BIOFIRE® Joint Infection (JI) Panel Testing

PURPOSE

This procedure provides instructions for testing synovial fluid (SF) using the BIOFIRE JI Panel Kit.

BACKGROUND

The BIOFIRE® Joint Infection (JI) Panel is a multiplexed nucleic-acid-based, *in vitro* diagnostic test intended for use with BIOFIRE® FILMARRAY® 2.0 and BIOFIRE® FILMARRAY® TORCH Systems for the simultaneous qualitative detection and identification of multiple bacterial and yeast nucleic acids and select antimicrobial resistance genes from synovial fluid (SF) obtained from individuals suspected to have a joint infection.

The following organisms are identified using the BIOFIRE JI Panel:

GRAM POSITIVE BACTERIA		
Anaerococcus prevotii/vaginalis	*Finegoldia magna*	*Streptococcus* spp.
Clostridium perfringens	*Parvimonas micra*	*Streptococcus agalactiae*
Cutibacterium avidum/granulosum	*Peptoniphilus*	*Streptococcus pneumoniae*
Enterococcus faecalis	*Peptostreptococcus anaerobius*	*Streptococcus pyogenes*
Enterococcus faecium	*Staphylococcus aureus*	
	Staphylococcus lugdunensis	
GRAM NEGATIVE BACTERIA		
Bacteroides fragilis	*Kingella kingae*	*Proteus* spp.
Citrobacter	*Klebsiella aerogenes*	*Pseudomonas aeruginosa*
Enterobacter cloacae complex	*Klebsiella pneumoniae* group	*Salmonella* spp.
Escherichia coli	*Morganella morganii*	*Serratia marcescens*
Haemophilus influenzae	*Neisseria gonorrhoeae*	
YEAST		
Candida		
Candida albicans		

The BIOFIRE JI Panel contains assays for the detection of genetic determinants associated with *S. aureus* resistance to methicillin *(mecA/C* in conjunction with the SCC*mec* right extremity junction [MREJ]), enterococcal resistance to vancomycin *(vanA* and *vanB)* and some mechanisms of gram-negative bacterial resistance to ß-lactams including penicillins, cephalosporins, monobactams, and carbapenems ($_{bla}$CTX-M, $_{bla}$IMP, $_{bla}$KPC, $_{bla}$NDM, $_{bla}$OXA-48-like, $_{bla}$VIM). Detection of these genetic determinants can aid in the identification of potentially antimicrobial-resistant organisms in synovial fluid samples. The antimicrobial resistance gene or marker detected may or may not be associated with the agent responsible for disease. Negative results for these select antimicrobial resistance gene assays do not indicate susceptibility, as multiple mechanisms of resistance to methicillin, vancomycin, and ß-lactams exist.

ANTIMICROBIAL RESISTANCE GENES			
CTX-M	KPC	NDM	*vanA/B*
IMP	*mecA/C* and MREJ (MRSA)	OXA-48-like	VIM

PRINCIPLE OF THE PROCEDURE

The BIOFIRE JI Panel is indicated as an aid in the diagnosis of specific agents of joint infection and results should be used in conjunction with other clinical and laboratory findings. Negative results may be due to infection with pathogens that are not detected by this test, pathogens present below the limit of detection of the assay, or infection that may not be detected in a synovial fluid specimen. Positive results do not rule out co-infection with other organisms. The BIOFIRE JI Panel is not intended to monitor treatment for joint infections.

Culture of synovial fluid is necessary to recover organisms for susceptibility testing and epidemiological typing, to identify organisms in the synovial fluid that are not detected by the BIOFIRE JI Panel, and to further identify species in the genus, complex, or group results.

During a run, the BIOFIRE System:

- Lyses the sample by agitation (bead beading) in addition to chemical lysis mediated by the Sample Buffer.
- Extracts and purifies all nucleic acids from the sample using magnetic bead technology.
- Performs nested multiplex PCR by:
  - First performing a single, large volume, massively multiplexed reaction (PCR1)
  - Then performing multiple simultaneous second-stage PCR reactions (PCR2) in the array to amplify sequences within the PCR1 products
- Uses endpoint melting curve data to detect and generate a result for each target on the BIOFIRE JI Panel array.

SAMPLE REQUIREMENTS

The following table describes the requirements for specimen collection, preparation, and handling that will help ensure accurate test results.

Specimen Type	Synovial fluid (SF) collected according to standard technique.
Minimum Sample Volume	0.2 mL (200 µL)
Transport and Storage	Specimens should be tested with the BIOFIRE JI Panel as soon as possible[a]. If transport or storage is required, specimens can be held: • Refrigerated for up to 7 days (2-8 °C)

[a] The performance validation included the evaluation of clinical synovial fluid specimens frozen for up to 20 months. However, longer frozen storage may be acceptable. Please follow your institutions rules and protocols regarding sample storage validation.

NOTE: *Storage of SF specimen at room temperature is not recommended.*

NOTE: *SF specimens should not be centrifuged, pre-processed, or placed into transport media or treated with anticoagulants before testing. The panel is not intended for use with synovial fluid in media/broths as these solutions may contain contaminating nucleic acids (bioburden) that can generate false positive results.*

NOTE: *Bleach can damage organisms/nucleic acids within the specimen, potentially causing false negative results. Contact between bleach and specimens during collection, disinfection, and testing procedures should be avoided.*

MATERIALS

The following table describes the requirements for specimen collection, preparation, and handling that will help ensure accurate test results.

MATERIALS PROVIDED	MATERIALS REQUIRED BUT NOT PROVIDED
Each kit contains sufficient reagents to test 30 samples (30-test kit; RFIT-ASY-0138): • Individually packaged BIOFIRE JI Panel pouches • Single-use (1mL) Sample Buffer ampoules • Single-use pre-filled (1.5mL) Hydration Injection Vials (**blue**) • Single-use Sample Injection Vials (**red**) • Individually packaged Transfer Pipettes	BIOFIRE® System including: • BIOFIRE® 2.0 or BIOFIRE® TORCH and accompanying software • BIOFIRE® FILMARRAY® Pouch Loading Station 10% bleach solution or a similar disinfectant

QUALITY CONTROL

PROCESS CONTROL

Two process controls are included in each pouch:

1. **DNA PROCESS CONTROL**

   The DNA Process Control assay targets a DNA transcript from the yeast *Schizosaccharomyces pombe.* The yeast is present in the pouch in a freeze-dried form and becomes rehydrated when sample is loaded. The control material is carried through all stages of the test process, including lysis, nucleic acid purification, PCR1, dilution, PCR2, and DNA melting. A positive control result indicates that all steps carried out in the BIOFIRE JI Panel pouch were successful.

2. **PCR2 CONTROL**

   The PCR2 Control assay detects a DNA target that is dried into wells of the array along with the corresponding primers. A positive result indicates that PCR2 was successful.

Both control assays must be positive for the test run to pass. If the controls fail, the sample should be retested using a new pouch.

MONITORING TEST SYSTEM PERFORMANCE

The software will automatically fail the run if the melting temperature (Tm) for either the DNA Process Control or the PCR2 Control is outside of an acceptable range (77.6 - 81.6°C for the DNA Process Control and 74.2-78.2°C for the PCR2 Control). If required by local, state, or accrediting organization quality control requirements, users can monitor the system by trending Tm values for the control assays and maintaining records according to standard laboratory quality control practices. Refer to the appropriate BIOFIRE® FILMARRAY® System Operator's Manual for instructions on obtaining control assay Tm values. The PCR2 Control is used in several BIOFIRE pouch types and can, therefore, be used to monitor the system when multiple pouch types are used on the same BIOFIRE System.

