TABLE S1 Direct identification results by the MALDI BioTyper system and FilmArray BCID panel for 171 polymicrobial BSIs stratified by the causative species assortments

Species (no. with positive resistance determinant result) identified by the reference method, for *n* BSI episodes studied[a]	Species detected by the indicated method, for *n* BSI episodes (no. with positive resistance determinant result)[b]			No. of BSIs with the FilmArray BCID panel result interpreted as:	
	FilmArray BCID panel[c]	MALDI BioTyper system[c]		Complete ID	Partial ID
		Top match score of ≥1.8	Other species in top 10 matches list with scores of >1.7 to <1.8		
Gram-negative bacteria only					
A. baumannii + *K. pneumoniae* (1 *bla*$_{\text{KPC}}$), *n* = 1	*A. baumannii* + *K. pneumoniae*, *n* = 1 (1 *bla*$_{\text{KPC}}$)	*K. pneumoniae*, *n* = 1	None	1	0
A. baumannii + *P. mirabilis*, *n* = 1	*A. baumannii* + *Proteus* sp., *n* = 1	*P. mirabilis*, *n* = 1	None	1	0
A. baumannii + *P. stuartii*, *n* = 1	*A. baumannii*, *n* = 1[d]	*A. baumannii*, *n* = 1	None	0	1
A. baumannii + *S. marcescens*, *n* = 1	*A. baumannii* + *Serratia* sp., *n* = 1	*A. baumannii*, *n* = 1	*S. marcescens*, *n* = 1	1	0
C. freundii + *S. marcescens*, *n* = 1	*Serratia* sp., *n* = 1 (1 *mecA*)[e]	None	None	0	1
E. cloacae + *S. marcescens*, *n* = 1	*E. cloacae* complex + *Serratia* sp., *n* = 1	None	None	1	0
E. cloacae + *E. coli*, *n* = 1	*E. cloacae* complex + *E. coli*, *n* = 1	*E. cloacae*, *n* = 1	*E. coli*, *n* = 1	1	0
E. cloacae + *K. pneumoniae*, *n* = 1	*E. cloacae* complex + *K. pneumoniae*, *n* = 1	*K. pneumoniae*, *n* = 1	*E. cloacae*, *n* = 1	1	0
E. coli + *K. pneumoniae* (5 *bla*$_{\text{KPC}}$), *n* = 9	*E. coli* + *K. pneumoniae*, *n* = 9 (5 *bla*$_{\text{KPC}}$; 1 *mecA*)[e]	*E. coli*, *n* = 6; *K. pneumoniae*, *n* = 2; *E. coli* + *K. pneumoniae*, *n* = 1	*K. pneumoniae*, *n* = 2; *E. coli*, *n* = 6	9	0
E. coli + *M. morganii*, *n* = 1	*E. coli*, *n* = 1	None	None	0	1
E. coli + *P. mirabilis*, *n* = 1	*E. coli* + *Proteus* sp., *n* = 1	None	None	1	0
E. coli + *S. marcescens*, *n* = 1	*E. coli* + *Serratia* sp., *n* = 1	*E. coli*, *n* = 1	*S. marcescens*, *n* = 1	1	0
K. pneumoniae + *M. morganii*, *n* = 1	*K. pneumoniae*, *n* = 1	*K. pneumoniae*, *n* = 1	*M. morganii*, *n* = 1	0	1
K. pneumoniae + *P. mirabilis*, *n* = 2	*K. pneumoniae* + *Proteus* sp., *n* = 2	*K. pneumoniae*, *n* = 2	*P. mirabilis*, *n* = 2	2	0
K. pneumoniae (1 *bla*$_{\text{KPC}}$) + *P. aeruginosa*, *n* = 4	*K. pneumoniae* + *P. aeruginosa*, *n* = 4 (1 *bla*$_{\text{KPC}}$)	*K. pneumoniae*, *n* = 3	None	4	0
P. mirabilis + *P. aeruginosa*, *n* = 5	*Proteus* sp. + *P. aeruginosa*, *n* = 5	*P. mirabilis*, *n* = 2; *P. aeruginosa*, *n* = 2	None; *P. mirabilis*, *n* = 1	5	0
P. aeruginosa + *S. maltophilia*, *n* = 1	*P. aeruginosa*, *n* = 1	*P. aeruginosa*, *n* = 1	*S. maltophilia*	0	1
E. coli + *K. pneumoniae* (1 *bla*$_{\text{KPC}}$) + *P. mirabilis*, *n* = 1	*E. coli* + *K. pneumoniae* + *Proteus* sp., *n* = 1 (1 *bla*$_{\text{KPC}}$)	None		1	0
Total species = 69, *n* = 34	Total species = 64, *n* = 34	Total species = 28, *n* = 27	Not calculated	Total BSIs = 29	Total BSIs = 5
Gram-positive bacteria only					
E. faecalis + *B. cereus*, *n* = 1	Enterococcus, *n* = 1	*E. faecalis*, *n* = 1	None	0	1
E. faecalis + *E. gallinarum*, *n* = 1	Enterococcus, *n* = 1	None	*E. faecalis*, *n* = 1	1	0
E. faecalis + *St. aureus* (1 *mecA*), *n* = 1	Enterococcus + *St. aureus*, *n* = 1 (1 *mecA*)	*St. aureus*, *n* = 1	*E. faecalis*, *n* = 1	1	0
E. faecalis + *St. epidermidis* (6 *mecA*), *n* = 7	Enterococcus + CoNS, *n* = 7 (7 *mecA*)[e]	*St. epidermidis*, *n* = 2	*E. faecalis*, *n* = 1	7	0

