Original Research Paper

Evaluation of FISH for Blood Cultures under Diagnostic Real-Life Conditions

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Background: The study assessed a spectrum of previously published in-house fluorescence in-situ hybridization (FISH) probes in a combined approach regarding their diagnostic performance with incubated blood culture materials.

Methods: Within a two-year interval, positive blood culture materials were assessed with Gram and FISH staining. Previously described and new FISH probes were combined to panels for Gram-positive cocci in grape-like clusters and in chains, as well as for Gram-negative rod-shaped bacteria. Covered pathogens comprised *Staphylococcus* spp., such as *S. aureus*, *Micrococcus* spp., *Enterococcus* spp., including *E. faecium*, *E. faecalis*, and *E. gallinarum*, *Streptococcus* spp., like *S. pyogenes*, *S. agalactiae*, and *S. pneumoniae*, *Enterobacteriaceae*, such as *Escherichia coli*, *Klebsiella pneumoniae* and *Salmonella* spp., *Pseudomonas aeruginosa*, *Stenotrophomonas maltophilia*, and *Bacteroides* spp.

Results: A total of 955 blood culture materials were assessed with FISH. In 21 (2.2%) instances, FISH reaction led to non-interpretable results. With few exemptions, the tested FISH probes showed acceptable test characteristics even in the routine setting, with a sensitivity ranging from 28.6% (*Bacteroides* spp.) to 100% (6 probes) and a specificity of >95% in all instances.

Conclusion: If sophisticated rapid diagnostic methods like mass spectrometry from blood culture materials are not available, FISH provides an option for rapid differentiation for laboratories in resource-limited settings.

Keywords: fluorescence in-situ hybridization, blood culture, rapid diagnostics, molecular diagnostics, sepsis

Introduction

Fluorescence in-situ hybridization (FISH) is a diagnostic technique which allows the identification of pathogens on species or genus level by the binding of short fluorescence-tagged pathogen-specific DNA probes to ribosomal RNA of microorganisms. Subsequently, analysis is performed under a fluorescence microscope. Use of multi-well slides allows the application of whole panels of FISH probes with the same specimen in a parallel approach [1]. This procedure, the so-called multi-probe concept, allows the exclusion of auto-fluorescence and non-specific binding by assessing fluorescence intensity of probes, which should not lead to positive results. If positive signals are provided by different FISH probes leading to contradicting results, the overall result is "non-interpretable" but at least not "false positive" in this way.

Nearly 20 years ago, FISH was identified as an easy and rapid procedure to provide additional information in addition to Gram staining from positive blood culture materials. As early as at the beginning of the new millennium, small and in part poorly evaluated probe panels for the identification of blood culture pathogens were published [2], but insufficient standardization limited the implementation of the technique for the diagnostic routine setting [3].

Due to the experience that various previously published probes did not show acceptable performance characteristics in our hands, we started to develop new probes and to publish them individually [4–7]. Accordingly, some of the data presented here have partially been published in a pathogen-specific way. Now, the entire data-set is reevaluated in a concluding synopsis.

Due to the continuous evaluation process, the data are incoherent. This means that the probe sets were adjusted in the course of the study, if binding characteristics of individual probes were considered as inappropriate. In the here described assessment, only the results for the probes and screening algorithms, which were proven to be useful in our hands and could thus be used in the course of the whole evaluation, were described. Due to the stepwise, Gram-staining-dependent, species-specific evaluation approaches, the here described FISH assessments strongly overlap with previous reports [4–7]. However, the samples are not identical, and therefore, the results are not equal.

In the meantime, MALDI–TOF–MS (matrix assisted laser desorption ionization–time of flight–mass spectrometry) is the predominantly applied method for the early identification of pathogen species from incubated blood culture materials [8, 9]. Nevertheless, cost-efficient FISH could be an option for resource-limited settings, where expensive MALDI–TOF–MS equipment is not affordable, e.g., in non-industrialized tropical areas [1, 7]. However, this requires availability of a fluorescence microscope and of well-trained laboratory personnel, so manpower can compensate a lack of sophisticated technology.

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In the here described study, the diagnostic performance of predominantly published FISH probes for blood culture diagnostics was assessed during a two-year interval under real-life-like conditions in a diagnostic routine laboratory of a German university hospital.

Materials and Methods

Study Setting. During a two-year interval, positive blood cultures were assessed by FISH in addition to Gram staining, as soon as they were detected positive by automated blood culture. The FISH results were compared with the definite diagnostic results after cultural growth and biochemical identification via VITEK or API (bioMérieux, Marcy-l'Étoile, France). The study was performed at the Institute for Medical Microbiology of the University Hospital of Ulm.

Inclusion and Exclusion Criteria. Positive blood culture materials were included in the FISH assessment if they showed either Gram-positive cocci in grape-like clusters or Gram-positive cocci in doubles or chains or Gram-negative rod-shaped bacteria. Positive blood culture materials with other morphology of microorganisms in Gram-stain and negative blood culture materials were excluded. There was no exclusion of copy strains, and both aerobic and anaerobic cultures from the same patients were considered as distinct samples. However, materials were excluded from further assessment if they led to non-interpretable FISH results due to multiple positive FISH signals in spite of only one type of observed morphology in Gram-stain as it may occur due to autofluorescence phenomena or in the case of failed reactions of the internal control FISH. In such instances, FISH cannot be interpreted [1]. Applying these exclusion criteria, 21 samples had to be excluded as summarized in Table 1.

FISH Procedure. Depending on the results of Gram-staining of positively tested blood culture materials, different panels of FISH probes were applied, as shown in Table 2. Specific probes were labelled with the red fluorescence dye Cy3 (cyanine), while the pan-eubacterial probe, which was used as the internal reaction control, was labelled with the green fluorescence dye FAM (carboxyfluorescein). Competitor probes are non-labelled probes which are added to block non-specific probe binding to phylogenetically closely related organisms. For enterococci and *Salmonella* spp., 2 distinct FISH probes and, in the latter case, also 2 distinct probe-competitor-probe-combinations were available (Table 2).

FISH was performed as described [1]. In short, slides with blood culture material were fixed with 100% methanol and air-dried. If Gram-positive cocci were seen, permeabilization was performed for 5 min with a lysis buffer containing 1 mg/mL lysozyme and 2 μg/mL lysostaphine in 10 mM Tris HCl at 46 °C. No lysis was necessary for Gram-negative organisms. All probes were designed to work with 30% formamide in the hybridization buffer containing 0.9 M NaCl, 20 mM Tris HCl, and 0.01% sodium dodecyl sulphate (SDS). Hybridization time was 60 min, followed by washing for about 15 min with a washing buffer containing 0.102 M NaCl, 5 mM EDTA, 20 mM Tris HCl, and 0.01% SDS. Prior to assessment on a fluorescence microscope, counterstaining of the bacterial DNA was performed with 4′,6-diamidin-2-phenylindol (DAPI).

Table 1. Excluded strains due to non-interpretable results, i.e., multiple positive signals in the multi-probe approach or failed reactions in the internal control FISH

21 excluded strains	*Acinetobacter lwoffii* (*n* = 1) *Brevundimonas diminuta* (*n* = 1) *Comamonas acidovorans* (*n* = 1) *Enterococcus faecium* (*n* = 1) *Escherichia coli* (*n* = 1) *Flavimonas oryzihabitans* (*n* = 1) *Gemella haemolysans* (*n* = 2) *Koccuria* spp. (*n* = 1) *Micrococcus lylae* (*n* = 1) *Moraxella catarrhalis* (*n* = 2) *Moraxella osloensis* (*n* = 1) not further differentiated *Gemella* spp. (*n* = 1) not further differentiated Gram-negative rod-shaped bacteria (*n* = 2) not further differentiated *Pseudomonas* sp. (*n* = 1) *Pseudomonas aeruginosa* (*n* = 1) *Staphylococcus epidermidis* (*n* = 1) *Stomatococcus mucilaginosus* (*n* = 1) *Streptococcus mitis* (*n* = 1)

In Silico Evaluation of the FISH Probes. In silico evaluation of all tested FISH probes was performed using the software probecheck (http://131.130.66.200/cgi-bin/probecheck/content.pl?id=home). The results are shown in Supplementary material 1.

Statistical Assessment. Descriptive assessment was performed to calculate sensitivity, specificity, positive predictive value, and negative predictive value using the software Microsoft Excel®.

Ethical Standards. Not applicable because no patient data or primary sample materials were used.

Results

Assessed Blood Culture Materials and Identification Results by the Reference Methods. Altogether, a total of 733 pathogens from positive aerobic blood culture materials and 222 pathogens from positive anaerobic blood culture materials were included in the study during the two-year-assessment period. They comprised 33 materials with mixed bacterial cultures comprising 29 materials with double infections and 4 materials with triple infections.

Altogether, 955 Gram-positive cocci in grape-like clusters, doubles, or chains, as well as Gram-negative, rod-shaped bacteria were identified. As stated above, 21 out of 955 (2.2%) samples had to be excluded, applying the exclusion criteria. These excluded strains comprised *Acinetobacter lwoffii* (*n* = 1), *Brevundimonas diminuta* (*n* = 1), *Comamonas acidovorans* (*n* = 1), *Enterococcus faecium* (*n* = 1), *Escherichia coli* (*n* = 1), *Flavimonas oryzihabitans* (*n* = 1), *Gemella haemolysans* (*n* = 2), *Kocuria* spp. (*n* = 1), *Micrococcus lylae* (*n* = 1), *Moraxella catarrhalis* (*n* = 2), *M. osloensis* (*n* = 1), not further differentiated *Gemella* spp. (*n* = 1), not further differentiated Gram-negative rod-shaped bacteria (*n* = 2), not further differentiated *Pseudomonas* spp. (*n* = 1), *P. aeruginosa* (*n* = 1), *Staphylococcus epidermidis* (*n* = 1), *Stomatococcus mucilaginosus* (*n* = 1), and *Streptococcus mitis* (*n* = 1). The remaining 934 pathogens that were included into further assessment comprised 534 Gram-positive cocci in grape-like clusters, i.e., *Staphylococcus aureus* (*n* = 84), *S. auricularis* (*n* = 1), *S. capitis* (*n* = 1), *S. caprae* (*n* = 1), *S. cohnii* (*n* = 1), *S. epidermidis* (*n* = 356), *S. haemolyticus* (*n* = 10), *S. hominis* (*n* = 9), *S. saccharolyticus* (*n* = 1), *S. simulans* (*n* = 3), *Micrococcus luteus* (*n* = 10), and not further differentiated coagulase negative staphylococci (*n* = 57). Further, 148 Gram-positive cocci in doubles or chains were observed, comprising *Enterococcus faecalis* (*n* = 38), *E. faecium* (*n* = 41), *E. gallinarum* (*n* = 3), *Lactococcus lactis* (*n* = 3), not further differentiated alpha-hemolytic *Streptococcus* spp. (n = 2), *S. agalactiae* (n = 5), *S. anginosus* (*n* = 6), *S. dysgalactiae* (*n* = 3), *S. dysgalactiae* subsp. *equisimilis* (*n* = 1), *S. mitis* (*n* = 18), *S. oralis* (*n* = 4), *S. pneumoniae* (*n* = 16), *S. pyogenes* (*n* = 3), *S. salivarius* (*n* = 1), and *S. sanguis* (*n* = 4). Further, 252 Gram-negative rod-shaped bacteria were identified as *Acinetobacter baumannii* (*n* = 1), *A. lwoffii* (*n* = 2), *Bacteroides fragilis* (*n* = 4), *B. thetaiotaomicron* (*n* = 1), *Citrobacter freundii* (*n* = 4), *C. koseri* (*n* = 2), *Enterobacter*