EXTERNAL CONTROLS

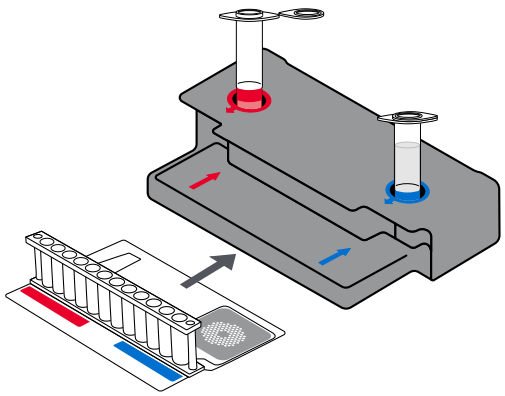
External controls should be used in accordance with laboratory protocols and the appropriate accrediting organization requirements, as applicable. Previously characterized positive samples or negative samples spiked with well-characterized organisms can be used as external positive controls. Commercial external control materials may be available from other manufacturers; these should be used in accordance with the manufacturers' instructions and appropriate accrediting organization requirements, as applicable.

PROCEDURE

Use clean gloves and other Personal Protective Equipment (PPE) when handling pouches and samples. Only prepare one BIOFIRE JI Panel pouch at a time and change gloves between samples and pouches. Once sample is added to the pouch, promptly transfer to the instrument to start the run. After the run is complete, discard the pouch in a biohazard container.

STEP 1: PREPARE POUCH

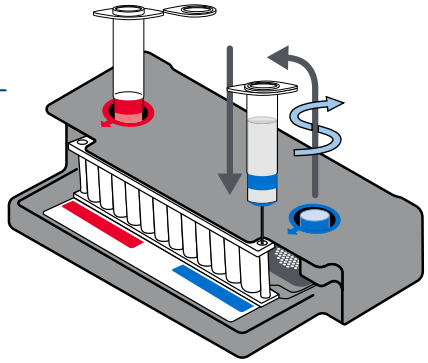
1. Thoroughly clean the work area and the Pouch Loading Station with freshly prepared 10% bleach (or suitable disinfectant) followed by a water rinse.
2. Remove the pouch from its vacuum-sealed package by tearing or cutting the notched outer packaging and opening the protective canister.



***NOTE:** The pouch may still be used even if the vacuum seal of the pouch is not intact. Attempt to hydrate the pouch using the steps in the Hydrate Pouch section. If hydration is successful, continue with the run. If hydration fails, discard the pouch and use a new pouch to test the sample.*

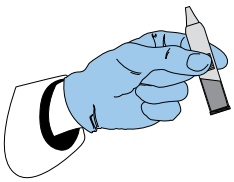
3. Check the expiration date on the pouch. Do not use expired pouches.
4. Insert the pouch into the Pouch Loading Station, aligning the red and blue labels on the pouch with the red and blue arrows on the Pouch Loading Station.
5. Place a red-capped **Sample Injection Vial** into the **red well** of the Pouch Loading Station.
6. Place a blue-capped **Hydration Injection Vial** into the **blue well** of the Pouch Loading Station.

STEP 2: HYDRATE POUCH



1. Unscrew the **Hydration Injection Vial** from the blue cap.
2. Remove the **Hydration Injection Vial**, leaving the blue cap in the Pouch Loading Station.
3. Insert the cannula tip of the **Hydration Injection Vial** into the **pouch hydration port** located directly below the blue arrow of the Pouch Loading Station.
4. Forcefully push down in a firm and quick motion to puncture seal until a faint "pop" is heard and there is an ease in resistance. Wait as the correct volume of Hydration Solution is pulled into the pouch by vacuum.
   - If the hydration solution is not automatically drawn into the pouch, repeat Step 2 to verify that the seal of the **pouch hydration port** was broken. If hydration solution is again not drawn into the pouch, discard the current pouch, retrieve a new pouch, and repeat from Step 1: Prepare Pouch.
5. Verify that the pouch has been hydrated.
   - Flip the barcode label down and check to see that fluid has entered the reagent wells (located at the base of the rigid plastic part of the pouch). Small air bubbles may be seen.
   - If the pouch fails to hydrate (dry reagents appear as white pellets), repeat Step 2 to verify that the seal of the **pouch hydration port** was broken. If hydration solution is still not drawn into the pouch, discard the current pouch, retrieve a new pouch, and repeat from Step 1: Prepare Pouch.

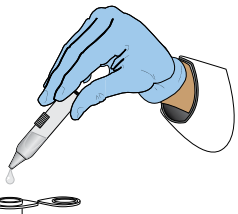
STEP 3: PREPARE SAMPLE MIX



1. Add Sample Buffer to the **Sample Injection Vial.**
   - Hold the Sample Buffer ampoule with the tip facing up.

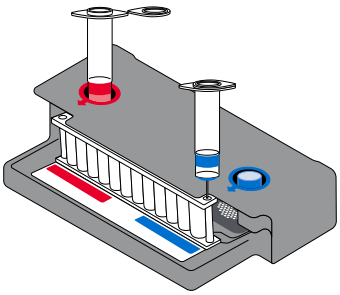
NOTE: *Avoid touching the ampoule tip during handling, as this may introduce contamination.*

- Firmly pinch at textured plastic tab on the side of the ampoule until the seal snaps.
- Invert the ampoule over the red-capped Sample Injection Vial and dispense Sample Buffer using a slow, forceful squeeze followed by a second squeeze.



NOTE: *Avoid squeezing the ampoule additional times to avoid foaming.*

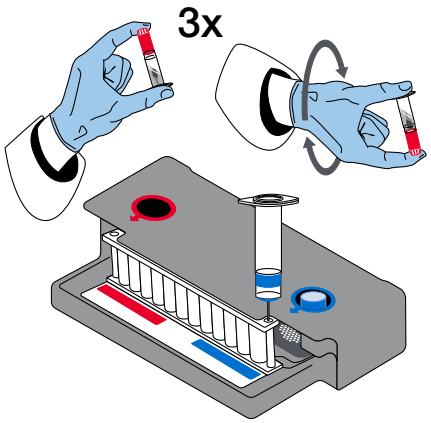
WARNING: The Sample Buffer is harmful if swallowed and can cause serious eye damage and skin irritation.



2. Mix the SF specimen by vortex or inversion.
3. Use the transfer pipette provided in the test kit to draw specimen to the second line (approximately 0.2 mL) of the transfer pipette.
4. Add the specimen to the Sample Buffer in the **Sample Injection Vial.**
5. Tightly close the lid of the **Sample Injection Vial** and discard the transfer pipette in a biohazard waste container.

NOTE: *DO NOT use the Transfer Pipette to mix the sample once it is loaded into the Sample Injection Vial.*

6. Remove the **Sample Injection Vial** from the Pouch Loading Station and invert the vial at least 3 times to mix.
7. Return the **Sample Injection Vial** to the **red well** of the Pouch Loading Station.

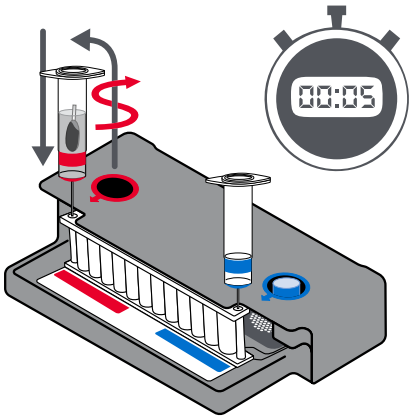


STEP 4: LOAD SAMPLE MIX

1. Slowly twist to unscrew the **Sample Injection Vial** from the red cap and wait for 5 seconds with the vial resting in the cap.

