



INSTRUCTION FOR USE

Urinary Tract Infections Panel PCR Kit

For Research Use Only



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1. INTENDED USE

For Research Use Only (RUO). Not for use in diagnostic procedures. No claim or representation is intended to provide information for the diagnosis, prevention, or treatment of disease. Furthermore, this test kit is not intended for the diagnosis of infectious diseases in animals.

The **MarinaBiolab Urinary Tract Infections Panel PCR Kit** is a multiplex, qualitative Real-Time Polymerase Chain Reaction (qPCR) test intended for the simultaneous detection and identification of multiple pathogenic nucleic acids in research samples. The kit enables qPCR results in less than one hour. It is designed to detect gene sequences from the following organisms:

Targets	
<i>Escherichia coli</i>	<i>Corynebacterium urealyticum</i>
<i>Streptococcus agalactiae</i>	<i>Enterococcus faecium</i>
<i>Klebsiella oxytoca</i>	<i>Enterococcus faecalis</i>
<i>Staphylococcus saprophyticus</i>	<i>Acinetobacter baumannii</i>
<i>Serratia marcescens</i>	<i>Proteus vulgaris</i>
<i>Proteus mirabilis</i>	<i>Staphylococcus aureus</i>
<i>Aerococcus urinae</i>	<i>Ureaplasma (Ureaplasma urealyticum/parvum)</i>
<i>Treponema pallidum</i>	<i>Providencia stuartii</i>
<i>Enterobacter cloacae</i>	<i>Candida albicans</i>
<i>Pseudomonas aeruginosa</i>	<i>Candida glabrata</i>
<i>Citrobacter freundii</i>	<i>Candida parapsilosis</i>
<i>Klebsiella aerogenes</i>	<i>Candida tropicalis</i>
<i>Klebsiella pneumoniae</i>	<i>Candida krusei</i>
<i>Morganella morganii</i>	<i>Candida auris</i>
Controls	
Human RNase P (IC)	
<i>Bacillus atrophaeus</i> (EC)	

2. PRINCIPLE of the PROCEDURE

DNA target regions are amplified using real-time PCR instruments, along with the specific primer and probe sets provided in the kit. During amplification, each probe binds to a specific target sequence located between the forward and reverse primers. During the extension phase of the PCR cycle, the 5' nuclease activity of Taq polymerase cleaves the probe, separating the reporter dye from the quencher and generating a fluorescent signal. With each cycle, more reporter dye molecules are released, resulting in an increase in fluorescence intensity. Fluorescence is measured at each cycle by the real-time PCR instrument. Probes labeled with distinct fluorophores are used to detect specific amplicons derived from both the target sequences and the internal control. The PCR instrument monitors the fluorescence signals in real time and interprets the data to provide a qualitative result for each target. A positive result for the presence of target DNA is indicated by the appearance of a real-time PCR amplification curve and a corresponding C_q (Quantification Cycle) value.

3. KIT COMPONENTS

The **MarinaBiolab Urinary Tract Infections Panel PCR Kit** consists of four main components:

1. qPCR Enzyme and Buffer Mix (qPCR Master Mix)
2. Forward, Reverse and Probe Oligo Mix (UTIP Oligo Mix 1-8)
3. A mixture of non-infectious DNA from artificial samples, including the targets listed in the table below (PC-UTIP)
4. DNase/RNase-Free Water (NTC)

The components of the kit are provided in Table 1-2.

Table 1. Kit components.

Component	Description	Quantity x Volume
		100 rxn MBLUTI004
qPCR Master Mix	Ready-to-use mix for qPCR	4 x 1000 µL
UTIP Oligo Mix 1-8	Primers and probes complementary to specific regions of the targets listed in the table above	8 x 250 µL
PC-UTIP	A mixture of non-infectious DNA from artificial samples, including the targets listed in the table below	2 x 400 µL
NTC	DNase/RNase-Free Water	2 x 400 µL

Table 2. Oligo Mix target organisms and detection channels.

Vial Name	Target	Channel
UTIP Oligo Mix 1	<i>Escherichia coli</i>	FAM/Green
	<i>Streptococcus agalactiae</i>	HEX/VIC/JOE/Yellow
	<i>Klebsiella oxytoca</i>	ROX/Texas Red/Orange
	Human RNase P (IC)	CY5/Red
UTIP Oligo Mix 2	<i>Staphylococcus saprophyticus</i>	FAM/Green
	<i>Serratia marcescens</i>	HEX/VIC/JOE/Yellow
	<i>Proteus mirabilis</i>	ROX/Texas Red/Orange
	<i>Aerococcus urinae</i>	CY5/Red
UTIP Oligo Mix 3	<i>Treponema pallidum</i>	FAM/Green
	<i>Enterobacter cloacae</i>	HEX/VIC/JOE/Yellow
	<i>Pseudomonas aeruginosa</i>	ROX/Texas Red/Orange
	<i>Citrobacter freundii</i>	CY5/Red

UTIP Oligo Mix 4	<i>Klebsiella aerogenes</i>	FAM/Green
	<i>Klebsiella pneumoniae</i>	HEX/VIC/JOE/Yellow
	<i>Morganella morganii</i>	ROX/Texas Red/Orange
	<i>Corynebacterium urealyticum</i>	CY5/Red
UTIP Oligo Mix 5	<i>Enterococcus faecium</i>	FAM/Green
	<i>Enterococcus faecalis</i>	HEX/VIC/JOE/Yellow
	<i>Acinetobacter baumannii</i>	ROX/Texas Red/Orange
	<i>Proteus vulgaris</i>	CY5/Red
UTIP Oligo Mix 6	<i>Staphylococcus aureus</i>	FAM/Green
	-	HEX/VIC/JOE/Yellow
	<i>Ureplasma (Ureaplasma urealyticum/parvum)</i>	ROX/Texas Red/Orange
	-	CY5/Red
UTIP Oligo Mix 7	<i>Candida albicans</i>	FAM/Green
	<i>Candida glabrata</i>	HEX/VIC/JOE/Yellow
	<i>Candida parapsilosis</i>	ROX/Texas Red/Orange
	<i>Providencia stuartii</i>	CY5/Red
UTIP Oligo Mix 8	<i>Candida tropicalis</i>	FAM/Green
	<i>Candida krusei</i>	HEX/VIC/JOE/Yellow
	<i>Candida auris</i>	ROX/Texas Red/Orange
	<i>Bacillus atrophaeus</i> (EC)	CY5/Red

The oligonucleotide set targeting the human *RNase P* (Internal Control: IC) and *Bacillus atrophaeus* (External Control: EC) are used to monitor sampling, nucleic acid extraction, and inhibition of qPCR. The kit also contains negative and positive control templates to evaluate contamination and the qPCR reagent stability, respectively.