Table 2. Applied FISH probe panels for blood culture diagnostics

Target organism	Probe sequence	Reference
Pan-eubacterial probe combined with all panels		
All bacteria	5‘-GCT-GCC-TCC-CGT-TAG-GAG-T-3‘	[27]
Panel for Gram-positive cocci in grape-like clusters		
Staphylococcus aureus	5’-GAA-GCA-AGC-TTC-TCG-TCC-G-3’	[3]
Staphylococcus spp.	5’-TCC-TCC-ATA-TCT-CTG-CGC-3’	[3]
Micrococcus spp.	5’-GTA-TCT-CTA-CGG-CGA-TCG-3’	This study
Panel for Gram-positive cocci in doubles or chains		
Enterococcus faecalis	5’-GAA-AGC-GCC-TTT-CAC-TCT-TAT-GC-3’	[4]
Enterococcus faecium	5’-TTC-ACA-CAA-TCG-TAA-CAT-CCT-A-3’	[4]
Enterococcus gallinarum	5’-ATT-CAC-AAC-TGT-GTA-ACA-TCC-TAT-3’	[4]
Enterococcus spp.	5’-CAC-CGC-GGG-TCC-ATC-CAT-CA-3’ and 5’-CAG-TTC-TCT-GCG-TCT-ACC-TC-3’	[4]
Streptococcus agalactiae	5’-GTA-AAC-ACC-AAA-CMT-CAG-CG-3’	[28]
Streptococcus pneumoniae	5’-GTG-ATG-CAA-GTG-CAC-CTT-3’ in combination with the competitor probe 5’-GTG-ATG-CAA-TTG-CAC-CTT-3’	[3]
Streptococcus pyogenes	5’-CTA-ACA-TGC-GTT-AGT-CTC-TC-3’	This study
Streptococcus spp.	5’-GTT-AGC-CGT-CCC-TTT-CTG-G-3’	[29]
Panel for Gram-negative rod-shaped bacteria		
Acinetobacter spp.	5’-TTA-GGC-CAG-ATG-GCT-GCC-3’	[6]
Bacteroides spp.	5’-CAT-CCT-TCA-CGC-TAC-TTG-GCT-GG-3’ in combination with the two competitor probes 5’-TCC-TTC-ACG-CGA-CTT-GGC-TGG-TT-3’ and 5’-TCC-TGC-ACG-CTA-CTT-GGC-TGG-T-3’	This study
Bacteroides spp. / *Prevotella* spp.	5’-CAT-CCT-TCA-CGC-TAC-TTG-GCT-GG-3’ in combination with the competitor probe 5’-TCC-TTC-ACG-CGA-CTT-GGC-TGG-TT-3’	This study
Enterobacteriaceae	5’-CCC-CCW-CTT-TGG-TCT-TGC-3’	[3]
Escherichia coli	5’-GCG-GGT-AAC-GTC-AAT-GAG-CAA-AGG-3’	This study
Klebsiella pneumoniae	5’-CCT-ACA-CAC-CAG-CGT-GCC-3’	[3]
Pseudomonas aeruginosa	5’-CCA-CTT-TCT-CCC-TCA-GGA-CG-3’	This study
Salmonella spp.	5’-TGC-GCT-TTT-GTG-TAC-GGG-GCT-3’ in combination with the competitor probe 5’-GTG-CAT-TTT-TGT-GTA-CGG-GGC-3’ and 5’-CTT-CAC-CTA-CGT-GTC-AGC-G-3’ in combination with the competitor probe 5’-TCA-CCT-ACA-TAT-CAG-CGT-GC-3’	[7]
Stenotrophomonas maltophilia	5’-GTC-GTC-CAG-TAT-CCA-CTG-C-3’	[26]

aerogenes (Klebsiella aerogenes) (*n* = 8), *E. amnigenus* (*n* = 1), *E. cloacae* (*n* = 12), *E. hormaechei* (*n* = 1), *Escherichia coli* (*n* = 126), *Klebsiella oxytoca* (*n* = 7), *K. pneumoniae* (*n* = 27), *Morganella morganii* (*n* = 1), not further differentiated *Acinetobacter* spp. (*n* = 6), not further differentiated *Bacteroides* spp. (*n* = 2), not further differentiated *Citrobacter* spp. (*n* = 1), not further differentiated *Pantoea* spp. (*n* = 1), *P. agglomerans* (*n* = 1), *Pseudomonas aeruginosa* (*n* = 30), *Salmonella* ser Bredeney (*n* = 1), *S.* ser Enteritidis (*n* = 3), *S.* ser Typhi (*n* = 2), *Serratia liquefaciens* (*n* = 1), *S. marcescens* (*n* = 4), and *Stenotrophomonas maltophilia* (*n* = 3) (Table 3).

In-silico Evaluation and Diagnostic Performance of the Assessed FISH Probes. Details of the in-silico evaluation of the assessed FISH probes are presented in the supplementary material (Supplementary material 1) and summarized in Table 4. As indicated in Table 4, potential cross-binding was considered as likely in the case of mismatches up to 2 bases. In-silico matching with the target organisms was 26.9–100% for the 0-mismatch range, 0–100% for the 1-base-mismatch range and 0–99.9% for the 2-bases-mismatch range (Table 4). Of note, even probes that showed good binding characteristics in the later in-vitro evaluation like the probe for *S. aureus* (Table 5) were associated with only moderate matching with deposited sequences in the in-silico evaluation (Table 4).

The in-vitro performance characteristics of the assessed FISH probes are detailed in Table 5. While the specificity of all described FISH approaches was better than 95%, sensitivity ranged from 28.6% for *Bacteroides* spp. to 100% for *Micrococcus* spp., *E. gallinarum*, *S. pyogenes*, *Acinetobacter* spp., *Klebsiella pneumoniae*, and *Salmonella* spp., respectively. Low percentage values, however, were influenced by disproportional high effects of single missed bindings in the case of species which were very rarely identified, like *S. agalactiae* (Table 5).

The details on lacking or incorrect binding of FISH probes are provided in Table 6. In detail, the *S. aureus* probe failed to bind to 3 *S. aureus* isolates. Of note, the *Staphylococcus* spp. probe was once erroneously used with Gram-positive cocci in chains and showed cross-binding with a *S. mitis* isolate. This erroneous use is not shown in Table 5. The probe altogether failed in the cases of 2 *S. aureus*, 3 *S. epidermidis*, and 4 not further identified *Staphylococcus* spp. The *E. faecalis* probe missed 2 *E. faecalis* isolates, and the *E. faecium* probe missed 8 *E. faecium* isolates. In contrast, the *E. gallinarum* probe showed cross-binding with 2 *E. faecium* isolates. The *Enterococcus* spp. probes failed to identify 3 *Enterococcus* spp. strains, i.e., 1 *E. faecalis* and 2 *E. faecium.* The *S. agalactiae* probe missed 1 *S. agalactiae* isolate, and the S. *pneumoniae* probe missed 2 *S. pneumoniae* isolates. The *S. pyogenes* probe showed cross-binding with 1 *S. anginosus* strain. The *Streptococcus* sp. probe missed 1 *S. mitis* but identified all 3 *Lactococcus lactis* isolates. Therefore, it has to be considered as a *Streptococcus* spp./*Lactococcus* spp. probe. The *Bacteroides* spp. probe missed 5 out of 7 *Bacteroides* spp., i.e., 3 *Bacteroides fragilis*, 1 *Bacteroides thetaiotaomicron,* and 1 not further identified *Bacteroides* sp. strain if used with both competitor probes against *Prevotella* spp. and *Porphyromonas* spp. If it was used as a *Bacteroides* spp./*Prevotella* spp. probe in conjunction with only the competitor probe against *Porphyromonas* spp., 3 out of 7 *Bacteroides* spp., i.e., 1 *Bacteroides fragilis* and 2 not further identified *Bacteroides* spp. were missed. The *Enterobacteriaceae* probe failed in 4 instances with 4 *E. coli.* The *Escherichia coli* probe missed 5 *E. coli* and showed cross-binding with 1 *Klebsiella oxytoca* isolate. The *Klebsiella pneumoniae* probe showed cross-binding with 1 *E. amnigenus* strain, 2 *Klebsiella oxytoca* strains, and 1 *Serratia marcescens*. The *P. aeruginosa* probe missed 3 *P. aeruginosa* isolates, and the *S. maltophilia* probe missed 1 out of 3 *S. maltophilia* in blood culture.

Discussion

The application of FISH for rapid blood culture diagnostics is not a new innovation. In parallel to MALDI–TOF–MS for rapid blood culture diagnostics, FISH was evaluated in various commercial and non-commercial approaches for this purpose.

Table 3. Distribution of species in samples which were included in the assessment

Groups	Species	Numbers of species
534 Gram-positive cocci in grape-like clusters	*Staphylococcus aureus*	84
	Staphylococcus auricularis	1
	Staphylococcus capitis	1
	Staphylococcus caprae	1
	Staphylococcus cohnii	1
	Staphylococcus epidermidis	356
	Staphylococcus haemolyticus	10
	Staphylococcus hominis	9
	Staphylococcus saccharolyticus	1
	Staphylococcus simulans	3
	Micrococcus luteus	10
	not further differentiated coagulase negative staphylococci	57
148 Gram-positive cocci in doubles or chains	*Enterococcus faecalis*	38
	Enterococcus faecium	41
	Enterococcus gallinarum	3
	Lactococcus lactis	3
	not further differentiated alpha-hemolytic *Streptococcus* spp.	2
	Streptococcus agalactiae	5
	Streptococcus anginosus	6
	Streptococcus dysgalactiae	3
	Streptococcus dysgalactiae subsp. *equisimilis*	1
	Streptococcus mitis	18
	Streptococcus oralis	4
	Streptococcus pneumoniae	16
	Streptococcus pyogenes	3
	Streptococcus salivarius	1
	Streptococcus sanguis	4
252 Gram-negative rod-shaped bacteria	*Acinetobacter baumannii*	1
	Acinetobacter lwoffii	2
	Bacteroides fragilis	4
	Bacteroides thetaiotaomicron	1
	Enterobacter aerogenes	8
	Enterobacter amnigenus	1
	Enterobacter cloacae	12
	Citrobacter freundii	4
	Enterobacter hormaechei	1
	Escherichia coli	126
	Citrobacter koseri	2
	Klebsiella pneumoniae	27
	Klebsiella oxytoca	7
	Morganella morganii	1
	not further differentiated *Acinetobacter* spp.	6
	not further differentiated *Bacteroides* spp.	2
	not further differentiated *Citrobacter* spp.	1
	not further differentiated *Pantoea* spp.	1
	Pantoea agglomerans	1
	Pseudomonas aeruginosa	30
	Salmonella ser Bredeney	1
	Salmonella ser Enteritidis	3
	Salmonella ser Typhi	2
	Serratia liquefaciens	1
	Serratia marcescens	4
	Stenotrophomonas maltophilia	3

Commercial applications comprise the use of patent-protected peptide-nucleic-acid (PNA)-FISH probes as developed and distributed by AdvanDx, Inc. (Vedbæk, Denmark) for the identification of pathogens in incubated blood culture materials. Respective PNA FISH approaches for the rapid diagnosis of blood culture pathogens comprised agents like *Acinetobacter* spp., *C. albicans*, *E. coli*, *K. pneumonia*, *P. aeruginosa*, and *S. aureus* [10–14].

Molecular beacon DNA probes for FISH-based blood culture diagnostics in a commercial hemo-FISH kit (miacom diagnostics, Düsseldorf, Germany) for both Gram-positive and Gram-negative pathogens have been introduced as well [15], next to various in-house approaches based on DNA FISH probes [5–7, 16–20].

For the presented study, in-silico evaluation of the probes was repeated with the updated database. The discrepancy, as exemplarily described for *S. aureus* in the Results section, between the observed in-vitro performance of the probes and the relatively poor in-silico matching is known from previous assessments. Even the current databases are not perfect, and older entries with wrong identifications are still included. Accordingly, in-vitro evaluations cannot be avoided.

This study assessed various published and few unpublished DNA FISH probes in a real-life-like observation at a German university hospital for their suitability for diagnostic FISH from blood culture materials. As detailed in the results, sensitivity and specificity in this real-life-like approach were slightly lower than suggested by previous evaluations under study conditions [16–0] including our own previous species-specific assessments [4–7]. Under the study conditions, cultured bacteria were directly tested by FISH in all contradictory cases, and in some cases, FISH was right in the end. In the here described assessment, such test repetition was not included, and the results were presented as obtained under routine-like conditions. Although phenotypical differentiation was used as reference standard for this assessment, it cannot be excluded that FISH results were nevertheless correct in some discrepant cases, as phenotypical methods can infrequently lead to incorrect results as well [21].