NOTE: *Waiting 5 seconds decreases the risk of dripping and contamination from the sample.*

2. Lift the **Sample Injection Vial**, leaving red cap in the well of the Pouch Loading Station, and insert the **Sample Injection Vial** cannula tip into the **pouch sample port** located directly below the red arrow of the Pouch Loading Station.
3. Forcefully push down in a firm and quick motion to puncture seal (a faint "pop" is heard) and sample is pulled into the pouch by vacuum.
4. Verify that the sample has been loaded.
   - Flip the barcode label down and check to see that fluid has entered the reagent well next to the sample loading port.
   - If the pouch fails to pull sample from the **Sample Injection Vial**, the pouch should be discarded. Retrieve a new pouch and repeat from Step 1: Prepare Pouch.
5. Discard the **Sample Injection Vial** and the **Hydration Injection Vial** in appropriate biohazard sharps container.



6. Record the Sample ID in the provided area on the pouch label (or affix a barcoded Sample ID) and remove the pouch from the Pouch Loading Station.

STEP 5: RUN POUCH

The BIOFIRE® FILMARRAY® Software includes step-by-step, on-screen instructions that guide the operator through performing a run. Refer to the appropriate BIOFIRE® FILMARRAY® System Operator's Manual for more detailed instructions.

BIOFIRE® 2.0

1. Ensure that the BIOFIRE 2.0 system (instrument and computer) is powered on and the software is launched.
2. Follow on-screen instructions and procedures described in the Operator's Manual to place the pouch in a module, enter pouch, sample, and operator information.
3. Pouch identification (Lot Number and Serial Number), Pouch Type, and Protocol information will be automatically entered when the barcode is scanned. If it is not possible to scan the barcode, the pouch Lot Number, Serial Number, Pouch Type, and Protocol can be manually entered from the information provided on the pouch label into the appropriate fields. To reduce data entry errors, it is strongly recommended that the pouch information be entered by scanning the barcode.

NOTE: ***When selecting a Pouch Type manually, ensure that the Pouch Type matches the label on the BIOFIRE JI Panel pouch.***

4. Enter the Sample ID. The Sample ID can be entered manually or scanned in by using the barcode scanner when a barcoded Sample ID is used.
5. If necessary, select and/or confirm the appropriate protocol for your sample type from the Protocol drop down list. The BIOFIRE JI Panel has a single protocol available in the drop-down list.
6. Enter a username and password in the Name and Password fields.

NOTE: ***The font color of the username is red until the username is recognized by the software.***

7. Review the entered run information on the screen. If correct, select Start Run. Once the run has started, the screen displays a list of the steps being performed by the instrument and the number of minutes remaining in the run.

NOTE: ***The bead-beater apparatus makes an audible, high-pitched noise during the first minute of operation.***

8. When the run is finished, follow the on-screen instructions to remove the pouch, then immediately discard it in a biohazard waste container.
9. The run file is automatically saved in the BIOFIRE® Software database, and the test report can be viewed, printed, and/or saved as a PDF file.

BIOFIRE® TORCH

1. Ensure that the BIOFIRE TORCH system is powered on.
2. Select an available Module on the touch screen or scan the barcode on the pouch using the barcode scanner.
3. Pouch identification (Lot Number and Serial Number), Pouch Type, and Protocol information will be automatically entered when the barcode is scanned. If it is not possible to scan the barcode, the pouch Lot Number, Serial Number, Pouch Type, and Protocol can be manually entered from the information provided on the pouch label into the appropriate fields. To reduce data entry errors, it is strongly recommended that the pouch information be entered by scanning the barcode.

***NOTE:** When selecting a Pouch Type manually, ensure that the Pouch Type matches the label on the BIOFIRE JI Panel pouch.*

4. Enter the Sample ID. The Sample ID can be entered manually or scanned in by using the barcode scanner when a barcoded Sample ID is used.
5. Insert the pouch into the available Module.
   - Ensure that the pouch fitment label is lying flat on top of pouch and not folded over. As the pouch is inserted, the module will grab onto the pouch and pull it into the chamber.
6. If necessary, select and/or confirm the appropriate protocol for your sample type from the Protocol drop down list. The BIOFIRE JI Panel has a single protocol available in the drop-down list.
7. Enter operator username and password, then select Next.

***NOTE:** The font color of the username is red until the username is recognized by the software.*

8. Review the entered run information on the screen. If correct, select Start Run. Once the run has started the screen displays a list of the steps being performed by the module and the number of minutes remaining in the run.

***NOTE:** The bead-beater apparatus can be heard as a high-pitched noise during the first minute of operation.*

9. At the end of the run, remove the partially ejected pouch, then immediately discard it in a biohazard waste container.
10. The run file is automatically saved in the BIOFIRE® Software database, and the test report can be viewed, printed, and/or saved as a PDF file.

ASSAY INTERPRETATION

When PCR2 is complete, the instrument performs a high-resolution DNA melting analysis on the PCR products and records the change in fluorescence signal generated in each well (for more information see appropriate BIOFIRE® System Operator's Manual). The BIOFIRE Software then performs several analyses and assigns a final assay result. The steps in the analyses are described below.

Analysis of melt curves. The BIOFIRE Software evaluates the DNA melt curve for each well of the PCR2 array to determine if a PCR product was present in that well. If the melt profile indicates the presence of a PCR product, then the analysis software calculates the melting temperature (Tm) of the curve and compares it against the expected Tm range for the assay. If the software determines that the Tm value falls inside the assay-specific Tm range, the melt curve is called positive. If the software determines that the melt curve is not in the appropriate Tm range, the melt curve is called negative.

Analysis of replicates. Once positive melt curves have been identified, the software evaluates the replicates for each assay to determine the assay result. For an assay to be called positive, two associated melt curves must be called positive, both Tm values must be similar. Assays that do not meet these criteria are called negative.

ORGANISM AND ANTIMICROBIAL RESISTANT GENE INTERPRETATION

Each positive and negative assay result is interpreted by the BIOFIRE Software to provide results for the identification of specific bacteria, yeast, and antimicrobial resistance (AMR) genes.

For most of the organism results reported by the BIOFIRE JI Panel, the result is qualitatively reported as Detected or Not Detected based on one assay. However, in some cases, determination of Detected and Not Detected results requires interpretation of more than one assay. Reporting of AMR genes with one or more applicable bacteria also requires interpretation based on more than one assay result, as discussed below.

***NOTE:** Polymicrobial specimens with four or more distinct organisms are possible but rare. If Detected results are reported for four or more organisms in a sample, a retest of the sample is recommended to confirm the polymicrobial result.*

GRAM POSITIVE BACTERIA		
Anaerococcus prevotii/vaginalis	*Finegoldia magna*	*Streptococcus* spp.
Clostridium perfringens	*Parvimonas micra*	*Streptococcus agalactiae*
Cutibacterium avidum/granulosum	*Peptoniphilus*	*Streptococcus pneumoniae*
Enterococcus faecalis	*Peptostreptococcus anaerobius*	*Streptococcus pyogenes*
Enterococcus faecium	*Staphylococcus aureus*	
	Staphylococcus lugdunensis	
GRAM NEGATIVE BACTERIA		
Bacteroides fragilis	*Kingella kingae*	*Proteus* spp.
Citrobacter	*Klebsiella aerogenes*	*Pseudomonas aeruginosa*
Enterobacter cloacae complex	*Klebsiella pneumoniae* group	*Salmonella* spp.
Escherichia coli	*Morganella morganii*	*Serratia marcescens*
Haemophilus influenzae	*Neisseria gonorrhoeae*	
YEAST		
Candida		
Candida albicans		

ANTIMICROBIAL RESISTANCE GENES			
CTX-M	KPC	NDM	*vanA/B*
IMP	*mecA/C* and MREJ (MRSA)	OXA-48-like	VIM

RESULT INTERPRETATION FOR GRAM-POSITIVE BACTERIA

The BIOFIRE JI Panel contains assays for the specific detection of several species of gram-positive anaerobic cocci (GPAC), and gram-positive anaerobic rod-shaped bacteria, the major *Enterococcus* species associated with joint infections *(Enterococcus faecium* and *Enterococcus faecalis)*, two clinically important *Staphylococci (S. aureus* and *S. lugdunensis)* and nearly all *Streptococcus* species, including specific identification of *S. agalactiae, S. pneumoniae,* and *S. pyogenes.*

Note that only a subset of *Peptoniphilus* species will be detected *(P. assacharolyticus, P. gorbachii, P. harei, P. indolicus, P. lacrimalis, and P. senegalensis)* but that nearly all species within the *Streptococcus* genus (*Streptococcus* spp.) are predicted to be detected by the panel (exceptions include *Streptococcus entericus, S. halitosis, S.hyovaginalis, S. minor,* and *S. pantholopis* and variant sequences identified *as S. equi, S. minor, S. oralis, S. sobrinus, S. suis,* and *S. uberis* that may be amplified less efficiently than others).