4. EQUIPMENT and MATERIALS REQUIRED but NOT PROVIDED

- 2-8°C Refrigerator
- ≤ -20°C Freezer
- ≤ -70°C Freezer (Optional)
- Vortex mixer
- Benchtop centrifuge with rotor for 1.5 mL tubes
- Benchtop mini centrifuge with rotor for PCR strips
- Benchtop plate centrifuge
- Biological Safety Cabinet (BSC)
- PCR cabinet for PCR Setup
- Adjustable Micropipettes: 1-10, 10-100, 100-1000 µL
- Sterile DNase/RNase free micropipettes tips - Compatible with the micropipettes
- Cold tube rack for microfuge tubes (1.5/2 mL) and for PCR tubes (0.1/0.2 mL)
- Disposable, powder-free, nitrile gloves
- Disposable (preferably) laboratory coat
- Surface decontaminants - Freshly diluted 10% bleach solution (0.5% NaClO)
- Applied Biosystems QuantStudio 5, 7, and 12K with Design & Analysis software and consumables
- Bio-Rad CFX96 Touch™/CFX96™ Dx/CFX Opus 96™/CFX Opus 96™ Dx/CFX384 Touch™/CFX Opus 384™ with Maestro software v1.1 and consumables
- Qiagen Rotor-Gene Q 5plex Platform with Rotor-Gene Q series software v2.1.0.9 and consumables
- Roche LightCycler 480 with software and consumables

5. WARNING and PRECAUTIONS

- The **MarinaBiolab Urinary Tract Infections Panel PCR Kit** is intended for research use only and should be used by professionally trained, qualified personnel. All procedures should be performed in accordance with Good Laboratory Practices (GLP).
- Biological material used for nucleic acid extraction should be handled as potentially infectious. Appropriate safety precautions are recommended when handling biological material (e.g., do not pipet by mouth; wear disposable gloves; disinfect hands after completing the test).
- Biological material should be inactivated before disposal (e.g., autoclaving). Disposable items should be autoclaved or incinerated after use.
- In the event of a spill involving potentially infectious materials, the spill should be immediately absorbed with paper tissue, and the affected area should be disinfected using a suitable standard disinfectant or 70% alcohol. Materials used for cleaning spills, including gloves, should be inactivated before disposal (e.g., autoclaving).
- Disposal of all samples, unused reagents and waste should be in accordance with country, federal, state, and local regulations.
- To avoid microbial contamination of reagents during aliquoting, it is recommended to use sterile, single-use pipettes and tips. Reagents that appear cloudy or show signs of microbial contamination should not be used.
- The kit should be stored away from nucleic acid sources and PCR amplicons to prevent contamination.
- Always check the expiration date on the kit. Do not use expired or improperly stored kits.
- Components in the kit should not be mixed with components from different lot numbers or from different manufacturers, even if they contain the same components.
- The kit components should be gently mixed before use by shaking.
- A common issue with PCR-based assays is false positive results caused by contamination from PCR amplicons. To minimize the risk of amplicon contamination:
 - Ensure separate work areas with dedicated apparatus are available for each stage of the procedure.
 - Do not open reaction tubes/plates post-amplification to avoid contamination with amplicons.
 - Discard used tubes/plates immediately in a biohazard container after completing the run.
 - Minimize handling of tubes/plates after testing.
 - Change gloves after handling used tubes/plates.

6. HANDLING, STORAGE, and STABILITY

- The **MarinaBiolab Urinary Tract Infections Panel PCR Kit** is shipped on dry ice. If any component, except the qPCR Master Mix, is not frozen upon arrival or if the outer packaging has been compromised during shipment, please contact **MarinaBiolab** or the local distributor immediately.
- Upon arrival, all components should be stored between -25°C and -15°C.
- Repeated freezing and thawing of the kit components may reduce detection quality. The kit can withstand up to 15 freeze/thaw cycles without impacting performance.
- When stored under the specified conditions, the kit remains stable until the expiration date printed on the package. The expiration date is 12 months from the date of manufacture.
- All components must be thawed at ambient temperature for at least 30 minutes before use.
- It is recommended to keep all components on ice when preparing the assay mixes.
- The primer and probe mixes contain fluorophore-labeled probes and should be protected from direct sunlight and prolonged exposure to ambient light.
- Do not use expired or improperly stored components.

7. TEST PROCEDURE

7.1. Sample Preparation and Nucleic Acid Extraction

Samples intended for nucleic acid isolation must be collected using appropriate cell collection systems. The performance of the kit is highly dependent on both the quantity and quality of the extracted nucleic acid. Ensure that the extraction method used is compatible with real-time PCR technology.

If the laboratory's established standard protocol is used for nucleic acid isolation, it must be validated by the end user.

For frozen samples or previously extracted nucleic acid, thaw only the amount required for testing on the same day. Avoid multiple freeze/thaw cycles, as these can compromise nucleic acid integrity. For best results, use the nucleic acid immediately after thawing.

7.2. PCR Reaction Preparation and Processing

- Completely thaw all components at room temperature for at least 30 minutes prior to use.
- Once thawed, keep all components on ice throughout the entire testing procedure.
- Determine the number of reactions needed and prepare a PCR plate layout accordingly.
- The plate layout should include the following:
 - Reactions for each test sample and extraction negative control.
 - PCR control reactions:
 - Positive Control (provided in the kit)
 - Negative (No Template) Control (NTC) (provided in the kit)
 - No Template Addition Control (NRC)
- Vortex and briefly centrifuge all components before each use.
- Prepare a master mix by combining the required components for the total number of reactions plus an additional 10% to account for pipetting variability.

Table 3. Reaction set-up.

Reaction Mix Component	1X Reaction (µL) per well
qPCR Master Mix	5 µL
UTIP Oligo Mix 1-8	2.5 µL
Template Nucleic Acid	2.5 µL
Total Reaction Volume	10 µL

- Add 5 µL of qPCR Master Mix and 2.5 µL of UTIP Oligo Mix 1-8 to each PCR tube.
- Add 2.5 µL of the isolated sample to the corresponding tubes.
- The final reaction volume should be 10 µL.
- Close the tubes, centrifuge briefly, then place them into the real-time PCR instrument.
- Proceed with amplification using the PCR profile outlined below.

Table 4. Amplification profile.

Step	Number of Cycles	Temperature	Time	Data Collection
Initial Denaturation	1	95 °C	10 sec	FAM/Green HEX/VIC/JOE/Yellow ROX/Texas Red/Orange CY5/Red
Denaturation	40	95 °C	5 sec	
Annealing/Extension		55 °C	15 sec	

8. INTERPRETATION OF RESULTS

MarinaBiolab Urinary Tract Infections Panel PCR Kit provides a qualitative result for the presence (Detected) or absence (Not Detected) of the target genes.

8.1. Calculation of Cq Values and Instrument-Specific Requirements

Configure the following instrument settings before evaluating the results.

Table 5. Instrument-specific settings.

