FilmArray GI panel were negative for Astrovirus. An additional two other false negatives had positive Astrovirus historical results from "other molecular methods."

b. Clinical specificity:

See section M.3a above.

c. Other clinical supportive data (when a. and b. are not applicable):

Not applicable.

4. Clinical cut-off:

Not applicable.

5. Expected values/Reference range:

All six geographically diverse clinical sites enrolled Prospective specimens that were being collected as part of routine patient care. The collection period for Enteric Viral Panel Prospective specimens ranged from November 2015 to April 2017. The study included 1873 Prospective specimens (818 unpreserved and 1055 Cary-Blair preserved). The observed prevalence based on the composite reference method and the expected value summaries as based on BD MAX Enteric Viral Panel assay results for the prospective study are summarized in the tables below.

Table 34: Observed Prevalence based on Composite Reference Method

Specimen Type	Site	Norovirus	Rotavirus	Adenovirus	Sapovirus	Astrovirus
Cary-Blair Preserved	ALB	3.4% (2/59)	0.0% (0/59)	0.0% (0/59)	0.0% (0/59)	1.7% (1/59)
	CIN	13.7% (53/387)	4.8% (19/392)	3.0% (12/394)	10.1% (39/387)	5.6% (22/394)
	JHU	8.2% (15/184)	3.8% (7/185)	0.5% (1/185)	0.0% (0/184)	1.1% (2/185)
	POR	3.9% (14/359)	1.7% (6/358)	0.8% (3/360)	3.1% (11/358)	1.9% (7/360)
	Total	8.5% (84/989)	3.2% (32/994)	1.6% (16/998)	5.1% (50/988)	3.2% (32/998)
Unpreserved	ALB	0.0% (0/1)	0.0% (0/1)	0.0% (0/1)	0.0% (0/1)	0.0% (0/1)
	CAL	4.7% (27/578)	1.0% (6/580)	0.7% (4/585)	3.6% (21/584)	4.8% (28/585)
	CIN	0.0% (0/2)	33.3% (1/3)	0.0% (0/3)	0.0% (0/3)	0.0% (0/3)
	JHU	10.3% (7/68)	0.0% (0/69)	0.0% (0/69)	0.0% (0/68)	0.0% (0/69)
	LUR	6.9% (7/101)	3.8% (4/104)	1.0% (1/104)	6.8% (7/103)	1.9% (2/104)
	POR	16.7% (2/12)	0.0% (0/12)	0.0% (0/13)	15.4% (2/13)	0.0% (0/13)
	Total	5.6% (43/762)	1.4% (11/769)	0.6% (5/775)	3.9% (30/772)	3.9% (30/775)
Combined	ALB	3.3% (2/60)	0.0% (0/60)	0.0% (0/60)	0.0% (0/60)	1.7% (1/60)
	CAL	4.7% (27/578)	1.0% (6/580)	0.7% (4/585)	3.6% (21/584)	4.8% (28/585)
	CIN	13.6% (53/389)	5.1% (20/395)	3.0% (12/397)	10..0% (39/390)	5.5% (22/397)
	JHU	8.7% (22/252)	2.8% (7/254)	0.4% (1/254)	0.0% (0/252)	0.8% (2/254)
	LUR	6.9% (7/101)	3.8% (4/104)	1.0% (1/104)	6.8% (7/103)	1.9% (2/104)
	POR	4.3% (16/371)	1.6% (6/370)	0.8% (3/373)	3.5% (13/371)	1.9% (7/373)
	Total	7.3% (127/1751)	2.4% (43/1763)	1.2% (21/1773)	4.5% (80/1760)	3.5% (62/1773)