***NOTE:** Peptoniphilus reactivity testing also included isolates described as Peptoniphilus allenii and Peptoniphilus grossensis (both detected), though neither is currently listed as a validly published species name.*

Based on *in silico* analysis and empirical testing each of the assays for detection of gram-positive bacteria is specific for detection of the indicated species with the exception of cross-reactivity with some rare near-neighbor species of *Anaerococcus* (multiple species), *Clostridium (C. baratii, C. cadaveris, C. disporicum C. fallax,* and *C. grantii),* and species of the *S. aureus* complex *(S. argenteus* and *S. schweitzeri).*

Results for most gram-positive bacteria are reported as Detected or Not Detected based on one corresponding assay result. If the assay is positive the test result will be Detected, and if the assay is negative, the test result will be Not Detected. Detection of gram-positive bacteria that is based on interpretation of more than one assay is described below.

CUTIBACTERIUM AVIDUM/GRANULOSUM

The BIOFIRE JI Panel contains two assays (Cutibacterium1 and Cutibacterium2) for the detection of these two specific *Cutibacterium* species. A positive result for one or both assays will generate a *Cutibacterium avidum/granulosum* Detected test result. *Cutibacterium avidum/granulosum* will be reported as Not Detected when both assays are negative.

STAPHYLOCOCCUS AUREUS

The BIOFIRE JI Panel contains two assays (Saureus1 and Saureus2) for the detection of *Staphylococcus aureus.* A positive result for one or both assays will generate a *Staphylococcus aureus* Detected test result. *Staphylococcus aureus* will be reported as Not Detected when both assays are negative

STREPTOCOCCUS SPP.

The BIOFIRE JI Panel contains four assays for the detection of *Streptococcus* species. Species-specific assays are included for the detection of *Streptococcus pyogenes* (Spyogenes), *Streptococcus agalactiae* (Sagalactiae), and *Streptococcus pneumoniae* (Spneumoniae). The fourth assay is a genus level assay (Streptococcus) designed to react with most *Viridans* group and other *Streptococcus* species that are not specifically identified by one of the other assays on the panel. The software integrates the results of all four *Streptococcus* assays into a *Streptococcus* spp. result. If all four assays are negative, the test result will be *Streptococcus* spp. Not Detected. Alternatively, if any of the four assays are positive, the test result will be *Streptococcus* spp. Detected and results for each species-specific assay will also be reported independently.

Table 3. Assay and Results Interpretation for the *Streptococcus* spp., *Streptococcus agalactiae, Streptococcus pneumoniae,* and *Streptococcus pyogenes* Test Results

BIOFIRE JI PANEL RESULTS	*Streptococcus* Assay	*S. agalactiae* Assay	*S. pneumonia* Assay	*S. pyogenes* Assay	DESCRIPTION
Streptococcus spp. Not Detected *Streptococcus agalactiae* Not Detected *Streptococcus pneumoniae* Not Detected *Streptococcus pyogenes* Not Detected	**NEGATIVE**	**NEGATIVE**	**NEGATIVE**	**NEGATIVE**	No *Streptococcus* species detected in the sample
Streptococcus spp. Detected *Streptococcus agalactiae* Not Detected *Streptococcus pneumoniae* Not Detected *Streptococcus pyogenes* Not Detected	**POSITIVE**	**NEGATIVE**	**NEGATIVE**	**NEGATIVE**	One or more *Streptococcus* species detected in the sample (not *S. agalactiae, S. pneumoniae, or S. pyogenes)*
Streptococcus spp. Detected *Streptococcus agalactiae* Detected *Streptococcus pneumoniae* Not Detected *Streptococcus pyogenes* Not Detected	**ANY RESULT**	**POSITIVE**	**NEGATIVE**	**NEGATIVE**	*Streptococcus agalactiae* detected in the sample. Note: additional *Streptococcus* species (not *S. pneumoniae* or *S. pyogenes)* may also be in the sample
Streptococcus spp. Detected *Streptococcus agalactiae* Not Detected *Streptococcus pneumoniae* Detected *Streptococcus pyogenes* Not Detected	**ANY RESULT**	**NEGATIVE**	**POSITIVE**	**NEGATIVE**	*Streptococcus pneumoniae* detected in the sample Note: additional *Streptococcus* species (not *S. agalactiae* or *S. pyogenes)* may also be in the sample
Streptococcus spp. Detected *Streptococcus agalactiae* Not Detected *Streptococcus pneumoniae* Not Detected *Streptococcus pyogenes* Detected	**ANY RESULT**	**NEGATIVE**	**NEGATIVE**	**POSITIVE**	*Streptococcus pyogenes* detected in the sample Note: additional *Streptococcus* species (not *S. agalactiae* or *S. pneumoniae)* may also be in the sample

***NOTE:** Multiple Streptococcus species assays may be positive in a single sample. If this occurs, the test result for each species with a positive assay will be reported as Detected.*

RESULTS INTERPRETATION FOR GRAM-NEGATIVE BACTERIA

The BIOFIRE JI Panel contains assays for the specific detection of many gram-negative aerobic and anaerobic species associated with joint infections. Species are identified individually *(Bacteroides fragilis, Escherichia coli, Haemophilus influenzae, Kingella kingae, Klebsiella aerogenes, Morganella morganii, Neisseria gonorrhoeae, Pseudomonas aeruginosa, Serratia marcescens),* or as multi-species complex, group, or genus results (*Enterobacter cloacae* complex, *Klebsiella pneumoniae* group, *Citrobacter, Proteus* spp., and *Salmonella* spp.).

Each species, complex, group, or genus result is reported as Detected or Not Detected based on an individual corresponding assay result. If the assay is positive, the result will be Detected; if the assay is negative, the result will be Not Detected.

Note that only a subset of species within the *Citrobacter* genus are expected to be detected as *Citrobacter* by the panel, including *C. braakii, C. europaeus, C. freundii, C. koseri, C. murliniae, C. pasteurii, C. portucalensis, C. werkmanii, and C. youngae.*

Based on testing and *in silico* analysis, the assays for gram-negative bacteria are specific for detection of the indicated genus, complex, group, or species, with the exception of the cross-reactivities with closely related species described below.