Instrument	Threshold Level	Other Settings
CFX96 Touch™/CFX96™ Dx/CFX Opus 96™/CFX Opus 96™ Dx/ CFX384 Touch™/CFX Opus 384™ (Bio-Rad)	500 RFU	-
Rotor-Gene Q 5plex Platform (QIAGEN)	0.02 RFU	Dynamic Tube: Active Slope Correct: Active Outlier Removal: 0
QuantStudio™ 5, 7 and 12K (Applied Biosystems™)	Auto	-
Roche LightCycler 480 (Roche)	Auto	-

The shape of the amplification curves should be evaluated. If the instrument's software assigns a Cq value to a sample and the curve is sigmoidal, the Cq value can be used in the final assessment. *Non-sigmoidal curves should be recorded as negative.*

A result is considered positive if the Cq value is ≤ 35 , or as determined by your laboratory's protocols.

8.2. Overall Validity of Detection

Table 6. Expected performance of controls.

Control Type	Used to Monitor	Signal	
		Target Channel	Internal/External Control Channel
Negative Control	Cross-contamination during extraction and reaction setup	-	-
No template addition	Reagent and/or environmental contamination	-	-
Positive Control	qPCR reaction setup and reagent integrity	+	+
Internal/External Control	To monitor the integrity of nucleic acid extraction and qPCR from each specimen	Not applicable	+

Before analyzing sample results, we recommend verifying the validity of the real-time PCR test. For each run, please confirm that the Positive and Negative controls performed as expected, based on the following criteria:

Table 7. Run validity/positive and negative control pass criteria.

Positive Control		Negative Control		Results	Recommendation
Target Channel	Internal/External Control Channel	Target Channel	Internal/External Control Channel		
+	+	-	-	VALID	Proceed with the interpretation of sample results.
Any of them is Negative		Not considered		INVALID	Contact the manufacturer, replenish the reagents, and repeat the reaction.
Not considered		Any of them is Positive		INVALID	Repeat the analysis, ensuring to follow the 'Warnings and Precautions' outlined in the IFU.

If any control fails to perform as described above, the run is considered invalid and must be repeated. If the issue persists, contact the manufacturer.

If all controls perform as expected, proceed with the interpretation of the results.

8.3. Interpretation of Unknown Specimen Results

The data generated by the instruments can be manually evaluated and reported using their software.

Table 8. Interpretation of unknown specimen results for DNA pathogens.

DNA Pathogens	Internal Control (<i>RNase P</i>)	External Control (<i>Bacillus atrophaeus</i>)	Results	Interpretation
Positive (+) (Cq<35)	Positive (+) (Cq<35)	Positive (+) (Cq<35)	Positive for Target	Target DNA is detected
Positive (+) (Cq<35)	Negative (-) (Cq≥35 or N/A)	Positive (+) (Cq<35)	Positive for Target	Target DNA is detected
Positive (+) (Cq<35)	Positive (+) (Cq<35)	Negative (-) (Cq≥35 or N/A)	Positive for Target	Target DNA is detected
Positive (+) (Cq<35)	Negative (-) (Cq≥35 or N/A)	Negative (-) (Cq≥35 or N/A)	Invalid	Repeat the test by re-extracting the sample. If the result remains invalid, consider collecting a new sample.
Negative (-) (Cq≥35 or N/A)	Positive (+) (Cq<35)	Positive (+) (Cq<35)	Negative for Target	Target DNA is not detected
Negative (-) (Cq≥35 or N/A)	Negative (-) (Cq≥35 or N/A)	Positive (+) (Cq<35)	Negative for Target	Target DNA is not detected
Negative (-) (Cq≥35 or N/A)	Positive (+) (Cq<35)	Negative (-) (Cq≥35 or N/A)	Negative for Target	Target DNA is not detected
Negative (-) (Cq≥35 or N/A)	Negative (-) (Cq≥35 or N/A)	Negative (-) (Cq≥35 or N/A)	Invalid	Repeat the test by re-extracting the sample. If the result remains invalid, consider collecting a new sample.

9. ASSAY LIMITATIONS

- The ***MarinaBiolab Urinary Tract Infections Panel PCR Kit*** is intended for use only by professionally trained and qualified staff.
- A false negative result may occur if the specimen is improperly collected, transported, or handled. False negatives can also occur if amplification inhibitors are present in the specimen or if insufficient numbers of organisms are present.
- Spontaneous mutations within the target sequences may result in failure to detect the target. While the test design mitigates this risk, if target detection failure is anticipated, it is recommended to test the specimen with a different assay that targets other sequences in the genome.
- There is a risk of false positive results due to cross-contamination by target viruses and/or bacteria, their nucleic acids or amplified products, or from non-specific signals in the assay. Proper handling of consumables, as outlined in the Warnings and Precautions section, is crucial to minimize this risk.
- This assay is qualitative and does not provide a quantitative assessment of the detected organism's concentration.
- All instruments (e.g., pipettes, real-time PCR cyclers) must be calibrated according to the manufacturer's instructions.

10. PERFORMANCE CHARACTERISTICS

10.1. Analytical Sensitivity (Limit of Detection, LoD)

The limit of detection (LoD) was defined as the concentration at which the test produces a positive result more than 95% of the time. Serial dilutions of the strains were tested, and the initial tentative LoD was confirmed with twenty (20) replicates. To ensure the accuracy of the LoD determination, if the initial detection rate was 100%, an additional twenty (20) replicates were performed at the next lower concentration until a detection rate of $\leq 95\%$ was achieved.

For nucleic acid extraction, a simulated research matrix was spiked with strains and processed using the Automatic Nucleic Acids Extraction Instrument. Testing was carried out on the CFX96 Touch™ (Bio-Rad) Real-Time PCR system. The confirmed LoDs for the strains tested, along with the corresponding LoDs for the **MarinaBiolab Urinary Tract Infections Panel PCR Kit** reportable targets, are presented in Table 9 below.

Table 9. Summary of LoD study results.

Analyte	Isolate ID/Source	LoD Concentration (copies/mL)	Detected/Total
<i>Escherichia coli</i>	ATCC 25922	3.5E+01 copies/mL	20/20 100%
<i>Streptococcus agalactiae</i>	ATCC 12386	6.7E+01 copies/mL	19/20 95%
<i>Klebsiella oxytoca</i>	ATCC 700324	2.6E+01 copies/mL	20/20 100%
<i>Staphylococcus saprophyticus</i>	Zeptomatrix 0804014	5.7E+01 copies/mL	20/20 100%
<i>Serratia marcescens</i>	ATCC 29021	2.1E+02 copies/mL	20/20 100%
<i>Proteus mirabilis</i>	Zeptomatrix 0801544	2.1E+02 copies/mL	20/20 100%
<i>Aerococcus urinae</i>	ATCC 51268	4.5E+01 copies/mL	20/20 100%
<i>Treponema pallidum</i>	In-house	6.9E+01 copies/mL	20/20 100%
<i>Enterobacter cloacae</i>	Zeptomatrix 0801830	7.4E+01 copies/mL	19/20 95%
<i>Pseudomonas aeruginosa</i>	ATCC 27853	6.7E+02 copies/mL	20/20 100%
<i>Citrobacter freundii</i>	Zeptomatrix 0801563	4.2E+01 copies/mL	20/20 100%
<i>Klebsiella aerogenes</i>	ATCC 13048	2.4E+02 copies/mL	20/20 100%