Table 35: Expected Values based on BD MAX Enteric Viral Panel Assay

Specimen Type	Site	Norovirus	Rotavirus	Adenovirus	Sapovirus	Astrovirus
Cary-Blair Preserved	ALB	7.7% (4/52)	0.0% (0/52)	0.0 (0/52)	1.9% (1/52)	1.9% (1/52)
	CIN	15.0% (59/394)	6.9% (27/394)	2.8% (11/394)	12.2% (48/394)	5.1% (20/394)
	JHU	9.8% (13/132)	4.5% (6/132)	0.8% (1/132)	1.5% (2/132)	0.8% (1/132)
	POR	3.9% (14/359)	1.9% (7/359)	0.8% (3/59)	2.5% (9/360)	2.2% (8/360)
	Total	9.6% (90/937)	4.3% (40/937)	1.6% (15/937)	6.4% (60/938)	3.2% (30/938)
Unpreserved	CAL	5.4% (31/574)	1.0% (6/574)	0.7% (4/574)	3.0% (17/575)	4.9% (28/575)
	CIN	0.0% (0/3)	33.3% (1/3)	0.0% (0/3)	0.0% (0/3)	0.0% (0/3)
	JHU	13.8% (9/65)	0.0% (0/65)	0.0% (0/65)	0.0% (0/63)	1.6% (1/63)
	LUR	10.1% (10/99)	5.1% (5/99)	1.0% (1/99)	7.9% (8/101)	1.0% (1/101)
	POR	23.1% (3/13)	7.7% (1/13)	0.0% (0/13)	15.4% (2/13)	0.0% (0/13)
	Total	7.0% (53/754)	1.7% (13/754)	0.7% (5/754)	3.6% (27/755)	4.0% (30/755)
Combined	ALB	7.7% (4/52)	0.0% (0/52)	0.0% (0/52)	1.9% (1/52)	1.9% (1/52)
	CAL	5.4% (31/574)	1.0% (6/574)	0.7% (4/574)	3.0% (17/575)	4.9% (28/575)
	CIN	14.9% (59/397)	7.1% (28/397)	2.8% (11/397)	12.1% (48/397)	5.0% (20/397)
	JHU	11.2% (22/197)	3.0% (6/197)	0.5% (1/197)	1.0% (2/195)	1.0% (2/195)
	LUR	10.1% (10/99)	5.1% (5/99)	1.0% (1/99)	7.9% (8/101)	1.0% (1/101)
	POR	4.6% (17/372)	2.2% (8/372)	0.8% (3/372)	2.9% (11/373)	2.1% (8/373)
	Total	8.5% (143/1691)	3.1% (53/1691)	1.2% (20/1691)	5.1% (87/1693)	3.5% (60/1693)

N. Instrument Name:

BD MAX System

O. System Descriptions:

1. Modes of Operation:

   Does the applicant's device contain the ability to transmit data to a computer, webserver, or mobile device?

   Yes ____X____ or No _____

   Does the applicant's device transmit data to a computer, webserver, or mobile device using wireless transmission?

   Yes _____ or No ____X____

2. Software:

   FDA has reviewed applicant's Hazard Analysis and software development processes for this line of product types:

   Yes ____X____ or No _____

   a. Level of Concern: Moderate
   b. Device Hazard Analysis: Acceptable

      The risks associated with the BD MAX Platform and Software were reviewed as part of previous premarket notifications—

      - K111860 (BD MAX Platform and Software with BD MAX GBS Assay)
      - DEN160001 (BD MAX Vaginal Panel and Software Updates)
      - K170308 (BD MAX Extended Enteric Bacterial Panel and Software Updates)

      The device hazard analysis submitted for the Enteric Viral Panel assay contains redacted hazards and Risk Control Measures that, according to BD, are not associated with the BD MAX system software for the ease of review by FDA.

      According to the risk region chart in the Hazard Analysis Report, BD identified 93, 14, and 0 hazards in green, yellow, and red risk regions, respectively. After accounting for appropriate mitigatins, where possible, all identified hazards are acceptable. Examples of appropriate mitigations include software changes implemented as a Risk Control Measures, proper device labeling, training of end users, and the results of clinical and analytical validation studies.

   c. Architecture Design Chart: Acceptable

      The architecture design chart for the BD MAX System and software was submitted as part of the original instrument clearance (K111860).

   d. Software Description: Acceptable

Each new BD MAX assay is developed with an Assay Definition File (ADF) containing the assay workflow parameters to run and report results for the assay on the BD MAX System. The ADF controls sample preparation cartridge loading, barcodes, result scripts, BANCS parameters and Master Mix parameters. The BD MAX Enteric Viral Panel Assay ADF (BD MAX ENT VIR 49 Version: 1) was released on Assay Release Key V2.38. The Assay Release Key is a compilation of released BD MAX assay ADFs.

There are no unresolved anomalies associated with the ADF developed for use with the BD MAX Enteric Viral Panel.