E. faecalis + *St. haemolyticus* (2 *mecA*), *n* = 2	Enterococcus + CoNS, *n* = 1 (1 *mecA*); CoNS, *n* = 1 (1 *mecA*)	None	*E. faecalis*, *n* = 1	1	1
E. faecium + *St. capitis*, *n* = 1	Enterococcus, *n* = 1	None	None	0	1
E. faecium (1 *vanA*) + *St. epidermidis* (1 *mecA*), *n* = 1	Enterococcus + CoNS, *n* = 1 (1 *vanA*/*B*; 1 *mecA*)	*E. faecium*, *n* = 1	None	1	0
E. gallinarum + *St. epidermidis*, *n* = 1	Enterococcus + CoNS, *n* = 1	*E. gallinarum*, *n* = 1	None	1	0
St. aureus (3 *mecA*) + *St. epidermidis* (3 *mecA*), *n* = 5	*St. aureus* + CoNS, *n* = 5 (3 *mecA*)	None	*St. aureus*, *n* = 3	5	0
St. aureus (1 *mecA*) + *St. haemolyticus* (2 *mecA*), *n* = 2	*St. aureus* + CoNS, *n* = 2 (2 *mecA*)	None	*St. aureus*, *n* = 1	2	0
St. aureus + *St. hominis* (1 *mecA*), *n* = 2	*St. aureus* + CoNS, *n* = 2 (1 *mecA*)	None	*St. aureus*, *n* = 1	2	0
St. aureus + *Str. pneumoniae*, *n* = 1	*St. aureus* + *Str. pneumoniae*, *n* = 1	None	*St. aureus*, *n* = 1	1	0
Str. agalactiae + *St. epidermidis*, *n* = 1	*Str. agalactiae* + CoNS, *n* = 1	*Str. agalactiae*, *n* = 1	None	1	0
Str. mitis + *St. epidermidis* (1 *mecA*), *n* = 1	Streptococcus + CoNS, *n* = 1 (1 *mecA*)	*Str. mitis*, *n* = 1	None	1	0
Str. pneumoniae + *St. epidermidis*, *n* = 1	*Str. pneumoniae* + CoNS, *n* = 1	*Str. pneumoniae*, *n* = 1	None	1	0
Total species = 56, *n* = 28	Total species = 53, *n* = 28	Total species = 9, *n* = 9	Not calculated	Total BSIs = 25	Total BSIs = 3
Gram-negative/Gram-positive bacteria					
A. baumannii + *E. faecalis*, *n* = 1	*A. baumannii* + Enterococcus, *n* = 1	*A. baumannii*, *n* = 1	None	1	0
A. baumannii + *St. aureus* (1 *mecA*), *n* = 1	*A. baumannii* + *St. aureus*, *n* = 1 (1 *mecA*)	*St. aureus*, *n* = 1	*A. baumannii*, *n* = 1	1	0
A. baumannii + *St. epidermidis* (1 *mecA*), *n* = 2	*A. baumannii* + CoNS, *n* = 2 (1 *mecA*)	*A. baumannii*, *n* = 2	None	2	0
A. baumannii + *St. haemolyticus* (1 *mecA*), *n* = 1	*A. baumannii* + CoNS, *n* = 1 (1 *mecA*)	*A. baumannii*, *n* = 1	None	1	0
Camp. rectus + *Parvimonas micra*, *n* = 1	None	None	None	0	0
C. freundii + *E. faecium*, *n* = 1	Enteric + Enterococcus, *n* = 1	None	None	1	0
C. koseri + *St. hominis* (1 *mecA*), *n* = 1	Enteric, *n* = 1 (1 *mecA*)[f]	None	*C. koseri*, *n* = 1	0	1
E. aerogenes + *E. faecalis*, *n* = 1	Enteric + Enterococcus, *n* = 1	*E. aerogenes*, *n* = 1	None	1	0