- *Bacteroides xylanisolvens,* a commensal species that naturally resides in the human intestine, can be mis-identified as *Bacteroides fragilis* due to non-specific interaction with the Bfragilis assay.
- The *Enterobacter cloacae* complex (ECC) is comprised of multiple species that may all be identified as *E. cloacae* by phenotypic laboratory methods. The Ecloacae assay will detect species and subspecies within the complex and may also react with other genetically related species (e.g. *E. bugandensis* and *E. chengduensis)* that have been more recently identified and may not be consistently designated as species of the ECC.
- The *E. coli* assay cross-reacts with *Shigella* species *(S. boydii, S. dysenteriae, S. flexneri,* and *S. sonnei);* which are practically indistinguishable from *E. coli* by both phenotypic and genetic analyses but are not generally associated with JI. Cross-reactivity has also been observed with *Escherichia fergusonii,* a rare but emerging veterinary and human pathogen, and *Escherichia albertii* (only at high concentration), a species more typically associated with gastrointestinal infections.
- *Haemophilus aegyptius*, a species formerly described as a subgroup or biotype of *Haemophilus influenzae,* is difficult to differentiate from *H. influenzae* by most laboratory methods and will be detected as *Haemophilus influenzae* by the BIOFIRE JI Panel due to cross-reactivity.
- *Kingella negevensis,* a recently identified species linked to pediatric joint infections that is closely related to, and likely to be mis-identified by standard laboratory methods as, *K. kingae* will also be detected as *Kingella kingae* by the BIOFIRE JI Panel due to cross-reactivity.
- The *Proteus* assay can cross-react with an insect-associated species *(Cosenzaea myxofaciens)* that was formerly classified as *Proteus myxofaciens.*

RESULTS INTERPRETATION FOR ANTIMICROBIAL RESISTANCE (AMR) GENES

The BIOFIRE JI Panel contains assays for the specific detection of several genetic determinants of resistance to multiple classes of antibiotics found in select gram-positive bacteria *(mecA/C* and MREJ (MRSA) and *vanA/B)* or gram-negative bacteria (CTX-M, IMP, KPC, NDM, OXA-48-like, and VIM). Results for the AMR genes are not reported unless an applicable bacterium (Table 4) is also detected, therefore the results are based on multiple assays, as described below.

The results for each of the antimicrobial resistance genes will be listed as:

- Detected – when an applicable bacterium is detected AND the antimicrobial resistance gene assay(s) are positive.
- Not Detected – when an applicable bacterium is detected AND the antimicrobial resistance gene assay(s) are negative.
- N/A – when all applicable bacteria are Not Detected, regardless of the result for the antimicrobial resistance gene assay(s).

Table 4. Antimicrobial Resistance (AMR) Genes and Applicable Bacteria

BIOFIRE JI PANEL AMR GENE RESULT	*Enterococcus faecalis*	*Enterococcus faecium*	*Staphylococcus aureus*	*Staphylococcus lugdunensis*	*Citrobacter*	*Enterobacter cloacae* complex	*Escherichia coli*	*Klebsiella aerogenes*	*Klebsiella pneumoniae* group	*Morganella morganii*	*Proteus* spp.	*Pseudomonas aeruginosa*	*Salmonella* spp.	*Serratia marcescens*
vanA/B	x	x												
mecA/C and MREJ (MRSA)			x											
CTX-M					x	x	x	x	x	x	x	x	x	x
IMP					x	x	x	x	x	x	x	x	x	x
KPC					x	x	x	x	x	x	x	x	x	x
NDM					x	x	x	x	x	x	x	x	x	x
OXA-48-like					x	x	x	x	x	x	x		x	x
VIM					x	x	x	x	x	x	x	x	x	x

NOTE: *Antimicrobial resistance can occur via multiple mechanisms. A Not Detected result for a genetic marker of antimicrobial resistance does not indicate susceptibility to associated antimicrobial drugs or drug classes. A Detected result for a genetic marker of antimicrobial resistance cannot be definitively linked to the microorganism(s) detected. Culture is required to obtain isolates for antimicrobial susceptibility testing, and BIOFIRE JI Panel results should be used in conjunction with culture results for the determination of susceptibility or resistance.*

Overall, testing and analysis of available sequence data demonstrate that each AMR gene assay will detect the majority of AMR gene types. However, there are some types and variant sequences that may be amplified less efficiently or may not be detected (MREJ types xv, xviii, xix, and xx; CTX-M-74, CTX-M-75, CTX-M-113, and CTX-M-151; IMP-31, IMP-35, and IIMP-46; OXA-54, OXA-416, and several OXA-48-like types that lack carbapenemase activity; VIM-7, VIM-39, VIM-45, VIM-46, VIM-61, VIM-65, and VIM-67).

Most AMR gene assays are specific for detection of the indicated AMR genes; however, cross-reactivity may be observed between AMR gene assays and related AMR genes (CTX-M with related $_{bla}$OXY, $_{bla}$RAHN, $_{bla}$KLU genes or some ampC sequences and *vanA/B* with *vanM).*

Each AMR gene result is associated with a single corresponding AMR gene assay (with the exception of the *mecA/C* and MREJ [MRSA] result) and one or more assay(s) for the detection of applicable bacteria. Table 5 - Table 7 describe how to interpret results for AMR genes and applicable bacteria. Table 5 describes how to interpret the *mecA/C* and MREJ assays in conjunction with detection of *S. aureus* for the *mecA/C* and MREJ (MRSA) result, Table 6 describes how to interpret a *vanA/B* AMR gene result with corresponding detection of *enterococci,* and Table 7 gives an example of how to interpret the KPC AMR gene result with various corresponding gram-negative bacteria. All other AMR genes that are reported with gram negative bacteria follow the same interpretation rules as indicated for KPC, according to the applicable bacteria indicated in Table 4.

mecA/C and MREJ (MRSA)

The *mecA/C* and MREJ (MRSA) result is intended to aid in the identification of methicillin-resistant *Staphylococcus aureus* (MRSA). When the Saureus1 and/or Saureus2 assay(s) are positive, the *mecA/C* and MREJ (MRSA) result will be reported as Detected or Not Detected based on whether the *mecA/C* and MREJa assays are positive or negative, respectively. If both Saureus1 and Saureus2 are negative, the *mecA/C* and MREJ (MRSA) results will be reported as N/A.

Table 5. Possible *mecA/C* and MREJ (MRSA) Results with Different *S. aureus*, *mecA/C,* and MREJ Assay Combinations

BIOFIRE JI PANEL TEST RESULT		Saureus 1 assay	Saureus 2 assay	*mecA/C* assay	MREJa assay
Staphylococcus aureus	Not Detected	NEGATIVE	NEGATIVE	ANY RESULT	ANY RESULT
mecA/C and MREJ (MRSA)	N/A				
Staphylococcus aureus	Detected	POSITIVE	ANY RESULT	POSITIVE	POSITIVE
mecA/C and MREJ (MRSA)	Detected[a]				
Staphylococcus aureus	Detected	ANY RESULT	POSITIVE	POSITIVE	POSITIVE
mecA/C and MREJ (MRSA)	Detected[a]				
Staphylococcus aureus	Detected	POSITIVE	ANY RESULT	NEGATIVE	NEGATIVE
mecA/C and MREJ (MRSA)	Not Detected				
Staphylococcus aureus	Detected	ANY RESULT	POSITIVE	NEGATIVE	NEGATIVE
mecA/C and MREJ (MRSA)	Not Detected				
Staphylococcus aureus	Detected	POSITIVE	ANY RESULT	POSITIVE	NEGATIVE
mecA/C and MREJ (MRSA)	Not Detected				
Staphylococcus aureus	Detected	POSITIVE	ANY RESULT	NEGATIVE	POSITIVE
mecA/C and MREJ (MRSA)	Not Detected				
Staphylococcus aureus	Detected	ANY RESULT	POSITIVE	POSITIVE	NEGATIVE
mecA/C and MREJ (MRSA)	Not Detected				
Staphylococcus aureus	Detected	ANY RESULT	POSITIVE	NEGATIVE	POSITIVE
mecA/C and MREJ (MRSA)	Not Detected				

vanA/B

The *vanA/B* result is intended to aid in the identification of vancomycin-resistant enterococci (VRE). When either or both *Enterococcus faecium* or *Enterococcus faecalis* are detected, the *vanA/B* result will be reported as Detected or Not Detected based on whether the *vanA/B* assay is positive or negative, respectively. If both the Efaecium and Efaecalis assays are negative, the *vanA/B* results will be reported as N/A.