The BD MAX System software automatically interprets test results. Results are reported for each of the analytes and for the Sample Processing Control. In the absence of positive sample processing control amplification, positive analyte results are maintained but any negative result is labeled unresolved "UNR". Results for each analyte are determined based on pre-extablished cut-off thresholds for both Ct.Score (amplification threshold cycle) and Cycle End point (end point fluorescence of each well).

e. Software Requirements Specifications: Acceptable

Extensive documentation was provided in the original K111860 submission with assay-specific updates to software and ADFs in DEN160001, K170308, and the current submission. No fundamental changes that affect safety or effectiveness are noted.

f. Software Development Environment: Acceptable

Extensive documentation was provided in the original K111860 submission with assay-specific updates to software and ADFs in DEN160001 and K170308. No fundamental changes that affect safety or effectiveness are noted.

g. Traceability Analysis: Acceptable

Both the original K111860 submission and subsequent submissions contain adequate documentation that links together design requirements and specifications to validation testing.

h. Verification and Validation (VnV) Testing: Acceptable

BD provided a Software VnV plan that details testing and implementation procedures for the release of V4.72A as well as the Assay Release Key V2.39A Software which contains updated BD MAX Vaginal Panel (MVP) Assay Definition Files. According to BD, the software version update to 4.72A is primarily to improve robustness of the MVP assay.

The sponsor states that an equivalence comparison for the BD MAX Enteric Viral Panel ADF will be performed to support the ADF parameters between the versions used in the performance studies and the final commercial release version.

Software validation includes integration testing of new features, regression testing to ensure retention of system performance and direct testing of bug fixes. Additional testing includes stress testing and resolution of unexpected results. All completeion criteria have been met for validation testing of the BD MAX Enteric Viral Panel System and Assay software and all expected results have been addressed and documented.

j. Revision Level History: Acceptable

BD MAX Enteric Viral Panel analytical and clinical studies were completed using the functionality of BD MAX System software version 4.60A or 4.61D and with BD MAX Enteric Viral Panel Assay Definition File "BD MAX Enteric Viral Panel IUO v1". The BD MAX Enteric Viral Panel assay kit will be distributed for use with the BD MAX System running System Software Version 4.60A (or greater). Additional enhancements, new features, and bug fixes are included in the upgrade to 4.72A.

A change to sample preparation script for the cleared BD MAX Vaginal Panel is noted in release version 4.72A. The Software change impact review provided by the sponsor suggests that this is to optimize workflow for interfering substances for version 2 of the MVP assay and no new hazards are introduced.

None of the changes incorporated into the latest software version would impact the BD MAX Enteric Viral Panel assay. The BD MAX ENT VIR 49 ADF was released on February 15, 2018 for use with the CE marked version of the BD MAX Enteric Viral Panel (CE Mark February 2018).

k. Unresolved Anomalies and Software Defects: Acceptable

In the Software Test Summary document, BD confirms passing results for all four test protocols (SP_MVP Scripting, Stress Test, IVD Regression Test, Windows Regression Test) using version 4.72A. Additionally, BD provides a list of all open Software Change Requests for this version of software release.

While no unresolved software anomalies remain to the assay-specific ADF component of the software, there is a total of 77 unresolved anomalies for the general instrument software -- 21 Serious, 41 Medium, and 15 low – that primarily affet user convenience and do not impact assay safety and effectiveness.

l. Off the Shelf Software (OTS)/Software of Unknown Pedigree (SOUP): Acceptable

The following third-party software components are used in the BD MAX instrument. Microsoft Windows 7, Microsoft Windows IoT10 64 bits, Microsoft SQL Server 2012 Express, Microsoft .NET framework, Microsoft Visual Studio 2010,

CylancePROTECT.

m. EMC Testing and Standards: Acceptable

The BD MAX System is an already cleared device and requires no further EMC testing.

3. Specimen Identification:

Barcode

4. Specimen Sampling and Handling:

Collected specimens, either unpreserved stool or stool stored in 15 mL Cary-Blair transport media, should be kept between 2 °C and 25 °C during transport. Protect against exposure to excessive heat.

Specimens can be stored for up to 120 hours (5 days) at 2–8 °C or for up to 48 hours at 2–25 °C before testing.

5. Calibration:

The system is calibrated on-site as part of the installation procedure, as well as during preventive maintenance that is offered with a service contract.

6. Quality Control:

The Sample Processing Control (SPC) is contained in the extraction tube and serves as verification that the extraction, amplification, and detection processes occurred appropriately.

Users may also add external controls in order to comply with applicable regulations. No external control materials are provided by the manufacturer and nor are they used by the BD MAX system for sample result interpretation.

As an external Negative control, the sponsor recommends commercially available material or a previously characterized negative specimen. As an external positive control, commercially available viral strains are purchaseable from Zeptometrix.

P. Other Supportive Instrument Performance Characteristics Data Not Covered In The "Performance Characteristics" Section above:

Not applicable.

Q. Proposed Labeling:

The labeling supports the finding of substantial equivalence for this device.

R. Conclusion:

The submitted information in this premarket notification is complete and supports a substantial equivalence decision.