E. cloacae + *E. faecalis*, *n* = 1	*E. cloacae* complex + Enterococcus, *n* = 1	*E. cloacae*, *n* = 1	*E. faecalis*, *n* = 1	1	0
E. coli + *B. cereus*, *n* = 1	*E. coli*, *n* = 1	*E. coli*, *n* = 1	None	0	1
E. coli + *Cl. perfringens*, *n* = 2	*E. coli*, *n* = 2	*E. coli*, *n* = 2	None	0	2
E. coli + *Cl. tertium*, *n* = 1	*E. coli*, *n* = 1[d]	*E. coli*, *n* = 1	None	0	1
E. coli + *E. faecalis*, *n* = 6	*E. coli* + Enterococcus, *n* = 6	*E. coli*, *n* = 3	*E. faecalis*, *n* = 1	6	0
E. coli + *E. faecium*, *n* = 4	*E. coli* + Enterococcus, *n* = 4	*E. coli*, *n* = 3	None	4	0
E. coli + *St. epidermidis* (2 *mecA*), *n* = 2	*E. coli* + CoNS, *n* = 2 (2 *mecA*)	*E. coli*, *n* = 1; *E. coli* + *St. epidermidis*, *n* = 1	None	2	0
E. coli + *Str. anginosus*, *n* = 1	*E. coli* + Streptococcus, *n* = 1	*E. coli*, *n* = 1	None	1	0
K. oxytoca + *Str. mitis*, *n* = 1	*K. oxytoca* + Streptococcus, *n* = 1	None	*K. oxytoca*, *n* = 1	1	0
K. pneumoniae (1 *bla*$_{\text{KPC}}$) + *E. faecalis*, *n* = 4	*K. pneumoniae* + Enterococcus, *n* = 4 (1 *bla*$_{\text{KPC}}$)	*K. pneumoniae*, *n* = 4	*E. faecalis*, *n* = 1	4	0
K. pneumoniae (1 *bla*$_{\text{KPC}}$) + *E. gallinarum*, *n* = 1	*K. pneumoniae* + Enterococcus, *n* = 1 (1 *bla*$_{\text{KPC}}$)	*K. pneumoniae*, *n* = 1	None	1	0
K. pneumoniae (1 *bla*$_{\text{KPC}}$) + *St. capitis* (1 *mecA*), *n* = 1	*K. pneumoniae*, *n* = 1 (1 *bla*$_{\text{KPC}}$; 1 *mecA*)[g]	*K. pneumoniae*, *n* = 1	None	0	1
K. pneumoniae + *St. epidermidis* (3 *mecA*), *n* = 3	*K. pneumoniae* + CoNS, *n* = 3 (3 *mecA*)	*K. pneumoniae*, *n* = 2; *K. pneumoniae* + *St. epidermidis*, *n* = 1	None	3	0
K. pneumoniae (1 *bla*$_{\text{KPC}}$) + *St. haemolyticus* (1 *mecA*), *n* = 1	*K. pneumoniae* + CoNS, *n* = 1 (1 *bla*$_{\text{KPC}}$; 1 *mecA*)	*K. pneumoniae*, *n* = 1	None	1	0
K. pneumoniae (2 *bla*$_{\text{KPC}}$) + *St. hominis* (2 *mecA*), *n* = 2	*K. pneumoniae* + CoNS, *n* = 2 (2 *bla*$_{\text{KPC}}$; 2 *mecA*)	*K. pneumoniae*, *n* = 2	None	2	0
M. morganii + *St. haemolyticus* (1 *mecA*), *n* = 1	CoNS, *n* = 1 (1 *mecA*)	None	None	0	1
P. mirabilis + *E. faecalis*, *n* = 2	*Proteus* sp. + Enterococcus, *n* = 2	None	None	2	0
P. mirabilis + *St. epidermidis* (2 *mecA*), *n* = 2	*Proteus* sp. + CoNS, *n* = 2 (2 *mecA*)	*P. mirabilis*, *n* = 2	None	2	0