Table 6. Possible *vanA/B* Test Results with Different Efaecium, Efaecalis and *vanA/B* Assay Results

BIOFIRE JI PANEL TEST RESULT		Efaecium assay	Efaecalis assay	*vanA/B* assay
Enterococcus faecium *Enterococcus faecalis* *vanA/B*	Not Detected Not Detected N/A	**NEGATIVE**	**NEGATIVE**	**ANY RESULT**
Enterococcus faecium *Enterococcus faecalis* *vanA/B*	Detected Not Detected Not Detected	**POSITIVE**	**NEGATIVE**	**POSITIVE**
Enterococcus faecium *Enterococcus faecalis* *vanA/B*	Not Detected Detected Not Detected	**NEGATIVE**	**POSITIVE**	**POSITIVE**
Enterococcus faecium *Enterococcus faecalis* *vanA/B*	Detected Detected Not Detected	**POSITIVE**	**POSITIVE**	**NEGATIVE**
Enterococcus faecium *Enterococcus faecalis* *vanA/B*	Detected Not Detected Detected	**POSITIVE**	**NEGATIVE**	**POSITIVE**
Enterococcus faecium *Enterococcus faecalis* *vanA/B*	Not Detected Detected Detected	**NEGATIVE**	**POSITIVE**	**POSITIVE**
Enterococcus faecium *Enterococcus faecalis* *vanA/B*	Detected Detected Detected	**POSITIVE**	**POSITIVE**	**POSITIVE**

CTX-M, IMP, KPC, NDM, OXA-48-like, and VIM

Detection and reporting of AMR genes with select gram-negative bacteria is intended to aid in the identification of bacteria with resistance to various antibiotics. When one or more of the applicable bacteria are detected, the AMR gene result will be reported as Detected or Not Detected based on whether the AMR gene assay is positive or negative. If all the assays for applicable bacteria are negative, the AMR gene results will be reported as N/A. An example of various assay combinations and KPC reporting is provided in Table 7 and similar interpretation is applicable to the other AMR genes.

Table 7. Possible KPC Test Results with Different Combinations of KPC and Applicable Bacterial Assay Result

BIOFIRE JI PANEL TEST RESULT		Citrobacter assay	Ecloacae assay	Ecoli assay	Kaerogenes assay	Kpneumoniae assay	Mmorganii assay	Proteus assay	Paeruginosa assay	Salmonella assay	Smarcescens assay	KPC assay	DESCRIPTION
Citrobacter	Not Detected	NEG	NEG	NEG	NEG	NEG	NEG	NEG	NEG	NEG	NEG	ANY RESULT	No applicable bacteria detected in the sample KPC results not applicable
Enterobacter cloacae complex	Not Detected												
Escherichia coli	Not Detected												
Klebsiella aerogenes	Not Detected												
Klebsiella pneumoniae group	Not Detected												
Morganella morganii	Not Detected												
Proteus spp.	Not Detected												
Pseudomonas aeruginosa	Not Detected												
Salmonella spp.	Not Detected												
Serratia marcescens	Not Detected												
KPC	N/A												

BIOFIRE JI PANEL TEST RESULT		Citrobacter assay	Ecloacae assay	Ecoli assay	Kaerogenes assay	Kpneumoniae assay	Mmorganii assay	Proteus assay	Paeruginosa assay	Salmonella assay	Smarcescens assay	KPC assay	DESCRIPTION
Citrobacter	Detected	POS	POS	POS	POS	POS	POS	POS	POS	POS	POS	NEG	Multiple gram-negative bacteria detected in the sample AND KPC not detected
Enterobacter cloacae complex	Detected												
Escherichia coli	Detected												
Klebsiella aerogenes	Detected												
Klebsiella pneumoniae group	Detected												
Morganella morganii	Detected												
Proteus spp.	Detected												
Pseudomonas aeruginosa	Detected												
Salmonella spp.	Detected												
Serratia marcescens	Detected												
KPC	Not Detected												
Citrobacter	Not Detected	POS	NEG	NEG	NEG	NEG	NEG	NEG	NEG	NEG	NEG	POS	*Citrobacter* detected in the sample AND KPC detected
Enterobacter cloacae complex	Not Detected												
Escherichia coli	Not Detected												
Klebsiella aerogenes	Not Detected												
Klebsiella pneumoniae group	Not Detected												
Morganella morganii	Not Detected												
Proteus spp.	Not Detected												
Pseudomonas aeruginosa	Not Detected												
Salmonella spp.	Not Detected												
Serratia marcescens	Not Detected												
KPC	Detected												
Citrobacter	Not Detected	NEG	POS	NEG	NEG	NEG	NEG	NEG	NEG	NEG	NEG	POS	One or more species of the *Enterobacter cloacae* complex detected in the sample AND KPC detected
Enterobacter cloacae complex	Not Detected												
Escherichia coli	Not Detected												
Klebsiella aerogenes	Not Detected												
Klebsiella pneumoniae group	Not Detected												
Morganella morganii	Not Detected												
Proteus spp.	Not Detected												
Pseudomonas aeruginosa	Not Detected												
Salmonella spp.	Not Detected												
Serratia marcescens	Not Detected												
KPC	Detected												

BIOFIRE JI PANEL TEST RESULT		Citrobacter assay	Ecloacae assay	Ecoli assay	Kaerogenes assay	Kpneumoniae assay	Mmorganii assay	Proteus assay	Paeruginosa assay	Salmonella assay	Smarcescens assay	KPC assay	DESCRIPTION
Citrobacter	Not Detected	NEG	NEG	POS	NEG	NEG	NEG	NEG	NEG	NEG	NEG	POS	*Escherichia coli* detected in the sample AND KPC detected
Enterobacter cloacae complex	Not Detected												
Escherichia coli	Not Detected												
Klebsiella aerogenes	Not Detected												
Klebsiella pneumoniae group	Not Detected												
Morganella morganii	Not Detected												
Proteus spp.	Not Detected												
Pseudomonas aeruginosa	Not Detected												
Salmonella spp.	Not Detected												
Serratia marcescens	Not Detected												
KPC	Detected												
Citrobacter	Not Detected	NEG	NEG	NEG	POS	NEG	NEG	NEG	NEG	NEG	NEG	POS	*Klebsiella aerogenes* detected in the sample AND KPC detected
Enterobacter cloacae complex	Not Detected												
Escherichia coli	Not Detected												
Klebsiella aerogenes	Not Detected												
Klebsiella pneumoniae group	Not Detected												
Morganella morganii	Not Detected												
Proteus spp.	Not Detected												
Pseudomonas aeruginosa	Not Detected												
Salmonella spp.	Not Detected												
Serratia marcescens	Not Detected												
KPC	Detected												
Citrobacter	Not Detected	NEG	NEG	NEG	NEG	POS	NEG	NEG	NEG	NEG	NEG	POS	One or more species in the *Klebsiella pneumoniae* group detected in the sample AND KPC detected
Enterobacter cloacae complex	Not Detected												
Escherichia coli	Not Detected												
Klebsiella aerogenes	Not Detected												
Klebsiella pneumoniae group	Not Detected												
Morganella morganii	Not Detected												
Proteus spp.	Not Detected												
Pseudomonas aeruginosa	Not Detected												
Salmonella spp.	Not Detected												
Serratia marcescens	Not Detected												
KPC	Detected												