Anyway, very poor performance characteristics with less than 80–90% matching were only observed, like in the case of sensitivity of the *S. maltophilia* probe, if only very few samples were part of the assessment. Individual false reactions had a lot of impact under these circumstances, an undeniable limitation of the presented single-center assessment. As impressively shown for the example of the *Bacteroides* spp. probe, increases in specificity due to the adding of several competitor probes [1] can lead to reduction of sensitivity to unacceptably low values. Further, there have been various changes in the taxonomy of anaerobic bacteria in the recent years, and the applied biochemical identification procedures were shown to be associated with limited reliability as well [22].

The assessment of the usefulness of FISH probes requires the consideration of various factors. For example, FISH-based differentiation of staphylococci was confirmed to show good performance characteristics under routine-like conditions. Only a small probe panel was necessary for the discrimination of Gram-positive cocci in grape-like clusters, and FISH allowed a clearly visible microscopic distinction between coagulase-negative staphylococci and the clinically much more relevant species, *Staphylococcus aureus*. Successful commercial applications have been described [23].

For microorganisms with other morphology in Gram stain, like yeasts, which were not in the scope of this assessment but detailed elsewhere [24–25], Gram-positive cocci in doubles or chains, or even Gram-negative rod-shaped bacteria, considerably larger probe panels are required for differentiation. Especially for Gram-negative bacteria, FISH-based differentiation without resistance data is also less likely to allow clear-cut therapeutic decisions just based on the species identity. For anaerobic bacteria, FISH-based identification using the described approach currently makes little sense due to poor performance and debatable therapeutic consequences. Anyway, identification of anaerobic bacteria is difficult with conventional phenotypic methods as well [22], potentially resulting in many incorrect entries in the databases. Next to this, nomenclature of these species is still in progress. If this

Table 4. In-silico matching of the assessed probes with target sequences in the 0-mismatch range (0 MM), the 1-base-mismatch range (1 MM), and the 2-bases-mismatch range (2 MM) (–, not matches indicated)

Probe[a]	Target organism	0 MM	1 MM	2 MM
ACS 16S 729	*Acinetobacter* spp.	61.7% 3114/5046	57.6% 276/479	9.7% 45/463
Entero all (variant 1: "A" at the wobble position)	*Enterobacterales*	58.1% 1906/3282	47.0% 7110/15123	51.0% 521/1022
Entero all (variant 2: "T" at the wobble position)	*Enterobacterales*	46.5% 6526/14023	55.7% 2220/3987	54.0% 594/1101
ENF 16S 191	*Enterococcus faecalis*	47.5% 322/678	18.8% 3/16	0% 0/1
ENU 23S 140 Beimfohr	*Enterococcus faecium*	97.3% 36/37	–	25.0% 1/4
EGA 16S 141	*Enterococcus gallinarum*	66.7% 2/3	–	–
ENC 16S 221	*Enterococcus* spp.	52.4% 1403/2677	11.7% 27/230	0.3% 4/1260
ENC 176 23S kurz	*Enterococcus* spp.	86.2% 125/145	0% 0/59	0% 0/999
ESC 16S 468	*Escherichia coli*	28.3% 1983/7009	29.5% 165/559	7.9% 3/38
Klpn23S	*Klebsiella pneumoniae*	82.1% 55/67	0% 0/7	0% 0/2403
Psae Ulm 16S 182	*Pseudomonas aeruginosa*	17.0% 747/4406	0.7% 8/1088	0.1% 6/4926
Sal 23S 331	*Salmonella* spp.	95.1% 273/287	75.0% 3/4	0% 0/2236
Sal Yer 23S 1705 Komp	none, prevention of cross-reaction with organisms other than *Salmonella* spp.	100% 2198/2198	87.5% 239/273	29.9% 120/401
SalYer 23S 1705	*Salmonella* spp.	94.9% 281/296	12.5% 34/271	0% 0/2246
Komp Sal 23S 331	none, prevention of cross-reaction with organisms other than *Salmonella* spp.	100% 2181/2181	94.8% 165/174	99.0% 308/311
Stalle 16S	*Staphylococcus* spp.	38.7% 2154/5571	0.9% 51/5484	0.02% 17/99651
Stau16S Kempf	*Staphylococcus aureus*	68.1% 451/662	25.0% 14/56	0% 0/1052
Stemal Hogardt	*Stenotrophomonas maltophilila*	26.9% 77/286	14.3% 315/2207	6.7% 81/1211
Saga (variant 1: "A" at the wobble position)	*Streptococcus agalactiae*	94.1% 32/34	65.0% 134/206	–
Saga (variant 2: "C" at the wobble position)	*Streptococcus agalactiae*	65.2% 135/207	93.9% 31/33	–
Spneu	*Streptococcus pneumoniae*	97.4% 683/701	1.6% 20/1220	0.3% 7/2050
Spn Komp	none, prevention of cross-reaction with bacteria other than *Streptococcus pneumoniae*	98.6% 1197/1214	74.8% 2051/2741	99.9% 2141/2144
Strep Franks = Str 16S 492 Jansen	*Streptococcus* spp.	43.6% 3725/8553	3.1% 39/1239	0.03% 10/39762
Bact 16 S 389	*Bacteroides* spp.	2.2% 463/21395	0.3% 27/9376	0.2% 17/9436
Bact Komp	none, prevention of cross-reaction with *Porphyromonas* spp.	99.3% 3110/3132	98.4% 29461/29941	99.9% 16677/16691
Bact Komp 2	none, prevention of cross-reaction with *Prevotella* spp.	100% 10857/10858	97.9% 21873/22351	99.5% 4896/4921
Mic	*Micrococcus* spp.	78.4% 355/453	34.0% 34/100	4.5% 24/528
Spy1	*Streptococcus pyogenes*	72.2% 143/198	100% 1/1	0% 0/2

[a] Probe names as stated in the supplementary material 1.

process is finished and better databases are available, designing better FISH probes for anaerobic bacteria may be possible in the future.

While the newly introduced *Bacterioides* spp. probe showed limited reliability, considerably better results were observed for the new probes for *Micrococcus* spp., for *S. pyogenes,* and, to a letter extent, for the probe targeting *P. aeruginosa*. Accordingly, these new probes represent useful additions to diagnostic FISH probe panels. In our hands, the newly introduced *S. pyogenes* probe was more reliable than the previously published one [26] (data not shown), and it could be useful to evaluate it with other sample materials as well.

For several published FISH probes and probe-competitor-probe combinations, acceptable performance characteristics could be shown. Accordingly, FISH can provide rapid preliminary pathogen identification from positive blood culture materials in resource-limited settings, where sophisticated and expensive approaches like MALDI–TOF–MS are not available for financial reasons. If published DNA-probes without patent protection are used, the price of material costs for a FISH reaction is less than one dollar if basic laboratory equipment like an incubator and a fluorescence microscope is available. The application of the multi-probe concept as described above reduces the risk of false positive results, making this algorithm based on Gram-morphology highly useful for FISH-applications. As usual for molecular methods, however, in-house FISH probe panels have to be thoroughly evaluated for diagnostic purposes and cannot just be blindly taken from previous publications to be applied in the diagnostic routine setting.

Table 5. Performance characteristics of the assessed FISH probes

Target organism	Sensitivity (%; absolute numbers)	Specificity (%; absolute numbers)	Positive predictive value (%; absolute numbers)	Negative predicitive value (%; absolute numbers)
S. aureus	96.4, 81/84	100.0, 450/450	100.0, 81/81	99.3, 450/453
Staphylococcus spp.	98.3, 515/524	100.0, 10/10	100.0, 515/515	52.6, 10/19
Micrococcus spp.	100.0, 10/10	100.0, 524/524	100.0, 10/10	100.0, 524/524
E. faecalis	94.7, 36/38	100.0, 110/110	100.0, 36/36	98.2, 110/112
E. faecium	80.5, 33/41	100.0, 107/107	100.0, 33/33	93.0, 107/115
E. gallinarum	100.0, 3/3	98.6, 143/145	60.0, 3/5	100.0, 143/143
Enterococcus spp.	96.3, 79/82	100.0, 66/66	100.0, 79/79	95.7, 66/69
S. agalactiae	80.0, 4/5	100.0, 143/143	100.0, 4/4	99.3, 143/144
S. pneumoniae	87.5, 14/16	100.0, 132/132	100.0, 14/14	98.5, 132/134
S. pyogenes	100.0, 3/3	99.3, 144/145	75.0, 3/4	100.0, 144/144
Streptococcus spp.	98.4, 62/63	96.5, 82/85	95.4, 62/65	98.8, 82/83
Acinetobacter spp.	100.0, 9/9	100.0, 243/243	100.0, 9/9	100.0, 243/243
Bacteroides spp.	28.6, 2/7	100.0, 245/245	100.0, 2/2	98.0, 245/250
Bacteroides spp./ *Prevotella* spp.	57.1, 4/7	100.0, 245/245	100.0, 4/4	98.8, 245/248
Enterobacteriaceae	98.0, 199/203	100.0, 49/49	100.0, 199/199	92.5, 49/53
E. coli	96.0, 121/126	99.2, 125/126	99.2, 121/122	96.2, 125/130
Klebsiella pneumoniae	100.0, 27/27	98.2, 221/225	87.1, 27/31	100.0, 221/221
Pseudomonas aeruginosa	90.0, 27/30	100.0, 222/222	100.0, 27/27	98.7, 222/225
Salmonella spp.	100.0, 6/6	100.0, 246/246	100.0, 6/6	100.0, 246/246
Stenotrophomonas maltophilia	66.7, 2/3	100.0, 249/249	100.0, 2/2	99.6, 249/250

Table 6. Details of lacking or incorrect binding of specific FISH probes

Probe	Failed to identify	Cross bindings
S. aureus	3/84 *S. aureus*	
Staphylococcus spp.	2/84 *S. aureus* 3/356 *S. epidermidis* 4/57 not further differentiated coagulase negative staphylococci	1/18 *S. mitis*[a]
E. faecalis	2/38 E. *faecalis*	
E. faecium	8/41 *E. faecium*	
E. gallinarium		2/41 *E. faecium*
Enterococcus spp.	1/38 *E. faecalis* 2/41 *E. faecium*	
S. agalactiae	1/5 *S. agalactiae*	
S. pneumoniae	2/16 *S. pneumoniae*	
S. pyogenes		1/6 *S. anginosus*
Streptococcus spp.	1/18 *S. mitis*	3/3 *Lactococcus lactis*
Bacteroides sp. probe in conjunction with the competitor probes against *Prevotella* spp. and *Porphyromonas* spp.	3/4 *Bacteroides fragilis* 1/1 *Bacteroides thetaiotaomicron* 1/2 B*acteroides* spp.	
Bacteroides sp./*Prevotella* sp. probe in conjunction with only the competitor probe against *Porphyromonas* spp.	2/2 *Bacteroides* spp. 1/4 *Bacteroides fragilis*	
Enterobacteriaceae	4/126 *E. coli*	
Escherichia coli	5/126 *E. coli*	1/7 *Klebsiella oxytoca*
Klebsiella pneumoniae		1/1 *E. amnigenes* 2/7 *Klebsiella oxytoca* 1/4 *Serratia marcescens*
P. aeruginosa	3/30 *P. aeruginosa*	
S. maltophilia	1/3 *S. maltophilia*	

[a] Not mentioned in Table 5, because the probe was erroneously used with streptococci.

Conclusions

In summary, the described FISH panel is a suitable approach for rapid preliminary identification of pathogens from blood culture materials, which could be useful for resource-limited settings. Individual misidentifications may occur. The demonstrated performance under diagnostic routine-like conditions confirms the suitability of the approach for the routine setting, apart from study conditions. However, FISH probe panels have to be thoroughly adapted to individual diagnostic needs. To our experience, FISH for the rapid identification of *S. aureus* was particularly useful.