<i>Klebsiella pneumoniae</i>	NCTC 13465	3.0E+01 copies/mL	20/20 100%
<i>Morganella morganii</i>	Zeptomatrix 0804010	4.8E+01 copies/mL	20/20 100%
<i>Corynebacterium urealyticum</i>	ATCC 43044	4.1E+01 copies/mL	20/20 100%
<i>Enterococcus faecium</i>	ATCC BAA-2127	4.5E+01 copies/mL	20/20 100%
<i>Enterococcus faecalis</i>	Zeptomatrix 0804216	3.6E+02 copies/mL	20/20 100%
<i>Acinetobacter baumannii</i>	ATCC 19606	1.7E+02 copies/mL	20/20 100%
<i>Proteus vulgaris</i>	Zeptomatrix 0810290CF	1.5E+02 copies/mL	20/20 100%
<i>Staphylococcus aureus</i>	ATCC 10832	5.5E+01 copies/mL	20/20 100%
<i>Ureaplasma urealyticum</i>	ATCC 27618	5.0E+01 copies/mL	20/20 100%
<i>Ureaplasma parvum</i>	ATCC 27815	4.0E+01 copies/mL	20/20 100%
<i>Providencia stuartii</i>	Zeptomatrix 0810452CF	4.5E+01 copies/mL	20/20 100%
<i>Candida albicans</i>	ATCC 10231	3.4E+02 copies/mL	20/20 100%
<i>Candida glabrata</i>	ATCC 90030	4.4E+01 copies/mL	20/20 100%
<i>Candida parapsilosis</i>	ATCC 22019	5.8E+01 copies/mL	20/20 100%
<i>Candida tropicalis</i>	ATCC 750	5.7E+01 copies/mL	20/20 100%
<i>Candida krusei</i>	ATCC 2159	6.8E+01 copies/mL	20/20 100%
<i>Candida auris</i>	ATCC MYA-5003	7.2E+01 copies/mL	19/20 95%

10.2. Device Equivalence Study

A device equivalence study was conducted to assess the differences in results obtained using the kit across various instruments. For this purpose, the same LoD determination study was repeated using the Bio-Rad CFX96™ Dx/CFX Opus 96™/CFX Opus 96™ Dx/CFX384 Touch™/CFX Opus 384™, Applied Biosystems QuantStudio 5, 7, and 12K, Qiagen Rotor-Gene Q 5plex Platform, and Roche LightCycler 480. Similar results were obtained at the 1x LoD concentration level of the targets in the device equivalence study across the different instruments.

10.3. Analytical Reactivity (Inclusivity)

10.3.1. In-Silico Analytical Reactivity

A BLAST search of the oligonucleotides was conducted on the genome sequences of *Escherichia coli*, *Streptococcus agalactiae*, *Klebsiella oxytoca*, *Staphylococcus saprophyticus*, *Serratia marcescens*, *Proteus mirabilis*, *Aerococcus urinae*, *Treponema pallidum*, *Enterobacter cloacae*, *Pseudomonas aeruginosa*, *Citrobacter freundii*, *Klebsiella aerogenes*, *Klebsiella pneumoniae*, *Morganella morganii*, *Corynebacterium urealyticum*, *Enterococcus faecium*, *Enterococcus faecalis*, *Acinetobacter baumannii*, *Proteus vulgaris*, *Staphylococcus aureus*, *Ureplasma (Ureaplasma urealyticum/parvum)*, *Providencia stuartii*, *Candida albicans*, *Candida glabrata*, *Candida parapsilosis*, *Candida tropicalis*, *Candida krusei*, and *Candida auris* using the Primer-BLAST tool on the NCBI database.

The aggregated results of all in-silico analyses performed using the NCBI database are provided in the table below. The melting temperatures (T_m) of the oligonucleotide sequences with a 1-base mismatch remain higher than the annealing temperature specified in the PCR cycle parameters of the kit. Therefore, single base mismatches in the sequences are not expected to impact the inclusivity of the test.

Table 10. In-silico analysis results performed in the NCBI database.

Target	Primer	Total number of target sequences	Ratio of the sequences without mismatch	Ratio of the sequences with 1 base mismatch	Ratio of the sequences with 2 base mismatches	Ratio of the sequences with 3 base mismatches
<i>Escherichia coli</i>	Sense Primer	5.547	99.25%	0.75%	0.00%	0.00%
<i>Escherichia coli</i>	Antisense Primer	5.579	99.65%	0.35%	0.00%	0.00%
<i>Escherichia coli</i>	Hydrolysis Probe	5.579	99.78%	0.22%	0.00%	0.00%
<i>Streptococcus agalactiae</i>	Sense Primer	226	99.95%	0.05%	0.00%	0.00%
<i>Streptococcus agalactiae</i>	Antisense Primer	236	100.00%	0.00%	0.00%	0.00%
<i>Streptococcus agalactiae</i>	Hydrolysis Probe	236	100.00%	0.00%	0.00%	0.00%
<i>Klebsiella oxytoca</i>	Sense Primer	150	99.74%	0.26%	0.00%	0.00%
<i>Klebsiella oxytoca</i>	Antisense Primer	158	99.56%	0.44%	0.00%	0.00%
<i>Klebsiella oxytoca</i>	Hydrolysis Probe	158	99.83%	0.27%	0.00%	0.00%
<i>Staphylococcus saprophyticus</i>	Sense Primer	26	99.52%	0.48%	0.00%	0.00%
<i>Staphylococcus saprophyticus</i>	Antisense Primer	26	97.52%	2.48%	0.00%	0.00%
<i>Staphylococcus saprophyticus</i>	Hydrolysis Probe	26	99.74%	0.26%	0.00%	0.00%