P. mirabilis + *St. haemolyticus* (2 *mecA*), *n* = 2	*Proteus* sp. + CoNS, *n* = 2 (2 *mecA*)	*P. mirabilis*, *n* = 2	None	2	0
P. aeruginosa + *E. faecalis*, *n* = 3	*P. aeruginosa* + Enterococcus, *n* = 3	*P. aeruginosa*, *n* = 2	*E. faecalis*, *n* = 1	3	0
P. aeruginosa + *E. faecium* (1 *vanA*), *n* = 2	*P. aeruginosa* + Enterococcus, *n* = 2 (1 *vanA/B*)	None	*P. aeruginosa*, *n* = 1	2	0
P. aeruginosa + *Listeria monocytogenes*, *n* = 1	*P. aeruginosa* + *Listeria monocytogenes*, *n* = 1	None	None	1	0
P. aeruginosa + *St. aureus* (1 *mecA*), *n* = 1	*P. aeruginosa* + *St. aureus*, *n* = 1 (1 *mecA*)	*St. aureus*, *n* = 1	None	1	0
P. aeruginosa + St. *capitis* (1 *mecA*), *n* = 1	*P. aeruginosa* + CoNS, *n* = 1 (1 *mecA*)	None	None	1	0
P. aeruginosa + *St. epidermidis* (4 *mecA*), *n* = 5	*P. aeruginosa* + CoNS, *n* = 5 (5 *mecA*)[e]	*P. aeruginosa*, *n* = 5	None	5	0
P. aeruginosa + *St. haemolyticus* (3 *mecA*), *n* = 3	*P. aeruginosa* + CoNS, *n* = 3 (3 *mecA*)	*P. aeruginosa*, *n* = 1	None	3	0
P. aeruginosa + *St. hominis* (1 *mecA*), *n* = 2	*P. aeruginosa* + CoNS, *n* = 2 (1 *mecA*)	*P. aeruginosa*, *n* = 2	None	2	0
P. aeruginosa + *Str. mitis*, *n* = 1	*P. aeruginosa* + Streptococcus, *n* = 1	None	None	1	0
P. aeruginosa + *Str. sanguinis*, *n* = 1	*P. aeruginosa* + Streptococcus, *n* = 1	None	*P. aeruginosa*, *n* = 1	1	0
S. marcescens + *St. hominis* (1 *mecA*), *n* = 1	*Serratia* sp.+ CoNS, *n* = 1 (1 *mecA*)	*S. marcescens*, *n* = 1	None	1	0
S. maltophilia + *St. haemolyticus* (1 *mecA*), *n* = 1	CoNS, *n* = 1 (1 *mecA*)	None	*S. maltophilia*, *n* = 1	0	1
A. baumannii + *E. faecalis* + *St. epidermidis* (1 *mecA*), *n* = 1	*A. baumannii* + Enterococcus + CoNS, *n* = 1 (1 *mecA*)	None	*A. baumannii*, *n* = 1	1	0
E. coli + *E. faecalis* + *E. faecium*, *n* = 1	*E. coli* + Enterococcus, *n* = 1	*E. coli* + *E. faecium*, *n* = 1	None	1	0
E. coli + *E. faecalis* + *St. aureus* (1 *mecA*), *n* = 1	*E. coli* + Enterococcus + *St. aureus*, *n* = 1 (1 *mecA*)	None	*E. coli*, *n* = 1	1	0
E. coli + *K. pneumoniae* + *E. faecalis*, *n* = 1	*E. coli* + *K. pneumoniae* + Enterococcus, *n* = 1	*K. pneumoniae*, *n* = 1	*E. coli*, *n* = 1	1	0
E. coli + *E. cloacae* + *E. faecalis*, *n* = 1	*E. coli* + *E. cloacae* complex+ Enterococcus, *n* = 1	*E. coli*, *n* = 1	None	1	0
K. pneumoniae (1 *bla*$_{\text{KPC}}$) + *E. faecalis* + *St. hominis* (1 *mecA*), *n* = 1	*K. pneumoniae* (1 *bla*$_{\text{KPC}}$) + Enterococcus + CoNS, *n* = 1 (1 *mecA*)	*K. pneumoniae*, *n* = 1	None	1	0
P. mirabilis + *E. faecalis* + *St. aureus* (1 *mecA*), *n* = 1	*Proteus* sp. + Enterococcus + *St. aureus*, *n* = 1 (1 *mecA*)	*P. mirabilis*, *n* = 1	None	1	0
P. mirabilis + *P. aeruginosa* + *E. faecalis*, *n* = 2	*Proteus* sp. + *P. aeruginosa* + Enterococcus, *n* = 2	*E. faecalis*, *n* = 1	*P. mirabilis*, *n* = 1	2	0
E. cloacae + *E. coli* + *K. oxytoca* + *Str. gallolyticus*, *n* = 1	*E. cloacae* complex + *E. coli* + *K. oxytoca* + Streptococcus, *n* = 1	None	*E. coli*, *n* = 1	1	0
K. pneumoniae (1 *bla*$_{\text{KPC}}$) + *P. mirabilis* + *St. aureus* (1 *mecA*) + *E. faecalis*, *n* = 1	*K. pneumoniae* + *Proteus* sp. + *St. aureus* + Enterococcus, *n* = 1 (1 *bla*$_{\text{KPC}}$; 1 *mecA*)	*K. pneumoniae*, *n* = 1	None	1	0
Total species = 173, *n* = 80	Total species = 163, *n* = 79	Total species = 58, *n* = 55	Not calculated	Total BSIs = 71	Total BSIs = 8
Bacteria (Gram-negative or Gram-positive)/Yeasts					
A. baumannii + *Candida albicans*, *n* = 1	*A. baumannii* + *Candida albicans*, *n* = 1	None	*A. baumannii*, *n* = 1	1	0
E. coli + *Candida albicans*, *n* = 2	*E. coli* + *Candida albicans*, *n* = 2	*E. coli*, *n* = 1	*E. coli*, *n* = 1	2	0
K. pneumoniae (1 *bla*$_{\text{KPC}}$) + *Candida albicans*, *n* = 1	*K. pneumoniae* + *Candida albicans*, *n* = 1 (1 *bla*$_{\text{KPC}}$)	*K. pneumoniae*, *n* = 1	None	1	0
P. aeruginosa + *Candida glabrata*, *n* = 1	*P. aeruginosa* + *Candida glabrata*, *n* = 1	*P. aeruginosa*, *n* = 1	None	1	0
E. faecalis + *Candida albicans*, *n* = 1	Enterococcus + *Candida albicans*, *n* = 1	*E. faecalis*, *n* = 1	None	1	0
St. epidermidis (4 *mecA*) + *Candida albicans*, *n* = 7	CoNS + *Candida albicans*, *n* = 7 (4 *mecA*)	*St. epidermidis*, *n* = 2	None	7	0
St. epidermidis (5 *mecA*) + *Candida parapsilosis*, *n* = 6	CoNS + *Candida parapsilosis*, *n* = 6 (5 *mecA*)	*St. epidermidis*, *n* = 1	None	6	0
St. epidermidis + *Candida tropicalis*, *n* = 2	CoNS + *Candida tropicalis*, *n* = 2	*St. epidermidis*, *n* = 1	None	2	0
St. haemolyticus (2 *mecA*) + *Candida albicans*, *n* = 2	CoNS + *Candida albicans*, *n* = 2 (2 *mecA*)	None	None	2	0
St. haemolyticus (1 *mecA*) + *Candida glabrata*, *n* = 1	CoNS + *Candida glabrata*, *n* = 1 (1 *mecA*)	None	None	1	0