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Authors' Contributions

AR performed the assessments and was mainly responsible for the publication. SP planned and conducted the experiments. MR also conducted the experiments. HF supervised and supported AR's assessments. All authors jointly wrote and corrected the manuscript.

Conflict of Interest

Nothing to report.

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Supplementary material 1: In-silico evaluation of the used FISH probes between August 2017 and May 2018 using the software probeCheck (http://131.130.66.200/cgi-bin/probecheck/content.pl?id=home, last assessed August 2018). Only specific probes were evaluated (not the pan-eubacterial probe which was used as internal control).

Name of the probe: ACS 16S 729

Target organism: *Acinetobacter* spp.

Sequence of the probe: TTA GGC CAG ATG GCT GCC

Date of *in-silico* assessment: March 2018

Mismatch count	Ribosomal RNA sequence corresponding to the probe	Matching with known sequences (without italics)
0 mm	GGC AGC CAU CUG GCC UAA	Acinetobacter antiviralis (1), Acinetobacter baumannii (401), Acinetobacter baylyi (14), Acinetobacter beijerinckii (8), Acinetobacter bereziniae (4), Acinetobacter bouvetii (4), Acinetobacter brisouii (1), Acinetobacter calcoaceticus (144), Acinetobacter genomosp. (5), Acinetobacter gerneri (2), Acinetobacter guillouiae (8), Acinetobacter gyllenbergii (3), Acinetobacter haemolyticus (13), Acinetobacter indicus (1), Acinetobacter johnsonii (93), Acinetobacter junii (42), Acinetobacter kyonggiensis (1), Acinetobacter lwoffii (66), Acinetobacter marinus (1), Acinetobacter nosocomialis (7), Acinetobacter oleivorans (7), Acinetobacter parvus (4), Acinetobacter pittii (17), Acinetobacter psychrotolerans (1), Acinetobacter radioresistens (40), Acinetobacter rhizosphaerae (5), Acinetobacter schindleri (12), Acinetobacter seohaensis (2), Acinetobacter septicus (5), Acinetobacter soli (8), Acinetobacter sp. (974), Acinetobacter tandoii (2), Acinetobacter tjernbergiae (4), Acinetobacter towneri (4), Acinetobacter ursingii (5), Acinetobacter venetianus (11), Aeromonas caviae (1), Alvinella pompejana symbiont (1), ant fungus garden metagenome (1), Arcobacter sp. (2), Arctic sea ice bacterium (1), Arthrobacter sp. (1), bacterium (48), Caenorhabditis remanei (1), Clostridium sp. (3), endosymbiont (various) (3), Enterobacter sp. (1), gamma proteobacterium (26), glacial ice bacterium (4), Kartchner Caverns bacterium (1),

		marine metagenome (1), Moraxellaceae Bacterium (2), Prolinoborus fasciculus (1), proteobacterium (various) (4), Pseudomonadales bacterium (1), Pseudomonas aeruginosa (1), Pseudomonas sp. (1), rainbow trout intestinal bacterium (1), Staphylococcus pasteuri (1), Stenotrophomonas sp. (1), Theobroma cacao (1), uncultured Acinetobacter sp. (1044), uncultured anaerobic bacterium (1), uncultured bacterium (1581), uncultured Bacteroidetes bacterium (1), uncultured Burkholderia sp. (1), uncultured compost bacterium (2), uncultured gamma proteobacterium (59), uncultured marine bacterium (9), uncultured microorganism (2), uncultured Moraxella sp. (5), uncultured Moraxellaceae bacterium (4), uncultured organism (123), uncultured prokaryote (5), uncultured proteobacterium (6), uncultured rumen bacterium (1), uncultured soil bacterium (6), unidentified (4), Vestimentiferan symbiont (1)
	NGC AGC CAU CUG GCC UAA	Acinetobacter baumannii (7), Acinetobacter junii (1), Acinetobacter radioresistens (8), Acinetobacter sp. (1), uncultured Acinetobacter sp. (6), uncultured bacterium (3)
	G**N**C AGC CAU CUG GCC UAA	Acinetobacter baumannii (1), uncultured Acinetobacter sp. (1)
	GGC A**N**C CAU CUG GCC UAA	Acinetobacter sp. (1), uncultured Acinetobacter sp. (1)
	GGC AGC CAU **N**UG GCC UAA	Acinetobacter sp. (1), uncultured Acinetobacter sp. (4)
	GGC AGC CAU CUG G**N**C UAA	Acinetobacter johnsonii (1)
	GGC AGC CAU CUG GC**N** UAA	Acinetobacter baumannii (8), Acinetobacter radioresistens (1), Acinetobacter sp. (1), uncultured Acinetobacter sp. (72), uncultured bacterium (2)
	GGC AGC CAU CUG GCC U**N**A	uncultured bacterium (1)
	GGC AGC CAU CUG GCC UA**N**	uncultured Acinetobacter sp. (1)
	NGC A**N**C CAU CUG GCC UAA	uncultured Acinetobacter sp. (2)
	NGC AGC CAU CUG **N**CC UAA	uncultured Acinetobacter sp. (1)
	NGC AGC CAU CUG G**N**C UAA	uncultured Acinetobacter sp. (1)
	NGC AGC CAU CUG GC**N** UAA	Acinetobacter baumannii (2), uncultured Acinetobacter sp. (7)
	G**N**C AGC CAU CUG GC**N** UAA	uncultured Acinetobacter sp. (7)
	GG**N** A**N**C CAU CUG GCC UAA	uncultured Acinetobacter sp. (1)
	GGC **NN**C CAU CUG GCC UAA	uncultured Acinetobacter sp. (1)
	GGC A**N**C CAU CUG **N**CC UAA	Acinetobacter sp. (1)
	GGC A**N**C CAU CUG GC**N** UAA	uncultured Acinetobacter sp. (1)
	GGC AGC C**N**U CUG G**N**C UAA	uncultured bacterium (1)
	GGC AGC C**N**U CUG GC**N** UAA	uncultured bacterium (1)
	GGC AGC CAU **N**UG GC**N** UAA	uncultured Acinetobacter sp. (1)

	GGC AGC CAU CUG **N**C**N** UAA	uncultured Acinetobacter sp. (1)
	GGC AGC CAU CUG G**N**C UA**N**	uncultured Acinetobacter sp. (1)
	GGC AGC CAU CUG GC**N** UA**N**	uncultured Acinetobacter sp. (2)
	NG**N** A**N**C CAU CUG GCC UAA	Acinetobacter junii (1)
	NGC **N**GC C**N**U CUG GCC UAA	uncultured Acinetobacter sp. (1)
	NGC AGC **N**AU CUG GC**N** UAA	uncultured Acinetobacter sp. (1)
	NGC AGC C**N**U CUG GC**N** UAA	uncultured bacterium (1)
	NGC AGC CAU CUG **NN**C UAA	uncultured bacterium (1)
	G**N**C AGC CAU CUG GC**N** UA**N**	uncultured Acinetobacter sp. (1), uncultured bacterium (1)
	GGC AGC CAU C**NN** G**N**C UAA	uncultured bacterium (1)
	GGC AGC CAU CUG G**NN N**AA	uncultured Acinetobacter sp. (1)
1 mm	**A**GC AGC CAU CUG GCC UAA	Acinetobacter baumannii (15), Acinetobacter baylyi (1), Acinetobacter junii (1), Acinetobacter radioresistens (4), Acinetobacter sp. (2), uncultured Acinetobacter sp. (123), uncultured Bacillus sp. (1), uncultured bacterium (19), uncultured Moraxella (5)
	CGC AGC CAU CUG GCC UAA	Acinetobacter baumannii (1), Acinetobacter guillouiae (1), Acinetobacter schindleri (1), Acinetobacter sp. (1), Acinetobacter tandoii (1), uncultured Acinetobacter sp. (27), uncultured bacterium (1), uncultured organism (1)
	UGC AGC CAU CUG GCC UAA	Acinetobacter calcoaceticus (1), Acinetobacter sp. (1), uncultured Acinetobacter sp. (9), uncultured bacterium (1), uncultured organism (1)
	G**A**C AGC CAU CUG GCC UAA	bacterium enrichment culture clone (1)
	G**C**C AGC CAU CUG GCC UAA	uncultured bacterium (2)
	GG**U** AGC CAU CUG GCC UAA	uncultured bacterium (3)
	GGC **G**GC CAU CUG GCC UAA	uncultured Acinetobacter sp. (2), uncultured bacterium (4)
	GGC A**A**C CAU CUG GCC UAA	Acinetobacter haemolyticus (1), uncultured bacterium (1)
	GGC A**C**C CAU CUG GCC UAA	Acinetobacter sp. (2), uncultured Acinetobacter sp. (1), uncultured bacterium (1)
	GGC A**U**C CAU CUG GCC UAA	Acinetobacter sp. (1)
	GGC AG**A** CAU CUG GCC UAA	uncultured bacterium (2)
	GGC AG**U** CAU CUG GCC UAA	uncultured Acinetobacter sp. (1)
	GGC AGC **G**AU CUG GCC UAA	Acinetobacter sp. (1)
	GGC AGC C**C**U CUG GCC UAA	Acinetobacter baumannii (1), Acinetobacter calcoaceticus (1), uncultured Acinetobacter sp. (1), uncultured bacterium (2)
	GGC AGC C**G**U CUG GCC UAA	Acinetobacter radioresistens (1), uncultured Acinetobacter sp. (1)
	GGC AGC C**U**U CUG GCC UAA	Acinetobacter sp. (26), Acinetobacter xiamenensis (2), Agitococcus lubricus (1),

		Alkanindiges hongkongensis (3), Alkanindiges illinoisensis (1), Alkanindiges sp. (1), Antarctic bacterium (2), gamma proteobacterium (1), Moraxellaceae bacterium (1), Perlucidibaca piscinae (2), uncultured Acinetobacter sp. (1), uncultured Alkanindiges sp. (2), uncultured bacterium (56), uncultured gamma proteobacterium (45), uncultured Moraxellaceae bacterium (1), uncultured Pseudomonadales bacterium (1), uncultured sludge bacterium (1), unidentified (2)
	GGC AGC CA**C** CUG GCC UAA	uncultured Acinetobacter sp. (2), uncultured bacterium (2)
	GGC AGC CAU **A**UG GCC UAA	Acinetobacter sp. (1)
	GGC AGC CAU **U**UG GCC UAA	uncultured organism (1)
	GGC AGC CAU C**A**G GCC UAA	uncultured bacterium (1)
	GGC AGC CAU C**C**G GCC UAA	Acinetobacter baumannii (1), uncultured Acinetobacter sp. (2)
	GGC AGC CAU CU**A** GCC UAA	uncultured Acinetobacter sp. (1), uncultured bacterium (1)
	GGC AGC CAU CU**C** GCC UAA	Acinetobacter calcoaceticus (1)
	GGC AGC CAU CU**U** GCC UAA	uncultured bacterium (1)
	GGC AGC CAU CUG **A**CC UAA	uncultured bacterium (2)
	GGC AGC CAU CUG **U**CC UAA	uncultured Acinetobacter sp. (1), uncultured bacterium (4)
	GGC AGC CAU CUG G**G**C UAA	Moraxellaceae bacterium (1), uncultured bacterium (1)
	GGC AGC CAU CUG G**U**C UAA	uncultured bacterium (3)
	GGC AGC CAU CUG GC**A** UAA	Acinetobacter junii (1), uncultured Acinetobacter sp. (3)
	GGC AGC CAU CUG GC**G** UAA	Acinetobacter baumannii (2), Acinetobacter sp. (2), uncultured Acinetobacter sp. (1), uncultured bacterium (1)
	GGC AGC CAU CUG GC**U** UAA	uncultured Acinetobacter sp. (3), uncultured bacterium (1)
	GGC AGC CAU CUG GCC **A**AA	Acinetobacter baumannii (1), uncultured Acinetobacter sp. (2), uncultured bacterium (3)
	GGC AGC CAU CUG GCC **C**AA	uncultured Acinetobacter sp. (2), uncultured bacterium (1)
	GGC AGC CAU CUG GCC U**G**A	Acinetobacter baumannii (1), Arthrobacter sp. (1), uncultured bacterium (5)
	GGC AGC CAU CUG GCC U**U**A	Acinetobacter calcoaceticus (1), uncultured bacterium (2), uncultured organism (2)
	GGC AGC CAU CUG GCC UA**G**	Acinetobacter schindleri (1), uncultured Acinetobacter sp. (1)
	GGC AGC CAU CUG GCC UA**U**	Acinetobacter calcoaceticus (1), Acinetobacter sp. (1), uncultured bacterium (4)
	AGC AGC CAU CUG G**N**C UAA	uncultured Acinetobacter sp. (2)
	AGC AGC CAU CUG GC**N** UAA	uncultured Acinetobacter sp. (2)
	AGC AGC CAU CUG GCC U**N**A	uncultured Acinetobacter sp. (2)
	CGC AGC CAU CU**N** GCC UAA	uncultured Acinetobacter sp. (1)
	UGC AGC CAU CUG GCC U**N**A	uncultured Acinetobacter sp. (1)
	GGC AGC **NU**U CUG GCC UAA	uncultured bacterium (1)