<i>Serratia marcescens</i>	Sense Primer	296	99.80%	0.20%	0.00%	0.00%
<i>Serratia marcescens</i>	Antisense Primer	296	99.80%	0.20%	0.00%	0.00%
<i>Serratia marcescens</i>	Hydrolysis Probe	292	99.82%	0.18%	0.00%	0.00%
<i>Proteus mirabilis</i>	Sense Primer	164	100.00%	0.00%	0.00%	0.00%
<i>Proteus mirabilis</i>	Antisense Primer	164	100.00%	0.00%	0.00%	0.00%
<i>Proteus mirabilis</i>	Hydrolysis Probe	160	99.80%	0.20%	0.00%	0.00%
<i>Aerococcus urinae</i>	Sense Primer	80	100.00%	0.00%	0.00%	0.00%
<i>Aerococcus urinae</i>	Antisense Primer	80	100.00%	0.00%	0.00%	0.00%
<i>Aerococcus urinae</i>	Hydrolysis Probe	76	100.00%	0.00%	0.00%	0.00%
<i>Treponema pallidum</i>	Sense Primer	538	99.64%	0.36%	0.00%	0.00%
<i>Treponema pallidum</i>	Antisense Primer	538	99.64%	0.36%	0.00%	0.00%
<i>Treponema pallidum</i>	Hydrolysis Probe	538	99.50%	0.50%	0.00%	0.00%
<i>Enterobacter cloacae</i>	Sense Primer	683	99.63%	0.37%	0.00%	0.00%
<i>Enterobacter cloacae</i>	Antisense Primer	669	99.12%	0.88%	0.00%	0.00%
<i>Enterobacter cloacae</i>	Hydrolysis Probe	669	99.82%	0.18%	0.00%	0.00%
<i>Pseudomonas aeruginosa</i>	Sense Primer	1.162	99.75%	0.25%	0.00%	0.00%
<i>Pseudomonas aeruginosa</i>	Antisense Primer	1.167	99.79%	0.21%	0.00%	0.00%
<i>Pseudomonas aeruginosa</i>	Hydrolysis Probe	1.167	99.84%	0.16%	0.00%	0.00%
<i>Citrobacter freundii</i>	Sense Primer	175	99.70%	0.30%	0.00%	0.00%
<i>Citrobacter freundii</i>	Antisense Primer	175	99.70%	0.30%	0.00%	0.00%
<i>Citrobacter freundii</i>	Hydrolysis Probe	168	99.90%	0.10%	0.00%	0.00%
<i>Klebsiella aerogenes</i>	Sense Primer	83	98.52%	1.48%	0.00%	0.00%
<i>Klebsiella aerogenes</i>	Antisense Primer	82	97.11%	2.89%	0.00%	0.00%
<i>Klebsiella aerogenes</i>	Hydrolysis Probe	82	96.85%	3.15%	0.00%	0.00%
<i>Klebsiella pneumoniae</i>	Sense Primer	2.816	100.00%	0.00%	0.00%	0.00%
<i>Klebsiella pneumoniae</i>	Antisense Primer	2.711	100.00%	0.00%	0.00%	0.00%
<i>Klebsiella pneumoniae</i>	Hydrolysis Probe	2.711	99.66%	0.34%	0.00%	0.00%
<i>Morganella morganii</i>	Sense Primer	81	99.84%	0.16%	0.00%	0.00%
<i>Morganella morganii</i>	Antisense Primer	81	99.84%	0.16%	0.00%	0.00%
<i>Morganella morganii</i>	Hydrolysis Probe	80	99.52%	0.48%	0.00%	0.00%
<i>Corynebacterium urealyticum</i>	Sense Primer	30	100.00%	0.00%	0.00%	0.00%
<i>Corynebacterium urealyticum</i>	Antisense Primer	30	100.00%	0.00%	0.00%	0.00%

<i>Corynebacterium urealyticum</i>	Hydrolysis Probe	30	100.00%	0.00%	0.00%	0.00%
<i>Enterococcus faecium</i>	Sense Primer	552	98.68%	1.32%	0.00%	0.00%
<i>Enterococcus faecium</i>	Antisense Primer	555	98.68%	1.32%	0.00%	0.00%
<i>Enterococcus faecium</i>	Hydrolysis Probe	555	98.46%	1.54%	0.00%	0.00%
<i>Enterococcus faecalis</i>	Sense Primer	575	100.00%	0.00%	0.00%	0.00%
<i>Enterococcus faecalis</i>	Antisense Primer	578	100.00%	0.00%	0.00%	0.00%
<i>Enterococcus faecalis</i>	Hydrolysis Probe	578	99.89%	0.11%	0.00%	0.00%
<i>Acinetobacter baumannii</i>	Sense Primer	1.703	99.35%	0.65%	0.00%	0.00%
<i>Acinetobacter baumannii</i>	Antisense Primer	1.701	99.89%	0.21%	0.00%	0.00%
<i>Acinetobacter baumannii</i>	Hydrolysis Probe	1.701	99.47%	0.53%	0.00%	0.00%
<i>Proteus vulgaris</i>	Sense Primer	155	99.83%	0.17%	0.00%	0.00%
<i>Proteus vulgaris</i>	Antisense Primer	155	99.83%	0.17%	0.00%	0.00%
<i>Proteus vulgaris</i>	Hydrolysis Probe	157	99.85%	0.15%	0.00%	0.00%
<i>Staphylococcus aureus</i>	Sense Primer	2.491	99.65%	0.35%	0.00%	0.00%
<i>Staphylococcus aureus</i>	Antisense Primer	2.703	99.74%	0.26%	0.00%	0.00%
<i>Staphylococcus aureus</i>	Hydrolysis Probe	2.703	99.62%	0.38%	0.00%	0.00%
<i>Ureplasma</i>	Sense Primer	90	99.90%	0.10%	0.00%	0.00%
<i>Ureplasma</i>	Antisense Primer	90	99.90%	0.10%	0.00%	0.00%
<i>Ureplasma</i>	Hydrolysis Probe	88	99.90%	0.10%	0.00%	0.00%
<i>Providencia stuartii</i>	Sense Primer	23	100.00%	0.00%	0.00%	0.00%
<i>Providencia stuartii</i>	Antisense Primer	23	100.00%	0.00%	0.00%	0.00%
<i>Providencia stuartii</i>	Hydrolysis Probe	22	100.00%	0.00%	0.00%	0.00%
<i>Candida auris</i>	Sense Primer	501	100,00%	0,00%	0.00%	0.00%
<i>Candida auris</i>	Antisense Primer	501	100,00%	0,00%	0.00%	0.00%
<i>Candida auris</i>	Hydrolysis Probe	499	100,00%	0,00%	0.00%	0.00%
<i>Candida krusei</i>	Sense Primer	1.415	100%	0.00%	0.00%	0.00%
<i>Candida krusei</i>	Antisense Primer	1.415	100%	0.00%	0.00%	0.00%
<i>Candida krusei</i>	Hydrolysis Probe	1.415	100%	0.00%	0.00%	0.00%
<i>Candida albicans</i>	Sense Primer	3.629	99.69%	0.31%	0.00%	0.00%
<i>Candida albicans</i>	Antisense Primer	3.728	98.85%	2.25%	0.00%	0.00%
<i>Candida albicans</i>	Hydrolysis Probe	3.728	98.52%	2.48%	0.00%	0.00%
<i>Candida parapsilosis</i>	Sense Primer	2.559	99.74%	0.26%	0.00%	0.00%

<i>Candida parapsilosis</i>	Antisense Primer	2.463	100%	0.00%	0.00%	0.00%
<i>Candida parapsilosis</i>	Hydrolysis Probe	2.463	100%	0.00%	0.00%	0.00%
<i>Candida tropicalis</i>	Sense Primer	1.164	98.40%	2.60%	0.00%	0.00%
<i>Candida tropicalis</i>	Antisense Primer	1.906	97.83%	2.17%	0.00%	0.00%
<i>Candida tropicalis</i>	Hydrolysis Probe	1.906	97.12%	2.88%	0.00%	0.00%
<i>Candida glabrata</i>	Sense Primer	763	100%	0.00%	0.00%	0.00%
<i>Candida glabrata</i>	Antisense Primer	1.111	99.20%	0.80%	0.00%	0.00%
<i>Candida glabrata</i>	Hydrolysis Probe	1.111	99.64%	0.36%	0.00%	0.00%

10.3.2. Wet-Test Analytical Reactivity

The analytical reactivity (inclusivity) of the **MarinaBiolab Urinary Tract Infections Panel PCR Kit** was demonstrated using a comprehensive panel that represents the temporal, evolutionary, and geographic diversity of each target organism.