BIOFIRE JI PANEL TEST RESULT		Citrobacter assay	Ecloacae assay	Ecoli assay	*Kaerogenes* assay	Kpneumoniae assay	Mmorganii assay	Proteus assay	Paeruginosa assay	Salmonella assay	Smarcescens assay	KPC assay	DESCRIPTION
Citrobacter	Not Detected	NEG	NEG	NEG	NEG	NEG	POS	NEG	NEG	NEG	NEG	POS	*Morganella morganii* detected in the sample AND KPC detected
Enterobacter cloacae complex	Not Detected												
Escherichia coli	Not Detected												
Klebsiella aerogenes	Not Detected												
Klebsiella pneumoniae group	Not Detected												
Morganella morganii	Not Detected												
Proteus spp.	Not Detected												
Pseudomonas aeruginosa	Not Detected												
Salmonella spp.	Not Detected												
Serratia marcescens	Not Detected												
KPC	Detected												
Citrobacter	Not Detected	NEG	NEG	NEG	NEG	NEG	NEG	POS	NEG	NEG	NEG	POS	*Pseudomonas aeruginosa* detected in the sample AND KPC detected
Enterobacter cloacae complex	Not Detected												
Escherichia coli	Not Detected												
Klebsiella aerogenes	Not Detected												
Klebsiella pneumoniae group	Not Detected												
Morganella morganii	Not Detected												
Proteus spp.	Not Detected												
Pseudomonas aeruginosa	Not Detected												
Salmonella spp.	Not Detected												
Serratia marcescens	Not Detected												
KPC	Detected												
Citrobacter	Not Detected	NEG	NEG	NEG	NEG	NEG	NEG	NEG	POS	NEG	NEG	POS	One or more *Proteus* species detected in the sample AND KPC detected
Enterobacter cloacae complex	Not Detected												
Escherichia coli	Not Detected												
Klebsiella aerogenes	Not Detected												
Klebsiella pneumoniae group	Not Detected												
Morganella morganii	Not Detected												
Proteus spp.	Not Detected												
Pseudomonas aeruginosa	Not Detected												
Salmonella spp.	Not Detected												
Serratia marcescens	Not Detected												
KPC	Detected												

BIOFIRE JI PANEL TEST RESULT		Citrobacter assay	Ecloacae assay	Ecoli assay	Kaerogenes assay	Kpneumoniae assay	Mmorganii assay	Proteus assay	Paeruginosa assay	Salmonella assay	Smarcescens assay	KPC assay	DESCRIPTION
Citrobacter	Not Detected	NEG	NEG	NEG	NEG	NEG	NEG	NEG	NEG	POS	NEG	POS	One or more *Salmonella* species detected in the sample AND KPC detected
Enterobacter cloacae complex	Not Detected												
Escherichia coli	Not Detected												
Klebsiella aerogenes	Not Detected												
Klebsiella pneumoniae group	Not Detected												
Morganella morganii	Not Detected												
Proteus spp.	Not Detected												
Pseudomonas aeruginosa	Not Detected												
Salmonella spp.	Not Detected												
Serratia marcescens	Not Detected												
KPC	Detected												
Citrobacter	Not Detected	NEG	NEG	NEG	NEG	NEG	NEG	NEG	NEG	NEG	POS	POS	*Serratia marcescens* detected in the sample AND KPC detected
Enterobacter cloacae complex	Not Detected												
Escherichia coli	Not Detected												
Klebsiella aerogenes	Not Detected												
Klebsiella pneumoniae group	Not Detected												
Morganella morganii	Not Detected												
Proteus spp.	Not Detected												
Pseudomonas aeruginosa	Not Detected												
Salmonella spp.	Not Detected												
Serratia marcescens	Not Detected												
KPC	Detected												

RESULTS INTERPRETATION FOR YEAST

The BIOFIRE JI Panel pouch contains two assays for the detection of *Candida* species. One species-specific assay (Calbicans) is included for the detection of *Candida albicans.* The second assay (Candida) is designed to detect some of the most clinically relevant *Candida* species, including *C. albicans, C. dubliniensis, C. glabrata, C. krusei, C. parapsilosis, C. orthopsilosis, C. metapsilosis, and C. tropicalis.* Based on *in silico* analysis and empirical testing, each assay is specific with no known cross-reactivity.

The software integrates the results of the Candida and Calbicans assays into the Candida test result, while the result for the species-specific Calbicans assay will be reported independently. If either of the two assays are positive, the test results will be *Candida* Detected (and *Candida albicans* Detected or Not Detected) and if both assays are negative, the result will be *Candida* Not Detected and *Candida albicans* Not Detected, as shown in Table 8.

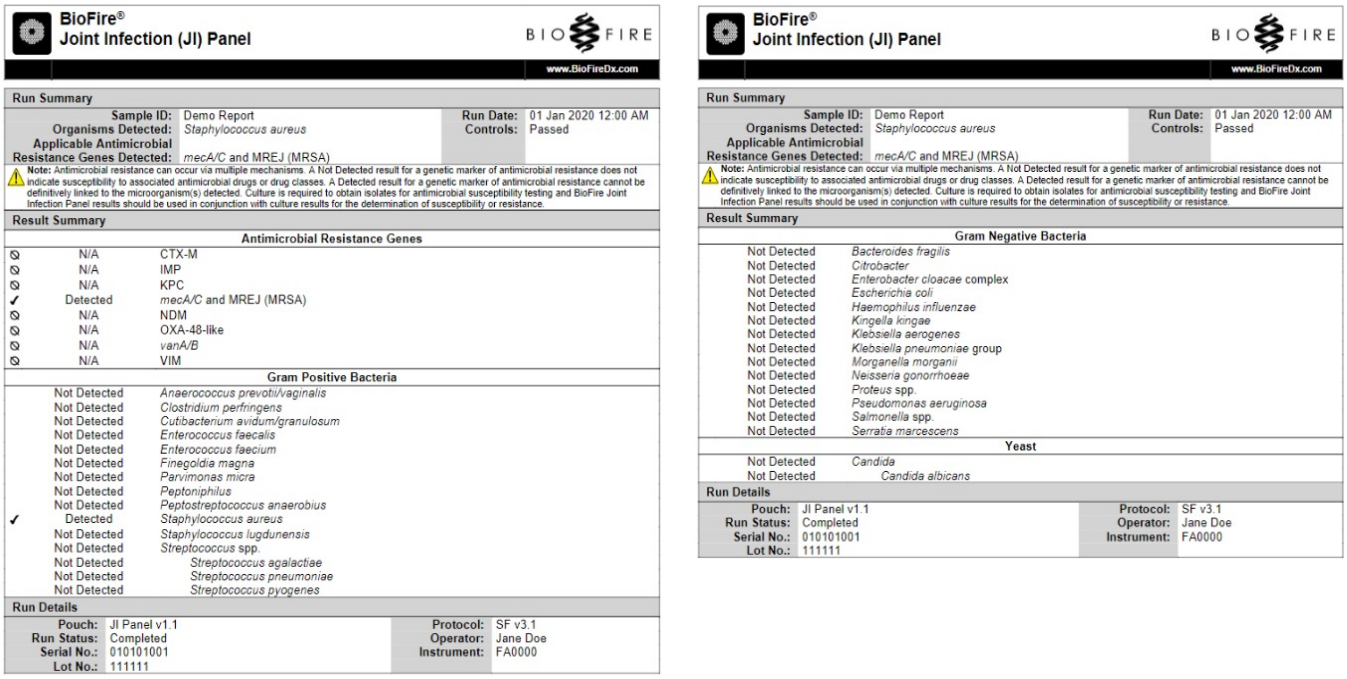
Table 8. Assay and Results Interpretation for the *Candida* and *Candida albicans* Test Results

BIOFIRE JI PANEL TEST RESULT		Candida assay	Calbicans assay
Candida *Candida albicans*	Not Detected Not Detected	NEGATIVE	NEGATIVE
Candida *Candida albicans*	Detected Detected	ANY RESULT	POSITIVE
Candida *Candida albicans*	Detected Not Detected	POSITIVE	NEGATIVE

NOTE: *According to recent taxonomic revisions, several Candida species are now classified in different genera, including Clavispora, Debaryomyces, Kluyveromyces, Meyerozyma, Nakaseomyces, Pichia, and Wickerhamomyces.*

STEP 6: BIOFIRE JI PANEL TEST REPORT

The two-page BIOFIRE JI Panel test report (Figure 1) is automatically displayed upon completion of a run and can be printed or saved as a PDF file. Each report contains a Run Summary, a Result Summary, and a Run Details section.