	GGC AGC CAU CUG **A**C**N** UAA	uncultured Acinetobacter sp. (1)
	GGC A**N**C C**U**U CUG G**N**C UAA	uncultured Acinetobacter sp. (1)
	GGC AG**N** CAU CU**C** G**N**C UAA	uncultured Acinetobacter sp. (1)
	GGC AGC CAU CUG G**N**C **NU**A	uncultured Acinetobacter sp. (1)
2 mm	**A**GC **G**GC CAU CUG GCC UAA	Acinetobacter junii (1)
	AGC AGC CA**A** CUG GCC UAA	uncultured Acinetobacter sp. (1)
	AGC AGC CAU CUG G**G**C UAA	uncultured Acinetobacter sp. (2)
	AGC AGC CAU CUG GC**U** UAA	uncultured bacterium (1), uncultured organism (1)
	AGC AGC CAU CUG GCC UA**C**	uncultured gamma proteobacterium (1)
	AGC AGC CAU CUG GCC UA**U**	uncultured Acinetobacter sp. (18), uncultured bacterium (1)
	CGC AGC CAU **U**UG GCC UAA	uncultured Acinetobacter sp. (1)
	CGC AGC CAU CUG GCC UA**U**	uncultured Acinetobacter sp. (3)
	UUC AGC CAU CUG GCC UAA	uncultured bacterium (1)
	UG**G** AGC CAU CUG GCC UAA	uncultured Acinetobacter sp. (1)
	UGC AGC CAU CUG GC**G** UAA	uncultured Acinetobacter sp. (1)
	UGC AGC CAU CUG GCC UA**U**	uncultured Acinetobacter sp. (1)
	G**A**C AGC CAU CUG GC**A** UAA	uncultured bacterium (1)
	G**C**C AGC CAU CUG GCC U**U**A	uncultured bacterium (1)
	GG**A** **G**GC CAU CUG GCC UAA	uncultured Acinetobacter sp. (1)
	GGC **GA**C CAU CUG GCC UAA	uncultured Pseudomonadales bacterium (1)
	GGC **GC**C CAU CUG GCC UAA	Acinetobacter sp. (1), uncultured soil bacterium (1)
	GGC **G**GC **U**AU CUG GCC UAA	uncultured bacterium (3)
	GGC **G**GC CA**C** CUG GCC UAA	uncultured bacterium (16), uncultured gamma proteobacterium (3), uncultured soil bacterium (1)
	GGC **G**GC CAU CUG G**A**C UAA	uncultured bacterium (1)
	GGC **G**GC CAU CUG G**U**C UAA	uncultured gamma proteobacterium (1)
	GGC **G**GC CAU CUG GCC UA**G**	uncultured spirochete (1)
	GGC A**A**C **A**AU CUG GCC UAA	uncultured bacterium (1)
	GGC AG**G** CAU CUG **C**CC UAA	bacterium (1)
	GGC AG**U** CAU CUG GCC **C**AA	uncultured candidate division bacterium (7)
	GGC AGC **UC**U CUG GCC UAA	uncultured Armatimonadetes bacterium (1), uncultured bacterium (1)
	GGC AGC **UU**U CUG GCC UAA	marine metagenome (1), uncultured bacterium (10), uncultured gamma proteobacterium (1), uncultured marine bacterium (1)

	GGC AGC **U**A**C** CUG GCC UAA	uncultured bacterium (3)
	GGC AGC **U**AU **G**UG GCC UAA	uncultured bacterium (1)
	GGC AGC **U**AU CUG G**A**C UAA	uncultured Verrucomicrobia bacterium (1)
	GGC AGC **U**AU CUG G**G**C UAA	uncultured bacterium (1)
	GGC AGC **U**AU CUG GCC **A**AA	uncultured bacterium (1)
	GGC AGC C**CC** CUG GCC UAA	endosymbiont (1), Methylobacillus glycogenes (1), Methylobacillus sp. (8), Methylovorus glucosetrophus (4), Methylovorus mays (1), Methylovorus menthalis (1), uncultured Aminomonas sp. (1), uncultured bacterium (24), uncultured beta proteobacterium (5), uncultured marine bacterium (5), uncultured Methylobacillus sp. (1), uncultured soil bacterium (1), unidentified (1)
	GGC AGC C**C**U C**G**G GCC UAA	Acinetobacter sp. (1)
	GGC AGC C**C**U CUG G**G**C UAA	uncultured bacterium (4)
	GGC AGC C**C**U CUG GC**A** UAA	Psychrobacter sp. (2)
	GGC AGC C**UC** CUG GCC UAA	Aminomonas aminovorus (1), bacterium (1), Methylobacillus flagellates (4), Methylobacillus pratensis (1), Methylobacillus sp. (2), uncultured bacterium (8), uncultured Pseudomonas sp. (2)
	GGC AGC C**U**U **U**UG GCC UAA	Acinetobacter sp. (1)
	GGC AGC C**U**U CUG GC**A** UAA	Acinetobacter sp. (1), Antarctic bacterium (1), Arctic seawater bacterium (1), bacterium (1), marine psychrotrophic bacterium (1), Moraxella sp. (1), Pseudoalteromonas sp. (2), Psychrobacter aff. glacinola (1), Psychrobacter arcticus (6), Psychrobacter cibarius (5), Psychrobacter cryohalolentis (6), Psychrobacter fozii (2), Psychrobacter frigidicola (2), Psychrobacter glacialis (1), Psychrobacter glacincola (6), Psychrobacter immobilis (6), Psychrobacter luti (1), Psychrobacter namhaensis (1), Psychrobacter okhotskensis (1), Psychrobacter phenylpyruvicus (1), Psychrobacter sp. (98), Psychrobacter urativorans (1), uncultured bacterium (22), uncultured gamma proteobacterium (3), uncultured marine bacterium (1), uncultured organism (1), uncultured proteobacterium (1)
	GGC AGC C**U**U CUG G**G**C UAA	Calyptogena fossajaponica gill thioautotophic symbiont (1)
	GGC AGC C**U**U CUG GC**U** UAA	uncultured bacterium (6)
	GGC AGC C**U**U CUG GCC **A**AA	uncultured bacterium (14), uncultured proteobacterium (1), uncultured soil bacterium (1)
	GGC AGC C**U**U CUG GCC **C**AA	uncultured bacterium (1)
	GGC AGC C**U**U CUG GCC U**G**A	uncultured Moraxellaceae bacterium (1), uncultured soil bacterium (1)
	GGC AGC CA**C** C**C**G GCC UAA	uncultured bacterium (1)
	GGC AGC CA**C** CUG GC**A** UAA	agricultural soil bacterium (1), Aquicella siphonis (2), uncultured Aquicella sp. (3), uncultured bacterium (19), uncultured Coxiellaceae bacterium (2), uncultured gamma proteobacterium (9), uncultured soil bacterium (1), unidentified (12)

	GGC AGC CA**C** CUG GC**G** UAA	uncultured Acinetobacter sp. (1)
	GGC AGC CA**C** CUG GC**U** UAA	uncultured bacterium (5), uncultured proteobacterium (2)
	GGC AGC CA**C** CUG GCC **A**AA	uncultured bacterium (1)
	GGC AGC CA**C** CUG GCC **C**AA	uncultured bacterium (1)
	GGC AGC CA**C** CUG GCC U**C**A	uncultured gamma proteobacterium (1)
	GGC AGC CA**C** CUG GCC U**G**A	uncultured soil bacterium (1)
	GGC AGC CAU **U**UG **C**CC UAA	Acinetobacter junii (2)
	GGC AGC CAU **U**UG GCC **A**AA	uncultured bacterium (1)
	GGC AGC CAU CUG G**A**C **G**AA	uncultured bacterium (1)
	GGC AGC CAU CUG G**A**C U**C**A	uncultured bacterium (1)
	GGC AGC CAU CUG G**A**C U**U**A	uncultured Acinetobacter sp. (1)
	GGC AGC CAU CUG G**U**C UA**G**	uncultured Acinetobacter sp. (1)
	GGC AGC CAU CUG GCC **CG**A	Acinetobacter radioresistens (1)
	GGC AGC CAU CUG GCC **CU**A	Acinetobacter johnsonii (1), uncultured bacterium (9)
	GGC AGC CAU CUG GCC U**UU**	Acinetobacter sp. (1)
	AGC **C**GC CAU CUG GCC **N**AA	uncultured Acinetobacter sp. (1)
	AGC A**U**C CAU CUG G**N**C UAA	uncultured Acinetobacter sp. (1)
	UGC A**U**C CAU CUG GC**N** UAA	uncultured Acinetobacter sp. (1)
	GGC AGC **UN**U CUG G**A**C UAA	uncultured gamma proteobacterium (1)

Name of the probe: Entero all

Target organism: *Enterobacterales*

Sequence of the probe: CCC CCW CTT TGG TCT TGC

Date of *in-silico* assessment: March 2018

Variant assessed here: CCC CCA CTT TGG TCT TGC

Mismatch count	**Ribosomal RNA sequence corresponding to the probe**	**Matching with known sequences (without italics)**
0 mm	GCA AGA CCA AAG UGG GGG	Bacillus megaterium (1), Bacillus sp. (4), Bacillus subtilis (1), bacterium (50), BEV proteobacterium (1), Biostraticola tofi (1), Brenneria goodwinii (3), Brenneria rubrifaciens (7), Brenneria salicis (1), Burkholderia cepacia (1), Candidatus Regiella insecticola (22), Candidatus Rohrkolberia cinguli (1), Candidatus Stammerula sp. (1), Cenchrus americanus (3), Cimex lectularius endosymbiont (4), Citrobacter sp. (1), Cronobacter dublinensis (2), Cronobacter muytjensii (21), Cronobacter sakazakii (1), Cronobacter sp. (1), Dickeya dadantii (8), Dickeya dianthicola (1), Dickeya dieffenbachiae (1), Dickeya sp. (8), Edwardsiella hoshinae (2), Edwardsiella ictaluri (29), Edwardsiella sp. (7), Edwardsiella tarda (76), endophytic bacterium (9), endosymbiont (various) (4), Enterobacter aerogenes (51), Enterobacter cloacae (8), Enterobacter helveticus (4), Enterobacter hormaechei (1), Enterobacter ludwigii (4), Enterobacter pulveris (4), Enterobacter sp. (37), Enterobacteriaceae bacterium (24), enterobacterium (1), Erwinia chrysanthemi (30), Erwinia mallotivora (1), Erwinia papayae (1), Erwinia psidii (2), Erwinia sp. (18), Erwinia tracheiphila (1), Escherichia blattae (2), Escherichia sp. (2), gamma proteobacterium (6), Gibbsiella quercinecans (5), Glossina pallidipes S-endosymbiont (1), human gut metagenome (2), Klebsiella alba (2), Klebsiella granulomatis (4), Klebsiella milletis (1), Klebsiella oxytoca (12), Klebsiella pneumoniae (270), Klebsiella singaporensis (2), Klebsiella sp. (337), Klebsiella variicola (17), Kluyvera ascorbata (19), Kluyvera cryocrescens (8), Kluyvera georgiana (3), Kluyvera intermedia (15), Kluyvera sp. (13), Leclercia sp. (5), Lonsdalea quercina (19), Lysinibacillus fusiformis (1), Nannospalax galili (1), nitrogen-fixing bacterium (1), Obesumbacterium sp. (1), Pantoea agglomerans (13), Pantoea ananatis (1), Pantoea calida (1), Pantoea cypripedii (10), Pantoea dispersa (14), Pantoea gaviniae (1), Pantoea sp. (39), Pantoea stewartii (17), Pantoea wallisii (2), Pectobacterium carotovorum (1), Pectobacterium sp. (1), Photorhabdus luminescens (18), Photorhabdus sp. (14), Photorhabdus temperata (37), primary endosymbiont (various) (7), proteobacterium (1), Pseudomonas aeruginosa (1), Pseudomonas sp. (5), Rahnella aquatilis (18), Rahnella sp. (3), rainbow trout intestinal bacterium (1), Raoultella ornithinolytica (28),