Each sample was tested in triplicate with the **MarinaBiolab Urinary Tract Infections Panel PCR Kit** at an initial concentration 3-fold higher than the LoD determined for each analyte. In cases where the expected targets were not detected in one or more replicates, concentrations 3-fold higher were evaluated.

The individual strains and the concentrations at which positive test results were obtained for all three replicates are presented by target organisms in Table 11 below.

Table 11. Results of the wet inclusivity test.

Variant/Type/Subtype/Lineage/Genotype/Species	Isolate ID/Source	xLoD Detected
<i>Escherichia coli</i>	ATCC 25922	1x
<i>Streptococcus agalactiae</i>	ATCC 12386	1x
<i>Klebsiella oxytoca</i>	ATCC 700324	1x
<i>Staphylococcus saprophyticus</i>	Zeptomatrix 0804014	1x
<i>Serratia marcescens</i>	ATCC 29021	1x
<i>Proteus mirabilis</i>	Zeptomatrix 0801544	1x
<i>Aerococcus urinae</i>	ATCC 51268	1x
<i>Treponema pallidum</i>	In-house	1x
<i>Enterobacter cloacae</i>	Zeptomatrix 0801830	1x
<i>Pseudomonas aeruginosa</i>	ATCC 27853	1x
<i>Citrobacter freundii</i>	Zeptomatrix 0801563	1x
<i>Klebsiella aerogenes</i>	ATCC 13048	1x
<i>Klebsiella pneumoniae</i>	NCTC 13465	1x

<i>Morganella morganii</i>	Zeptomatrix 0804010	1x
<i>Corynebacterium urealyticum</i>	ATCC 43044	1x
<i>Enterococcus faecium</i>	ATCC BAA-2127	1x
<i>Enterococcus faecalis</i>	Zeptomatrix 0804216	1x
<i>Acinetobacter baumannii</i>	ATCC 19606	1x
<i>Proteus vulgaris</i>	Zeptomatrix 0810290CF	1x
<i>Staphylococcus aureus</i>	ATCC 10832	1x
<i>Ureaplasma urealyticum</i>	ATCC 27618	1x
<i>Ureaplasma parvum</i>	ATCC 27815	1x
<i>Providencia stuartii</i>	Zeptomatrix 0810452CF	1x
<i>Candida albicans</i>	ATCC 10231	1x
<i>Candida glabrata</i>	ATCC 90030	1x
<i>Candida parapsilosis</i>	ATCC 22019	1x
<i>Candida tropicalis</i>	ATCC 750	1x
<i>Candida krusei</i>	ATCC 2159	1x
<i>Candida auris</i>	ATCC MYA-5003	1x

10.4. Analytical Specificity (Exclusivity)

10.4.1. In-Silico Analytical Specificity

Primers and probes designed for a target sequence may also bind to similar sequences if they closely match or differ by only a few base pairs from a non-targeted sequence. To ensure specificity to the target sequence, it is essential to screen the primers and probes against the reference database for the intended templates, as well as any databases that may contain potential contaminating templates.

Table 12. The results of On-Panel and Off-Panel organisms tested for cross-reactivity.

On-Panel/Off-Panel	Name of the organism	Cross Reactivity*		
		Forward	Probe	Reverse
On-Panel	<i>Escherichia coli</i>	None	None	None
On-Panel	<i>Streptococcus agalactiae</i>	None	None	None
On-Panel	<i>Klebsiella oxytoca</i>	None	None	None
On-Panel	<i>Staphylococcus saprophyticus</i>	None	None	None
On-Panel	<i>Serratia marcescens</i>	None	None	None
On-Panel	<i>Proteus mirabilis</i>	None	None	None

On-Panel	<i>Aerococcus urinae</i>	None	None	None
On-Panel	<i>Treponema pallidum</i>	None	None	None
On-Panel	<i>Enterobacter cloacae</i>	None	None	None
On-Panel	<i>Pseudomonas aeruginosa</i>	None	None	None
On-Panel	<i>Citrobacter freundii</i>	None	None	None
On-Panel	<i>Klebsiella aerogenes</i>	None	None	None
On-Panel	<i>Klebsiella pneumoniae</i>	None	None	None
On-Panel	<i>Morganella morganii</i>	None	None	None
On-Panel	<i>Corynebacterium urealyticum</i>	None	None	None
On-Panel	<i>Enterococcus faecium</i>	None	None	None
On-Panel	<i>Enterococcus faecalis</i>	None	None	None
On-Panel	<i>Acinetobacter baumannii</i>	None	None	None
On-Panel	<i>Proteus vulgaris</i>	None	None	None
On-Panel	<i>Staphylococcus aureus</i>	None	None	None
On-Panel	<i>Ureaplasma urealyticum</i>	None	None	None
On-Panel	<i>Ureaplasma parvum</i>	None	None	None
On-Panel	<i>Providencia stuartii</i>	None	None	None
On-Panel	<i>Candida albicans</i>	None	None	None
On-Panel	<i>Candida glabrata</i>	None	None	None
On-Panel	<i>Candida parapsilosis</i>	None	None	None
On-Panel	<i>Candida tropicalis</i>	None	None	None
On-Panel	<i>Candida krusei</i>	None	None	None
On-Panel	<i>Candida auris</i>	None	None	None
Off-Panel	<i>Staphylococcus epidermidis</i>	None	None	None
Off-Panel	<i>Staphylococcus haemolyticus</i>	None	None	None
Off-Panel	<i>Staphylococcus lugdunensis</i>	None	None	None
Off-Panel	<i>Streptococcus dysgalactiae</i>	None	None	None
Off-Panel	<i>Streptococcus pyogenes</i>	None	None	None
Off-Panel	<i>Fusarium solani</i>	None	None	None
Off-Panel	<i>Microsporium spp.</i>	None	None	None
Off-Panel	<i>Trichophyton spp.</i>	None	None	None
Off-Panel	<i>Acinetobacter iwoffi</i>	None	None	None