K. pneumoniae (1 *bla*$_{\text{KPC}}$) + *E. faecalis* + *Candida albicans*, *n* = 1	*K. pneumoniae* + Enterococcus + *Candida albicans*, *n* = 1 (1 *bla*$_{\text{KPC}}$)	*K. pneumoniae*, *n* = 1	None	1	0
S. maltophilia + *St. hominis* (1 *mecA*) + *Candida albicans*, *n* = 1	CoNS + *Candida albicans*, *n* = 1 (1 *mecA*)	None	*S. maltophilia*, *n* = 1	0	1
E. faecium + *St. haemolyticus* (1 *mecA*) + *Candida albicans*, *n* = 1	Enterococcus + CoNS + *Candida albicans*, *n* = 1 (1 *mecA*)	None	None	1	0
St. haemolyticus (1 *mecA*) + *Candida albicans* + *Candida krusei*, *n* = 1	CoNS + *Candida albicans* + *Candida krusei*, *n* = 1 (1 *mecA*)	None	None	1	0
A. baumannii + *E. faecalis* + *St. aureus* (1 *mecA*) + *Candida albicans*, *n* = 1	*A. baumannii* + Enterococcus + *St. aureus* + *Candida albicans*, *n* = 1 (1 *mecA*)	*St. aureus*, *n* = 1	None	1	0
Total species = 64, *n* = 29	Total species = 63, *n* = 29	Total species = 10, *n* = 10	Not calculated	Total BSIs = 28	Total BSIs = 1
Overall species = 362, *n* = 171	Overall species = 343, *n* = 170	Overall species = 105, *n* = 101	Not calculated	Overall BSIs = 153	Overall BSIs = 17