		Raoultella planticola (18), Raoultella sp. (23), Raoultella terrigena (7), Regiella symbiont (5), Salmonella enterica (1), secondary endosymbiont (various) (5), secondary symbiont (various) (16), Serratia fonticola (1), Serratia liquefaciens (1), Serratia rubidaea (8), Serratia sp. (5), Serratia symbiotica (28), Shigella flexneri (1), Shimwellia blattae (2), Sitophilus zeamais (1), Sodalis glossinidius (6), Sodalis secondary endosymbiont (various) (2), Tatumella citrea (3), Tatumella morbirosei (3), Tatumella punctata (1), Tatumella terrea (3), Thorsellia anophelis (1), uncultured actinomycete (1), uncultured bacterium (1127), uncultured Citrobacter sp. (2), uncultured compost bacterium (1), uncultured Edwardsiella sp. (1), uncultured Enterobacter sp. (7), uncultured Enterobacteriaceae bacterium (19), uncultured Erwinia sp. (7), uncultured gamma proteobacterium (4), uncultured Klebsiella sp. (449), uncultured Kluyvera sp. (4), uncultured organism (23), uncultured Pantoea sp. (3), uncultured proteobacterium (4), uncultured Rahnella sp. (10), uncultured Raoultella sp. (10), uncultured rumen bacterium (1), uncultured Serratia sp. (1), uncultured soil bacterium (1), uncultured Xanthomonadaceae bacterium (1), uncultured Yersinia sp. (1), unidentified (10), Xenorhabdus poinarii (2), Yersinia sp. (1)
	NCA AGA CCA AAG UGG GGG	Raoultella terrigena (1)
	GC**N** AGA CCA AAG UGG GGG	Pantoea dispersa (1), Pantoea septica (2), Photorhabdus luminescens (1), Raoultella terrigena (2)
	GCA AGA **N**CA AAG UGG GGG	Yersinia kristensenii (1)
	GCA AGA CCA AAG **N**GG GGG	Klebsiella pneumoniae (1)
	GCA AGA CCA AAG UGG GG**N**	uncultured bacterium (1)
1 mm	**A**CA AGA CCA AAG UGG GGG	Enterobacteriaceae bacterium (1), uncultured bacterium (3), uncultured Klebsiella sp. (3)
	CCA AGA CCA AAG UGG GGG	Klebsiella pneumoniae (1)
	UCA AGA CCA AAG UGG GGG	Erwinia chrysanthemi (2)
	G**A**A AGA CCA AAG UGG GGG	Candidatus Baumannia cicadellinicola (1), Candidatus Ecksteinia adelgidicola (2), Candidatus Kleidoceria schneideri (6), Candidatus Regiella insecticola (1), secondary endosymbiont (various) (2), Serratia symbiotica (3), uncultured bacterium (5), uncultured organism (2), uncultured Rahnella sp. (1), uncultured Sodalis sp. (1)
	G**U**A AGA CCA AAG UGG GGG	Candidatus Baumannia cicadellinicola (1), Candidatus Moranella endobia (1), Candidatus Schneideria nysicola (11), Candidatus Stammerula sp. (5), Candidatus Stammerula tephritidis (14), Enterobacteriaceae bacterium (14), Klebsiella pneumoniae (1), Pantoea sp. (1), Planococcus citri gamma-proteobacterial endosymbiont (1), primary endosymbiont (1), secondary endosymbiont (various) (4), secondary symbiont (1), Serratia symbiotica (4), symbiont (11),

		uncultured bacterium (2), uncultured Pantoea sp. (5), uncultured proteobacterium (1), uncultured Sodalis sp. (1)
	GC**G** AGA CCA AAG UGG GGG	Bacteriophage (2), Candidatus Hamiltonella defensa (17), Enterobacteriaceae bacterium (1), Erwinia sp. (1), Hamiltonella symbiont (6), male-killer in Chilomenes sexmaculatus (1), Pantoea agglomerans (7), Pantoea dispersa (2), Pantoea sp. (2), Pantoea stewartii (1), Photorhabdus asymbiotica (16), Photorhabdus luminescens (70), Photorhabdus sp. (5), Photorhabdus temperata (1), secondary endosymbiont (7), secondary symbiont (10), uncultured bacterium (142), uncultured Enterobacteriaceae bacterium (1), uncultured Erwinia sp. (2), uncultured organism (1), uncultured Photorhabdus sp. (1)
	GC**U** AGA CCA AAG UGG GGG	Candidatus Baumannia cicadellinicola (2), Pantoea sp. (1)
	GCA **G**GA CCA AAG UGG GGG	Klebsiella pneumoniae (1), Raoultella ornithinolytica (1), uncultured bacterium (3), uncultured Pantoea sp. (1)
	GCA A**A**A CCA AAG UGG GGG	primary endosymbiont (1), secondary endosymbiont (1)
	GCA AG**G** CCA AAG UGG GGG	uncultured bacterium (3)
	GCA AGA **G**CA AAG UGG GGG	Aranicola sp. (9), bacterium (6), Brenneria nigrifluens (4), Brenneria sp. (7), Enterobacteriaceae bacterium (10), Erwinia persicina (5), Erwinia sp. (1), Erwinia toletana (9), Ewingella americana (4), Hafnia sp. (4), Klebsiella sp. (1), lobster gut bacterium (1), Margalefia venezuelensis (1), Nevskia ramosa (2), Pantoea oleae (3), Pantoea septica (1), Pantoea sp. (1), Rahnella aquatilis (10), Rahnella genomosp. (2), Rahnella sp. (36), Serratia grimesii (1), Tiedjeia arctica (1), uncultured Aeromonas sp. (1), uncultured bacterium (67), uncultured compost bacterium (1), uncultured Ewingella sp. (1), uncultured gamma proteobacterium (6), uncultured marine bacterium (1), uncultured Pantoea sp. (1), uncultured Rahnella sp. (7), uncultured Serratia sp. (7), uncultured Yersinia sp. (1), Yersinia aldovae (3), Yersinia aleksiciae (2), Yersinia enterocolitica (1), Yersinia frederiksenii (7), Yersinia intermedia (6), Yersinia kristensenii (15), Yersinia mollaretii (5), Yersinia pestis (156), Yersinia pseudotuberculosis (55), Yersinia rohdei (7), Yersinia ruckeri (21), Yersinia similis (5), Yersinia sp. (12)
	GCA AGA **U**CA AAG UGG GGG	uncultured bacterium (1)
	GCA AGA C**A**A AAG UGG GGG	Klebsiella pneumoniae (1)
	GCA AGA C**U**A AAG UGG GGG	Sodalis glossinidius (7), uncultured Klebsiella sp. (1)
	GCA AGA CC**G** AAG UGG GGG	Klebsiella pneumoniae (1), Klebsiella sp. (1)
	GCA AGA CCA **G**AG UGG GGG	Klebsiella sp. (2), uncultured bacterium (1), uncultured Klebsiella sp. (1)
	GCA AGA CCA A**G**G UGG GGG	Klebsiella sp. (2), Rahnella sp. (1)
	GCA AGA CCA A**U**G UGG GGG	uncultured bacterium (1)
	GCA AGA CCA AA**A** UGG GGG	Candidatus Baumannia cicadellinicola (1)
	GCA AGA CCA AAG **A**GG GGG	Acinetobacter radioresistens (1), Acinetobacter sp. (1), Ajellomyces capsulatus (1), Aranicola sp. (1),

		Bacillus subtilis (2), bacterium (129), Brenneria alni (1), Brenneria lupinicola (1), Brenneria nigrifluens (2), Brenneria rubrifaciens (1), Budvicia sp. (1), Buttiauxella agrestis (1), Candidatus Cuticobacterium kirbyi (1), Cedecea davisae (4), Cedecea lapagei (1), Cedecea neteri (2), Cedecea sp. (1), Citrobacter amalonaticus (10), Citrobacter braakii (5), Citrobacter farmeri (10), Citrobacter freundii (91), Citrobacter gillenii (3), Citrobacter koseri (7), Citrobacter murliniae (7), Citrobacter rodentium (11), Citrobacter sedlakii (4), Citrobacter sp. (96), Citrobacter werkmanii (3), Citrobacter youngae (2), Cloning vector (1), Clonorchis sinensis (1), Cronobacter sakazakii (13), cucurbit yellow vine disease bacterium (1), Curtobacterium plantarum (1), Desulfovibrio sp. (2), Dickeya dadantii (7), Dickeya sp. (6), Dickeya zeae (1), endophytic bacterium (41), endosymbiont (various) (6), Enteric Group (1), Enterobacter aerogenes (23), Enterobacter amnigenus (19), Enterobacter arachidis (1), Enterobacter asburiae (37), Enterobacter cancerogenus (24), Enterobacter cloacae (183), Enterobacter cowanii (7), Enterobacter endosymbiont (2), Enterobacter gergoviae (2), Enterobacter hormaechei (41), Enterobacter kobei (2), Enterobacter ludwigii (27), Enterobacter mori (2), Enterobacter nimipressuralis (1), Enterobacter oryzae (10), Enterobacter pyrinus (2), Enterobacter radicincitans (3), Enterobacter sp. (576), Enterobacter turicensis (3), Enterobacteria phage (7), Enterobacteriaceae bacterium (37), Enterobacterial endosymbiont (4), Enterobacteriales bacterium (3), enterobacterium (1), Erwinia aphidicola (1), Erwinia chrysanthemi (13), Erwinia psidii (1), Escherichia (1), Escherichia albertii (21), Escherichia coli (2104), Escherichia fergusonii (26), Escherichia hermannii (13), Escherichia senegalensis (1), Escherichia sp. (50), Escherichia vulneris (4), estrogen-degrading bacterium (1), Flavobacterium sp. (1), gamma proteobacterium (18), Gram-negative bacterium (1), Grimontella senegalensis (1), Grimontella sp. (2), Haemophilus sp. (1), Hafnia alvei (1), human gut metagenome (5), iron-reducing enrichment clone (1), Klebsiella oxytoca (127), Klebsiella pneumoniae (8), Klebsiella sp. (41), Kluyvera ascorbata (1), Leclercia adecarboxylata (16), Leclercia sp. (5), Lonsdalea quercina (2), Mangrovibacter plantisponsor (1), Mangrovibacter sp. (1), marine bacterium (1), marine metagenome (1), midgut symbiont (1), Morganella morganii (1), nitrogen-fixing bacterium (1), Oryza sativa Indica Group (4), Paenibacillus durus (1), Pantoea agglomerans (231), Pantoea ananatis (105), Pantoea anthophila (5), Pantoea brenneri (2), Pantoea conspicua (3), Pantoea cypripedii (3), Pantoea deleyi (1), Pantoea dispersa (2), Pantoea eucalypti (5), Pantoea sp. (138), Pantoea stewartii (1), Pantoea vagans (11), Paracoccus sp. (1), Pectobacterium atrosepticum (1), Pectobacterium cacticida (3), Pectobacterium carotovorum (6), Pectobacterium wasabiae (1), Phage Gifsy (7), Photorhabdus luminescens (1), Phytobacter diazotrophicus (2), Pragia fontium (1), proteobacterium (1), proteobacterium symbiont (2), Proteus vulgaris (1), Pseudomonas fluorescens (11), Pseudomonas putida (2), Pseudomonas sp. (7), Pseudomonas syringae (1), rainbow trout intestinal bacterium (1), Raoultella ornithinolytica (1), Raoultella planticola (1), Raoultella sp. (1),