Off-Panel	<i>Acinetobacter nosocomialis</i>	None	None	None
Off-Panel	<i>Stenotrophomonas maltophilia</i>	None	None	None
Off-Panel	<i>Moraxella catarrhalis</i>	None	None	None
Off-Panel	<i>Pasteurella stomatis</i>	None	None	None
Off-Panel	<i>Epidermophyton floccosum</i>	None	None	None
Off-Panel	<i>Finnegoldia magna</i>	None	None	None
Off-Panel	<i>Bartonella henselae</i>	None	None	None
Off-Panel	<i>Haemophilus influenzae</i>	None	None	None
Off-Panel	<i>Candida sojae</i>	None	None	None
Off-Panel	<i>Candida oregonensis</i>	None	None	None
Off-Panel	<i>Malessezia restricta</i>	None	None	None
Off-Panel	<i>Peptoniphilus harei</i>	None	None	None
Off-Panel	<i>Peptoniphilus ivorii</i>	None	None	None
Off-Panel	<i>Peptostreptococcus prevotii</i>	None	None	None
Off-Panel	<i>Peptostreptococcus anaerobius</i>	None	None	None
Off-Panel	<i>Listeria monocytogenes</i>	None	None	None
Off-Panel	<i>Candida lusitanae</i>	None	None	None
Off-Panel	<i>Kingella kingae</i>	None	None	None
Off-Panel	<i>Chlamydia trachomatis</i>	None	None	None
Off-Panel	<i>Legionella dumoffii</i>	None	None	None
Off-Panel	<i>Corynebacterium diphtheriae</i>	None	None	None
Off-Panel	<i>Neisseria meningitidis</i>	None	None	None

* Homology should be <80% between the cross-reactivity microorganisms and the test primers/ probe(s).

10.4.2. Wet-Test Analytical Specificity

The potential for non-specific amplification by assays designed to detect analytes was evaluated by testing high concentrations of organisms or nucleic acids using the **MarinaBiolab Urinary Tract Infections Panel PCR Kit**. On-panel organisms were tested to assess potential intra-panel cross-reactivity, while off-panel organisms were tested to evaluate the specificity of the panel. Off-panel organisms included normal flora, pathogens that may be present in specimens, and genetically related species to those detected by the **MarinaBiolab Urinary Tract Infections Panel PCR Kit**. The concentration of organisms tested (in triplicate) was at least 1.0E+06 CFU/mL for bacteria, fungi, and parasites, and at least 1.0E+05 units/mL for viruses. For certain organisms that were not available for laboratory testing, in silico analysis of the organism's whole genome sequences was used. The on-panel and off-panel organisms tested are listed in Table 13 and Table 14.

Table 13. On-Panel organisms tested for evaluation of *MarinaBiolab Urinary Tract Infections Panel PCR Kit* analytical specificity.

Organism	Isolate ID/Source	Cross Reactivity Detected
<i>Escherichia coli</i>	ATCC 25922	None
<i>Streptococcus agalactiae</i>	ATCC 12386	None
<i>Klebsiella oxytoca</i>	ATCC 700324	None
<i>Staphylococcus saprophyticus</i>	Zeptomatrix 0804014	None
<i>Serratia marcescens</i>	ATCC 29021	None
<i>Proteus mirabilis</i>	Zeptomatrix 0801544	None
<i>Aerococcus urinae</i>	ATCC 51268	None
<i>Treponema pallidum</i>	In-house	None
<i>Enterobacter cloacae</i>	Zeptomatrix 0801830	None
<i>Pseudomonas aeruginosa</i>	ATCC 27853	None
<i>Citrobacter freundii</i>	Zeptomatrix 0801563	None
<i>Klebsiella aerogenes</i>	ATCC 13048	None
<i>Klebsiella pneumoniae</i>	NCTC 13465	None
<i>Morganella morganii</i>	Zeptomatrix 0804010	None
<i>Corynebacterium urealyticum</i>	ATCC 43044	None
<i>Enterococcus faecium</i>	ATCC BAA-2127	None
<i>Enterococcus faecalis</i>	Zeptomatrix 0804216	None
<i>Acinetobacter baumannii</i>	ATCC 19606	None
<i>Proteus vulgaris</i>	Zeptomatrix 0810290CF	None
<i>Staphylococcus aureus</i>	ATCC 10832	None
<i>Ureaplasma urealyticum</i>	ATCC 27618	None
<i>Ureaplasma parvum</i>	ATCC 27815	None
<i>Providencia stuartii</i>	Zeptomatrix 0810452CF	None
<i>Candida albicans</i>	ATCC 10231	None
<i>Candida glabrata</i>	ATCC 90030	None
<i>Candida parapsilosis</i>	ATCC 22019	None
<i>Candida tropicalis</i>	ATCC 750	None
<i>Candida krusei</i>	ATCC 2159	None
<i>Candida auris</i>	ATCC MYA-5003	None

Table 14. Off-Panel organisms were tested for evaluation of *MarinaBiolab Urinary Tract Infections Panel PCR Kit* analytical specificity.

Organism	Isolate ID/Source	Cross Reactivity Detected
<i>Acinetobacter calcoaceticus</i>	ATCC 23055	None
<i>Staphylococcus epidermidis</i>	Zeptomatrix 0804281	None
<i>Staphylococcus haemolyticus</i>	Zeptomatrix 0801591	None
<i>Staphylococcus lugdunensis</i>	Zeptomatrix 0801555	None
<i>Streptococcus dysgalactiae</i>	Zeptomatrix 0801516	None
<i>Streptococcus pyogenes</i>	Zeptomatrix 0801512	None
<i>Fusarium solani</i>	Zeptomatrix 0801806	None
<i>Acinetobacter iwoffii</i>	Zeptomatrix 0801909	None
<i>Stenotrophomonas maltophilia</i>	Zeptomatrix 0801569	None
<i>Moraxella catarrhalis</i>	Zeptomatrix 0801509	None
<i>Candida sojae</i>	Zeptomatrix 0801825	None
<i>Listeria monocytogenes</i>	Zeptomatrix 0804339	None
<i>Chlamydia trachomatis</i>	Zeptomatrix 0801775	None
<i>Acinetobacter baumannii</i>	ATCC 19606	None
<i>Legionella pneumophila</i>	Zeptomatrix 0801530	None
<i>Neisseria gonorrhoeae</i>	ATCC 19424	None
<i>Neisseria meningitidis</i>	ATCC 13090	None
<i>Aspergillus flavus</i>	Zeptomatrix 0801598	None

10.5. Interferences

The potential for endogenous or exogenous substances, which may be present in research samples or introduced during sample collection and handling, to interfere with the accurate detection of analytes was evaluated through select direct testing on the *MarinaBiolab Urinary Tract Infections Panel PCR Kit*. The findings were extrapolated from the interference evaluation of the kit.