The MALDI BioTyper is one of the systems commercially available for matrix-assisted laser desorption ionization time of flight mass spectrometry (MALDI-TOF MS) analysis; BCID, blood culture identification; BSI, bloodstream infection; ID, identification; CoNS, coagulase-negative staphylococcus.

[a] Isolates were identified using a reference method which consisted of Gram-stain microscopic examination and subcultures on routine media, followed by MALDI-TOF MS analysis of bacterial or yeast colonies. Additionally, ID conventional phenotypical tests and/or sequencing analyses of the 16S rRNA and *rpoB* genes (for bacterial isolates) and the ITS1-5.8S-ITS2 rRNA gene regions (for yeast isolates) were performed whenever necessary.

[b] For some of the listed species, the FilmArray BCID panel provided results to the levels of genus or group of microorganisms. According to the manufacturer's product insert, isolates identified as Enterococcus were potentially belonging to *Enterococcus* species, such as *E. casseliflavus*, *E. durans*, *E. faecalis*, *E. faecium*, and *E. gallinarum*; isolates identified as CoNS were potentially belonging to *Staphylococcus* species, such as *S. capitis*, *S. caprae*, *S. cohnii*, *S. epidermidis*, *S. haemolyticus*, *S. hominis*, *S. kloosii*, *S. lugdunensis*, *S. microti*, *S. nepalensis*, *S. saccharolyticus*, *S. saprophyticus*, *S. simiae*, *S. warneri*, and *S. xylosus*; isolates identified as Enteric were potentially belonging to enteric species, such as *Cedeceae davisiae*, *Citrobacter* spp., *Cronobacter sakazakii*, *Enterobacter* spp., *Kluyvera ascorbata*, *Leclercia adecarboxylata*, *Raoultella* spp., *Salmonella* spp., *Shigella* spp., and *Yokenella regensburgei*; isolates identified as Streptococcus were potentially belonging to *Streptococcus* species, such as *S. anginosus*, *S. equinus*, *S. gallolyticus*, *S. gordonii*, *S. mitis*, *S. mutans*, *S. oralis*, *S. parasanguinis*, *S. salivarius*, *S. sanguinis*, and *S. uberis*.

[c] BC testing by FilmArray BCID panel was performed according to the diagnostic algorithm presented in this study, whereas BC testing by MALDI BioTyper system was performed only for comparison purpose, unless in those BCs that were initially classified as monomicrobial infections based on the Gram stain results. Only MALDI BioTyper system results that yielded score values of ≥1.8 were considered as valid IDs to the species level.

[d] Additionally, a CoNS organism was identified by the FilmArray BCID panel method.

[e] The *mecA* resistance determinant was falsely detected in 1 episode.

[f] The *mecA* resistance determinant was correctly detected, despite the absence of detection for the corresponding CoNS organism (*St. hominis*).

[g] The *mecA* resistance determinant was correctly detected, despite the absence of detection for the corresponding CoNS organism (*St. capitis*).