		Rhodopseudomonas palustris (1), rumen bacterium enrichment culture clone (2), ruminal bacterium (1), Salmonella bongori (10), Salmonella enterica (433), Salmonella sp. (27), Salmonella subterranea (1), selenate-reducing bacterium (1), Serratia entomophila (1), Serratia marcescens (230), Serratia nematodiphila (8), Serratia sp. (212), Serratia symbiont (various) (4), Serratia ureilytica (4), Shigella boydii (74), Shigella dysenteriae (37), Shigella flexneri (188), Shigella sonnei (47), Shigella sp. (28), Streptomyces sp. (1), Strongylocentrotus purpuratus (1), Strongyloides ratti (1), swine fecal bacterium (9), swine manure bacterium (2), synthetic construct (14), uncultured Azoarcus sp. (1), uncultured Bacillus sp. (1), uncultured bacterium (4909), uncultured Citrobacter sp. (383), uncultured Cronobacter sp. (1), uncultured endophytic bacterium (1), uncultured Enterobacter sp. (228), uncultured Enterobacteriaceae bacterium (27), uncultured Erwinia sp. (1), uncultured Escherichia sp. (20), uncultured Firmicutes bacterium (2), uncultured gamma proteobacterium (353), uncultured Klebsiella sp. (129), uncultured marine bacterium (6), uncultured microorganism (1), uncultured organism (1702), uncultured Pantoea sp. (15), uncultured Parabacteroides sp. (4), uncultured Pectobacterium sp. (1), uncultured prokaryote (4), uncultured proteobacterium (4), uncultured Pseudomonas sp. (1), uncultured Psychrobacter sp. (1), uncultured Salmonella sp. (15), uncultured Serratia sp. (129), uncultured sheep mite bacterium (6), uncultured Shigella sp. (66), uncultured soil bacterium (41), uncultured Stenotrophomonas sp. (2), uncultured Streptomyces sp. (1), uncultured Tolumonas sp. (1), uncultured Verrucomicrobia bacterium (1), uncultured Yersinia sp. (1), unidentified (63), Yersinia sp. (1), Yokenella regensburgei (6)
	GCA AGA CCA AAG **C**GG GGG	Aquamonas haywardensis (1), Budvicia sp. (1), Enterobacteriaceae bacterium (25), Pantoea agglomerans (1), Sodalis glossinidius (2), Tatumella ptyseos (5), Tatumella punctata (4), Tatumella sp. (3), uncultured bacterium (53), uncultured Enterobacteriaceae bacterium (13), uncultured gamma proteobacterium (4), uncultured Pseudomonas sp. (1)
	GCA AGA CCA AAG **G**GG GGG	Pantoea sp. (1), Serratia marcescens (1), uncultured bacterium (6), uncultured Citrobacter sp. (1), uncultured gamma proteobacterium (1), uncultured Klebsiella sp. (1), uncultured Shigella sp. (1), uncultured Verrucomicrobiales bacterium (1)
	GCA AGA CCA AAG U**A**G GGG	uncultured Klebsiella sp. (1)
	GCA AGA CCA AAG UG**A** GGG	Edwardsiella tarda (1), endosymbiont (7)
	GCA AGA CCA AAG UGG **A**GG	Klebsiella sp. (2), primary endosymbiont (1), uncultured bacterium (2)
	GCA AGA CCA AAG UGG G**A**G	uncultured bacterium (2)
	GCA AGA CCA AAG UGG GG**A**	Serratia symbiotica (1), uncultured bacterium (4)
	NCA AGA CCA AAG **A**GG GGG	Citrobacter sp. (1), Enterobacter sp. (2), Enterobacteriaceae bacterium (1), Pantoea agglomerans (1),

		uncultured bacterium (1)
	GNA AGA GCA AAG UGG GGG	Rahnella aquatilis (2), Yersinia aleksiciae (1)
	GNA AGA CCA AAG AGG GGG	Citrobacter sedlakii (1), Escherichia coli (1), Pantoea agglomerans (1)
	GCN AGA CCA AAG AGG GGG	Pantoea endophytica (1)
	GCA NGA CCA AAG AGG GGG	Enterobacteriaceae bacterium (1)
	GCA AGA CCN AAG AGG GGG	swine fecal bacterium (1)
	GCA AGA CCA AAN AGG GGG	Serratia marcescens (1)
	GCA AGA CCA AAG ANG GGG	Escherichia coli (1), Pseudomonas fluorescens (1)
	GCA AGA CCA AAG AGG NGG	uncultured bacterium (2)
	GCA AGA CCA AAG AGG GNG	Escherichia coli (1)
	NNA AGA CCA AAG AGG GGG	uncultured soil bacterium (1)
	NCN AGA CCA AAG AGG GGG	uncultured Enterobacter sp. (1)
	GCA AGN NCA AAG AGG GGG	Escherichia coli (1)
2 mm	AAA AGA CCA AAG UGG GGG	Buchnera aphidicola (6)
	AUA AGA CCA AAG UGG GGG	Candidatus Baumannia cicadellinicola (1), endosymbiont (1)
	ACA AGA CCA AAG AGG GGG	Citrobacter sp. (1), Enterobacter sp. (2), Enterobacteriaceae bacterium (1), Serratia sp. (1), uncultured bacterium (6), uncultured Klebsiella sp. (4), uncultured organism (9), uncultured Pantoea sp. (1)
	ACA AGA CCA AAG GGG GGG	Enterobacter sp. (1)
	CUA AGA CCA AAG UGG GGG	gamma-symbiont (1)
	CCA AGA CCA AAG AGG GGG	Achromobacter xylosoxidans (1), Citrobacter freundii (1), endophytic bacterium (1), Enterobacter sp. (1), gamma proteobacterium (1), Pantoea agglomerans (1), rape rhizosphere bacterium (1), uncultured bacterium (2), uncultured gamma proteobacterium (1), uncultured organism (4), Xenorhabdus nematophila (1)
	UUA AGA CCA AAG UGG GGG	secondary endosymbiont (1)
	UCA GGA CCA AAG UGG GGG	Gibbsiella quercinecans (1)
	UCA AGA ACA AAG UGG GGG	Chloroidium saccharophilum (1)
	UCA AGA CCA AAG AGG GGG	Enterobacter sp. (4), gamma proteobacterium (1), Pantoea agglomerans (4), Pantoea sp. (5), selenate-reducing bacterium (1), uncultured bacterium (2), uncultured organism (2), unidentified (3), Yokenella sp. (1)
	GAG AGA CCA AAG UGG GGG	Candidatus Baumannia cicadellinicola (1), primary endosymbiont (2), secondary endosymbiont (1), uncultured gamma proteobacterium (2)
	GAU AGA CCA AAG UGG GGG	uncultured bacterium (9)

	G**A**A A**A**A CCA AAG UGG GGG	Acyrthosiphon pisum (2), Buchnera aphidicola (36), Buchnera sp. (6), Triticum aestivum (1), uncultured bacterium (3), uncultured Buchnera sp. (1), unidentified (1)
	G**A**A AGA **G**CA AAG UGG GGG	Bacterium (2), endophyte bacterium (1), Enterobacteriaceae bacterium (2), Erwinia (1), Ewingella americana (19), Nevskia soli (2), Nevskia sp. (1), Pantoea sp. (1), Pectobacterium carotovorum (13), Rahnella aquatilis (18), Rahnella genomosp. (1), Rahnella sp. (58), symbiont (various) (4), uncultured bacterium (26), uncultured eubacterium (1), uncultured gamma proteobacterium (3), uncultured Rahnella sp. (8), uncultured rape rhizosphere bacterium (1), unidentified (2), Yersinia aleksiciae (1), Yersinia massiliensis (2), Yersinia sp. (2)
	G**A**A AGA **U**CA AAG UGG GGG	Blochmannia endosymbiont (1), Candidatus Steffania adelgidicola (2), uncultured bacterium (1)
	G**A**A AGA C**U**A AAG UGG GGG	uncultured bacterium (1)
	G**A**A AGA CCA AA**A** UGG GGG	Candidatus Baumannia cicadellinicola (2)
	G**A**A AGA CCA AAG **A**GG GGG	Escherichia coli (6), Pantoea sp. (1), uncultured bacterium (3), uncultured organism (25), uncultured Citrobacter sp. (3), uncultured Pantoea sp. (1), uncultured Salmonella sp. (1)
	G**A**A AGA CCA AAG **C**GG GGG	Budvicia aquatica (1), Candidatus Baumannia cicadellinicola (2), secondary endosymbiont (1), uncultured bacterium (1)
	G**A**A AGA CCA AAG U**A**G GGG	uncultured proteobacterium (1)
	G**A**A AGA CCA AAG UGG GG**A**	Sodalis-like symbiont of Nippolachnus piri (1)
	G**G**A AGA CCA AAG **A**GG GGG	Pantoea sp. (1), uncultured bacterium (1)
	G**UG** AGA CCA AAG UGG GGG	Hamiltonella endosymbiont (2), secondary endosymbiont (various) (9)
	G**UU** AGA CCA AAG UGG GGG	Candidatus Baumannia cicadellinicola (1)
	G**U**A **G**GA CCA AAG UGG GGG	uncultured bacterium (2)
	G**U**A A**A**A CCA AAG UGG GGG	Candidatus Ishikawaella capsulata (8), Ishikawaella symbiont (5), uncultured Pantoea sp. (1)
	G**U**A AGA **G**CA AAG UGG GGG	bacterium (1), Rahnella aquatilis (3), Rahnella sp. (1), uncultured bacterium (13), uncultured Erwinia sp. (21), uncultured gamma proteobacterium (2), uncultured Rahnella sp. (1), Yersinia aleksiciae (3), Yersinia bercovieri (5), Yersinia intermedia (4)
	G**U**A AGA C**U**A AAG UGG GGG	Candidatus Stammerula sp. (1)
	G**U**A AGA CCA AA**A** UGG GGG	Baumannia cicadellinicola (2), Candidatus Baumannia cicadellinicola (6)
	G**U**A AGA CCA AAG **A**GG GGG	Escherichia coli (1), Shigella sp. (2), uncultured bacterium (6), uncultured Enterobacter sp. (5), uncultured Klebsiella sp. (2), uncultured organism (2)
	G**U**A AGA CCA AAG **C**GG GGG	Enterobacteriaceae bacterium (2), secondary endosymbiont (1)
	G**U**A AGA CCA AAG **G**GG GGG	uncultured Verrucomicrobia bacterium (1)
	G**U**A AGA CCA AAG UG**A** GGG	Candidatus Curculioniphilus endosymbiont (various) (19), Serratia symbiotica (1)
	GC**C** AGA CCA AAG **A**GG GGG	bacterium (1), uncultured bacterium (1), uncultured organism (1)