Potentially interfering substances were evaluated using contrived samples spiked with the substance of interest. Results from samples containing the substance were compared to those from control samples without the substance. The substances tested included endogenous compounds that may be present in samples at normal or elevated levels (e.g., blood, mucus/mucin, human genomic DNA), various commensal or infectious microorganisms, medications, washes or topical applications, swabs and transport media used for sample collection, and substances employed to clean, decontaminate, or disinfect work areas. Each substance was added to contrived samples containing representative organisms at concentrations near (3x) the LoD. The concentration of each substance added to the samples was equal to or greater than the highest level expected in research samples, and each sample was tested in triplicate.

None of the substances tested were found to interfere with the **MarinaBiolab Urinary Tract Infections Panel PCR Kit**.

Table 15. Evaluation of potentially interfering substances on the **MarinaBiolab Urinary Tract Infections Panel PCR Kit**.

Substance Tested	Concentration Tested	Observed Interference
Endogenous Substances		
Whole Blood	10% v/v	No Interference
Human serum	5% v/v	No Interference
Human Urine	-	No Interference
Competitive Microorganisms		
<i>Escherichia coli</i>	1.0E+06 CFU/mL	No Interference
<i>Streptococcus agalactiae</i>	1.0E+06 CFU/mL	No Interference
<i>Klebsiella oxytoca</i>	1.0E+06 CFU/mL	No Interference
<i>Staphylococcus saprophyticus</i>	1.0E+06 CFU/mL	No Interference
<i>Serratia marcescens</i>	1.0E+06 CFU/mL	No Interference
<i>Proteus mirabilis</i>	1.0E+06 CFU/mL	No Interference
<i>Aerococcus urinae</i>	1.0E+06 CFU/mL	No Interference
<i>Treponema pallidum</i>	1.0E+06 CFU/mL	No Interference
<i>Enterobacter cloacae</i>	1.0E+06 CFU/mL	No Interference
<i>Pseudomonas aeruginosa</i>	1.0E+06 CFU/mL	No Interference
<i>Citrobacter freundii</i>	1.0E+06 CFU/mL	No Interference
<i>Klebsiella aerogenes</i>	1.0E+06 CFU/mL	No Interference
<i>Klebsiella pneumoniae</i>	1.0E+06 CFU/mL	No Interference
<i>Morganella morganii</i>	1.0E+06 CFU/mL	No Interference
<i>Corynebacterium urealyticum</i>	1.0E+06 CFU/mL	No Interference
<i>Enterococcus faecium</i>	1.0E+06 CFU/mL	No Interference
<i>Enterococcus faecalis</i>	1.0E+06 CFU/mL	No Interference
<i>Acinetobacter baumannii</i>	1.0E+06 CFU/mL	No Interference
<i>Proteus vulgaris</i>	1.0E+06 CFU/mL	No Interference
<i>Staphylococcus aureus</i>	1.0E+06 CFU/mL	No Interference
<i>Ureaplasma urealyticum</i>	1.0E+06 CFU/mL	No Interference
<i>Ureaplasma parvum</i>	1.0E+06 CFU/mL	No Interference
<i>Providencia stuartii</i>	1.0E+06 CFU/mL	No Interference
<i>Candida albicans</i>	1.0E+06 CFU/mL	No Interference

<i>Candida glabrata</i>	1.0E+06 CFU/mL	No Interference
<i>Candida parapsilosis</i>	1.0E+06 CFU/mL	No Interference
<i>Candida tropicalis</i>	1.0E+06 CFU/mL	No Interference
<i>Candida krusei</i>	1.0E+06 CFU/mL	No Interference
<i>Candida auris</i>	1.0E+06 CFU/mL	No Interference
Exogenous Substances		
Feminine Spray/talcum powder	5% v/v	No Interference
Phenazopyridine Hydrochloride (Pyridium)	10 µg/mL	No Interference
Ascorbic acid	0.6 mmol/L	No Interference
High pH	pH = 8.0	No Interference
Low pH	pH = 4.0	No Interference
<u>Antibiotic Pool</u> Amoxicillin trihydrate Metronidazole Tetracycline Hydrochloride Sodium Cefotaxime	1 mg/mL (Each)	No Interference
Specimen Collection Materials		
Urine Tubes (BD Vacutainer® 364992)	N/A	No Interference
Starplex™ Scientific Urine Preservative Tube (22046414)	N/A	No Interference

11. TROUBLESHOOTING

Problem	Cause	Solution
Target-specific and/or internal control (IC) signals were detected in the Negative Control well.	Contamination may arise from the environment, contamination of extraction and/or qPCR reagents, or well-to-well cross-contamination. The signal observed is not true target amplification, but rather background curves generated by the software of the qPCR instrument.	Repeat the qPCR using fresh reagents. Follow the general GLP guidelines in a PCR lab (e.g., decontaminate all surfaces and instruments with sodium hypochlorite or ethanol, and ensure filter tips are used and changed between samples). It is recommended to set up the qPCR reactions in a separate area, where no RNA/DNA is handled, and with equipment designated solely for pre-PCR activities. Ignore the Cq value of the No Template Control (NTC) if the amplification curve appears to be background noise rather than a true signal. If the issue persists, contact Technical Support.
No IC signal is detected, but a target-specific signal is observed in the sample wells.	A high copy number of target nucleic acid in the samples leads to preferential amplification of the target-specific nucleic acid.	No action is required. The result is considered positive.
The Positive Control did not meet the criteria for acceptable values specified by the kit, rendering the assay invalid.	The Positive Control was not stored under the recommended conditions. The kit has expired.	Check the kit label for the recommended storage conditions and expiration date. Replace the Positive Control. If necessary, use a new kit.
High Cq values were observed in the repeated samples.	The frozen samples were not mixed properly after thawing. Nucleic acids may be degraded.	Ensure frozen samples are thawed with mild agitation to guarantee thorough mixing. Make sure samples are stored correctly and are not subjected to multiple freeze-thaw cycles.
Target-specific and/or IC signals were detected after 35 cycles in the Positive Control.	Incorrect qPCR set-up or the kit reagents may have been compromised (e.g., improper storage or more than 15 freeze-thaw cycles).	Replace the control. If the problem persists, contact Technical Support.
No target-specific or IC signals were detected in the sample wells.	Sampling, extraction, or inhibition problem.	Dilute the nucleic acid isolate 1:10 and repeat the qPCR. If the diluted sample does not show a positive result in the IC channel, request a new sample and repeat the nucleic acid extraction. If necessary, repeat the nucleic acid extraction and the qPCR. If the issue persists, request a new sample, repeat the nucleic acid extraction and qPCR. If the problem continues, contact Technical Support.

12. EXPLANATION of SYMBOLS

Symbol	Title of Symbol	Symbol	Title of Symbol
	Research Use Only		Use-by date
	Manufacturer		Batch code
	Negative control		Non-sterile
	Positive control		Consult instructions for use or consult electronic instructions for use
	Control		Caution
	Temperature limit		Catalogue number
	Keep away from sunlight		Do not use if package is damaged and consult instructions for use
	Keep dry		Keep upright
	Contains sufficient for <n> tests		Protect from heat and radioactive sources

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