BioFire® Joint Infection (JI) Panel — www.BioFireDx.com

Run Summary

Sample ID:	Demo Report	Run Date:	01 Jan 2020 12:00 AM
Organisms Detected:	*Staphylococcus aureus*	Controls:	Passed
Applicable Antimicrobial Resistance Genes Detected:	*mecA/C* and MREJ (MRSA)		

⚠ **Note:** Antimicrobial resistance can occur via multiple mechanisms. A Not Detected result for a genetic marker of antimicrobial resistance does not indicate susceptibility to associated antimicrobial drugs or drug classes. A Detected result for a genetic marker of antimicrobial resistance cannot be definitively linked to the microorganism(s) detected. Culture is required to obtain isolates for antimicrobial susceptibility testing and BioFire Joint Infection Panel results should be used in conjunction with culture results for the determination of susceptibility or resistance.

Result Summary

Antimicrobial Resistance Genes

⊘	N/A	CTX-M
⊘	N/A	IMP
⊘	N/A	KPC
✓	Detected	*mecA/C* and MREJ (MRSA)
⊘	N/A	NDM
⊘	N/A	OXA-48-like
⊘	N/A	*vanA/B*
⊘	N/A	VIM

Gram Positive Bacteria

	Not Detected	*Anaerococcus prevotii/vaginalis*
	Not Detected	*Clostridium perfringens*
	Not Detected	*Cutibacterium avidum/granulosum*
	Not Detected	*Enterococcus faecalis*
	Not Detected	*Enterococcus faecium*
	Not Detected	*Finegoldia magna*
	Not Detected	*Parvimonas micra*
	Not Detected	*Peptoniphilus*
	Not Detected	*Peptostreptococcus anaerobius*
✓	Detected	*Staphylococcus aureus*
	Not Detected	*Staphylococcus lugdunensis*
	Not Detected	*Streptococcus* spp.
	Not Detected	*Streptococcus agalactiae*
	Not Detected	*Streptococcus pneumoniae*
	Not Detected	*Streptococcus pyogenes*

Run Details

Pouch:	JI Panel v1.1	Protocol:	SF v3.1
Run Status:	Completed	Operator:	Jane Doe
Serial No.:	010101001	Instrument:	FA0000
Lot No.:	111111		

BioFire® Joint Infection (JI) Panel — www.BioFireDx.com

Run Summary

Sample ID:	Demo Report	Run Date:	01 Jan 2020 12:00 AM
Organisms Detected:	*Staphylococcus aureus*	Controls:	Passed
Applicable Antimicrobial Resistance Genes Detected:	*mecA/C* and MREJ (MRSA)		

⚠ **Note:** Antimicrobial resistance can occur via multiple mechanisms. A Not Detected result for a genetic marker of antimicrobial resistance does not indicate susceptibility to associated antimicrobial drugs or drug classes. A Detected result for a genetic marker of antimicrobial resistance cannot be definitively linked to the microorganism(s) detected. Culture is required to obtain isolates for antimicrobial susceptibility testing and BioFire Joint Infection Panel results should be used in conjunction with culture results for the determination of susceptibility or resistance.

Result Summary

Gram Negative Bacteria

Not Detected	*Bacteroides fragilis*
Not Detected	*Citrobacter*
Not Detected	*Enterobacter cloacae* complex
Not Detected	*Escherichia coli*
Not Detected	*Haemophilus influenzae*
Not Detected	*Kingella kingae*
Not Detected	*Klebsiella aerogenes*
Not Detected	*Klebsiella pneumoniae* group
Not Detected	*Morganella morganii*
Not Detected	*Neisseria gonorrhoeae*
Not Detected	*Proteus* spp.
Not Detected	*Pseudomonas aeruginosa*
Not Detected	*Salmonella* spp.
Not Detected	*Serratia marcescens*

Yeast

Not Detected	*Candida*
Not Detected	*Candida albicans*

Run Details

Pouch:	JI Panel v1.1	Protocol:	SF v3.1
Run Status:	Completed	Operator:	Jane Doe
Serial No.:	010101001	Instrument:	FA0000
Lot No.:	111111		

Figure 1. BIOFIRE JI Panel Example Test Report (Page 1 – on left; Page 2 – on right)

RUN SUMMARY

The Run Summary section of the test report provides the Sample ID, time and date of the run, control results, and an overall summary of the test results. Any organism with a Detected result will be listed in the corresponding field of the summary. If all of the organism assays were negative, then 'None' will be displayed in the Organisms Detected field. If an organism was detected and an applicable antimicrobial resistance gene assay was positive, the applicable antimicrobial resistance gene will be listed as Detected in the corresponding field of the summary. If all of the applicable antimicrobial resistance gene assays were negative, then 'None' will be displayed in the Applicable Antimicrobial Resistance Genes Detected field. Controls are listed as Passed, Failed, or Invalid. Table 9 provides additional information for each of the possible control field results.

CONTROL RESULT	EXPLANATION	ACTION
PASSED	The run was successfully completed AND Both pouch controls were successful.	None Report the results provided on the test report.
FAILED	The run was successfully completed BUT At least one of the pouch controls (RNA Process Control and/or PCR2 Control) failed.	Repeat the test using a new pouch. If the error persists, contact Technical Support for further instruction.
INVALID	The controls are invalid because the run did not complete. (Typically this indicates a software or hardware error).	Note the Run Status field in the Run Details section of the report. Refer to the appropriate BIOFIRE® operator's manual or contact Technical Support for further instruction. Once the error is resolved, repeat the test or repeat the test using another module, if available

RESULT SUMMARY

The Result Summary section of the test report lists the result for each target tested by the panel. Possible results for each organism are Detected, Not Detected, or Invalid. Possible results for each antimicrobial resistance gene are Detected, Not Detected, N/A, or Invalid. Table 10 provides an explanation for each interpretation and any follow-up necessary to obtain a final result

CONTROL RESULT	EXPLANATION	ACTION
DETECTED[a]	The run was successfully completed AND The pouch controls were successful (Passed) AND The assay(s) for the organism (or antimicrobial resistance gene) were POSITIVE[a]	Report results.
NOT DETECTED	The run was successfully completed AND The pouch controls were successful (Passed) AND The assay(s) for the organism (or antimicrobial resistance gene) were NEGATIVE	Report results.

INVALID	The pouch controls were not successful (Failed) OR The run did not complete successfully (Run Status displayed as: Aborted, Incomplete, Instrument Error, or Software Error)	See Table 9 for instruction.
N/A Antimicrobial Resistance Genes only	The run was successfully completed AND The pouch controls were successful (Passed) AND The assay(s) for the organism(s) that are applicable to the antimicrobial resistance gene were NEGATIVE, so the results of the antimicrobial resistance gene are not applicable to the test results.	Report results.

[a] If four or more organisms are detected in a specimen, retesting is recommended to confirm the polymicrobial result

RUN DETAILS

The Run Details section provides additional information about the run, including pouch information (type, lot number, and serial number), Run Status (Completed, Incomplete, Aborted, Instrument Error, or Software Error), the protocol that was used to perform the test, the identity of the operator that performed the test, and the instrument used to perform the test.

CHANGE SUMMARY

It is possible to edit the Sample ID once a run has completed. If this information has been changed, an additional section called Change Summary will be added to the test report. This Change Summary section lists the field that was changed, the revised entry, the original entry, the operator that made the change, and the date that the change was made. Sample ID is the only field of the report that can be changed.

Change Summary				
Field	**Changed To**	**Changed From**	**Operator**	**Date**
[1]Sample ID	New Example Id	Old Example Id	Anonymous	06 Apr 2020

REFERENCES/RELATED DOCUMENTS

BIOFIRE® Joint Infection (JI) Instructions for Use, (BFR0000-8303-01), bioMérieux, Inc.