	GC**G** A**C**A CCA AAG UGG GGG	uncultured proteobacterium (1)
	GC**G** AGA **G**CA AAG UGG GGG	Erwinia sp. (2), uncultured bacterium (8)
	GC**G** AGA CCA AA**C** UGG GGG	Photorhabdus luminescens (1)
	GC**G** AGA CCA AAG **A**GG GGG	Enterobacter sp. (2), Pantoea endophytica (1), Pseudomonas sp. (1), uncultured bacterium (7), uncultured Citrobacter sp. (2), uncultured sheep mite bacterium (1)
	GC**G** AGA CCA AAG **C**GG GGG	Bacteriophage (1), Pseudomonas flectens (2)
	GC**G** AGA CCA AAG **G**GG GGG	Enterobacter sp. (1)
	GC**G** AGA CCA AAG UG**U** GGG	Cronobacter sp. (1)
	GC**G** AGA CCA AAG UGG G**A**G	uncultured bacterium (1)
	GC**U** AGA CCA AA**A** UGG GGG	Candidatus Baumannia cicadellinicola (1)
	GCA **C**GA CCA AAG **A**GG GGG	Pantoea agglomerans (1), Pantoea sp. (1), uncultured organism (2)
	GCA **G**GA CCA AAG **A**GG GGG	Enterobacter nickellidurans (1), Escherichia coli (1), Pantoea agglomerans (1), Salmonella enterica (4), uncultured bacterium (8), uncultured Serratia sp. (1)
	GCA **U**GA CCA AAG **A**GG GGG	uncultured bacterium (1)
	GCA A**A**A CCA AAG **A**GG GGG	Escherichia coli (2), Pantoea sp. (1), Shigella dysenteriae (5), uncultured bacterium (3), uncultured beta proteobacterium (2), uncultured gamma proteobacterium (3), uncultured Shigella sp. (1)
	GCA A**A**A CCA AAG U**A**G GGG	Buchnera aphidicola (1)
	GCA AG**C** **A**CA AAG UGG GGG	Rahnella sp. (1)
	GCA AG**C** CCA AAG **A**GG GGG	uncultured bacterium (2)
	GCA AG**G** **G**CA AAG UGG GGG	Hafnia sp. (1)
	GCA AG**G** CCA AAG **A**GG GGG	Citrobacter sp. (1), Enterobacter cloacae (1), Pseudomonas sp. (1), uncultured bacterium (5), uncultured Citrobacter sp. (1)
	GCA AG**G** CCA AAG **C**GG GGG	uncultured Enterobacteriaceae bacterium (1)
	GCA AG**U** CCA AAG **A**GG GGG	uncultured bacterium (1)
	GCA AGA **GG**A AAG UGG GGG	uncultured bacterium (4)
	GCA AGA **G**CA A**G**G UGG GGG	Yersinia ruckeri (1)
	GCA AGA **G**CA AAG **A**GG GGG	bacterium (3), Enterobacteriaceae bacterium (1), Erwinia chrysanthemi (2), Erwinia sp. (7), Erwinia tracheiphila (1), Listonella anguillarum (1), Nevskia ramosa (1), Nevskia sp. (7), Oryza sativa Indica Group (1), Pantoea cedenensis (6), Pantoea sp. (1), Pectobacterium atrosepticum (1), Pectobacterium carotovorum (124), Pectobacterium sp. (4), uncultured bacterium (18), uncultured Erwinia sp. (11), uncultured gamma proteobacterium (2)
	GCA AGA **G**CA AAG **G**GG GGG	uncultured bacterium (1)
	GCA AGA **U**CA AAG **A**GG GGG	uncultured bacterium (2)

	GCA AGA **U**CA AAG U**C**G GGG	uncultured bacterium (1), uncultured Verrucomicrobia bacterium (2)
	GCA AGA **U**CA AAG U**U**G GGG	uncultured bacterium (1)
	GCA AGA **U**CA AAG UGG **A**GG	uncultured Verrucomicrobia bacterium (2)
	GCA AGA **U**CA AAG UGG GG**C**	Klebsiella sp. (1)
	GCA AGA C**A**A AAG **A**GG GGG	Pantoea agglomerans (2), uncultured bacterium (1)
	GCA AGA C**G**A AAG **A**GG GGG	Enterobacteriaceae bacterium (1)
	GCA AGA C**U**A AAG **A**GG GGG	Escherichia coli (3), Shigella sonnei (4), uncultured bacterium (2), uncultured Serratia sp. (1)
	GCA AGA CC**C** AAG **A**GG GGG	Shigella sonnei (1)
	GCA AGA CC**G** AAG **A**GG GGG	Enterobacter aerogenes (1), Enterobacter sp. (2), Serratia marcescens (1), uncultured bacterium (2), uncultured organism (6)
	GCA AGA CC**U** AAG **A**GG GGG	Serratia marcescens (2)
	GCA AGA CCA **C**AG **A**GG GGG	uncultured bacterium (1)
	GCA AGA CCA **G**AG **A**GG GGG	Escherichia albertii (1), uncultured bacterium (6), uncultured Citrobacter sp. (1), uncultured organism (3), uncultured sheep mite bacterium (2)
	GCA AGA CCA A**C**G **A**GG GGG	uncultured bacterium (1)
	GCA AGA CCA A**C**G **C**GG GGG	unidentified thrip gut bacterium (1)
	GCA AGA CCA A**G**G **A**GG GGG	Pantoea sp. (1), uncultured bacterium (3), uncultured gamma proteobacterium (1), uncultured organism (4)
	GCA AGA CCA A**G**G **C**GG GGG	uncultured Enterobacteriaceae bacterium (1)
	GCA AGA CCA A**U**G **A**GG GGG	uncultured bacterium (3), Vestimentiferan symbiont (1)
	GCA AGA CCA AA**A** **A**GG GGG	bacterium enrichment culture clone (6), endosymbiont of Sphenophorus levis (1), Enterobacter sp. (1), Escherichia coli (2), Pantoea sp. (1), Serratia marcescens (1), Shigella boydii (2), Shigella sp. (1), uncultured bacterium (59), uncultured Escherichia sp. (1), uncultured Shigella sp. (4)
	GCA AGA CCA AA**U** **A**GG GGG	uncultured bacterium (1)
	GCA AGA CCA AAG **AA**G GGG	Enterobacter cloacae (1), uncultured bacterium (2)
	GCA AGA CCA AAG **AU**G GGG	Enterobacter sp. (1)
	GCA AGA CCA AAG **A**G**A** GGG	Pantoea sp. (1), uncultured bacterium (3), uncultured gamma proteobacterium (1)
	GCA AGA CCA AAG **A**G**C** GGG	Shigella sonnei (1)
	GCA AGA CCA AAG **A**G**U** GGG	Orbus hercynius (1)
	GCA AGA CCA AAG **A**GG **A**GG	Salmonella enterica (1), uncultured bacterium (1), uncultured Klebsiella sp. (1), uncultured organism (1)
	GCA AGA CCA AAG **A**GG **U**GG	uncultured bacterium (1)
	GCA AGA CCA AAG **A**GG G**A**G	Enterobacter sp. (1), uncultured bacterium (1)
	GCA AGA CCA AAG **A**GG G**C**G	uncultured bacterium (1)
	GCA AGA CCA AAG **A**GG G**U**G	Escherichia coli (1), uncultured bacterium (1)

	GCA AGA CCA AAG **A**GG GG**A**	Escherichia coli (7), Shigella flexneri (2), uncultured bacterium (13), uncultured Citrobacter sp. (2), uncultured organism (1)
	GCA AGA CCA AAG **A**GG GG**U**	Escherichia coli (8), uncultured bacterium (3), uncultured gamma proteobacterium (1), uncultured organism (1), unidentified (1)
	GCA AGA CCA AAG **CA**G GGG	gamma proteobacterium (1), Panacagrimonas perspica (1), uncultured bacterium (3), uncultured soil bacterium (1)
	GCA AGA CCA AAG **CC**G GGG	uncultured Xanthomonadaceae bacterium (6)
	GCA AGA CCA AAG **CU**G GGG	gamma proteobacterium (3), Solimonas flava (1), Solimonas soli (3), Solimonas variicoloris (1), uncultured Acidobacteria bacterium (1), uncultured bacterium (4)
	GCA AGA CCA AAG **GA**G GGG	Enterobacter hormaechei (1)
	GCA AGA CCA AAG UG**A** **A**GG	Serratia symbiotica (1)
	GCA AG**N** C**A**A AAG **A**GG GGG	Pantoea agglomerans (1)

Name of the probe: Entero all

Target organism: *Enterobacterales*

Sequence of the probe: CCC CCW CTT TGG TCT TGC

Date of *in-silico* assessment: March 2018

Variant assessed here: CCC CCT CTT TGG TCT TGC

Mismatch count	**Ribosomal RNA sequence corresponding to the probe**	**Matching with known sequences (without italics)**
0 mm	GCA AGA CCA AAG AGG GGG	Acinetobacter radioresistens (1), Acinetobacter sp. (1), Ajellomyces capsulatus (1), Aranicola sp. (1), Bacillus subtilis (2), bacterium (129), Brenneria alni (1), Brenneria lupinicola (1), Brenneria nigrifluens (2), Brenneria rubrifaciens (1), Budvicia sp. (1), Buttiauxella agrestis (1), Candidatus Cuticobacterium kirbyi (1), Cedecea davisae (4), Cedecea lapagei (1), Cedecea neteri (2), Cedecea sp. (1), Citrobacter amalonaticus (10), Citrobacter braakii (5), Citrobacter farmeri (10), Citrobacter freundii (91), Citrobacter gillenii (3), Citrobacter koseri (7), Citrobacter murliniae (7), Citrobacter rodentium (11), Citrobacter sedlakii (4), Citrobacter sp. (96), Citrobacter werkmanii (3), Citrobacter youngae (2), Cloning vector (1), Clonorchis sinensis (1), Cronobacter sakazakii (13), cucurbit yellow vine disease bacterium (1), Curtobacterium plantarum (1), Desulfovibrio sp. (2), Dickeya dadantii (7), Dickeya sp. (6), Dickeya zeae (1), endophytic bacterium (41), endosymbiont (various) (6), Enteric Group (1), Enterobacter aerogenes (23), Enterobacter amnigenus (19), Enterobacter arachidis (1), Enterobacter asburiae (37), Enterobacter cancerogenus (24), Enterobacter cloacae (183), Enterobacter cowanii (7), Enterobacter endosymbiont (2), Enterobacter gergoviae (2), Enterobacter hormaechei (41), Enterobacter kobei (2), Enterobacter ludwigii (27), Enterobacter mori (2), Enterobacter nimipressuralis (1), Enterobacter oryzae (10), Enterobacter pyrinus (2), Enterobacter radicincitans (3), Enterobacter sp. (576), Enterobacter turicensis (3), Enterobacteria phage (7), Enterobacteriaceae bacterium (37), Enterobacterial endosymbiont (4), Enterobacteriales bacterium (3), enterobacterium (1), Erwinia aphidicola (1), Erwinia chrysanthemi (13), Erwinia psidii (1), Escherichia (1), Escherichia albertii (21), Escherichia coli (2104), Escherichia fergusonii (26), Escherichia hermannii (13), Escherichia senegalensis (1), Escherichia sp. (50), Escherichia vulneris (4), estrogen-degrading bacterium (1), Flavobacterium sp. (1), gamma proteobacterium (18), Gram-negative bacterium (1), Grimontella senegalensis (1), Grimontella sp. (2), Haemophilus sp. (1), Hafnia alvei (1), human gut metagenome (5), iron-reducing enrichment clone (1), Klebsiella oxytoca (127), Klebsiella pneumoniae (8), Klebsiella sp. (41), Kluyvera ascorbata (1),

		Leclercia adecarboxylata (16), Leclercia sp. (5), Lonsdalea quercina (2), Mangrovibacter plantisponsor (1), Mangrovibacter sp. (1), marine bacterium (1), marine metagenome (1), midgut symbiont (1), Morganella morganii (1), nitrogen-fixing bacterium (1), Oryza sativa Indica Group (4), Paenibacillus durus (1), Pantoea agglomerans (231), Pantoea ananatis (105), Pantoea anthophila (5), Pantoea brenneri (2), Pantoea conspicua (3), Pantoea cypripedii (3), Pantoea deleyi (1), Pantoea dispersa (2), Pantoea eucalypti (5), Pantoea sp. (138), Pantoea stewartii (1), Pantoea vagans (11), Paracoccus sp. (1), Pectobacterium atrosepticum (1), Pectobacterium cacticida (3), Pectobacterium carotovorum (6), Pectobacterium wasabiae (1), Phage Gifsy (7), Photorhabdus luminescens (1), Phytobacter diazotrophicus (2), Pragia fontium (1), proteobacterium (1), proteobacterium symbiont (2), Proteus vulgaris (1), Pseudomonas fluorescens (11), Pseudomonas putida (2), Pseudomonas sp. (7), Pseudomonas syringae (1), rainbow trout intestinal bacterium (1), Raoultella ornithinolytica (1), Raoultella planticola (1), Raoultella sp. (1), Rhodopseudomonas palustris (1), rumen bacterium enrichment culture clone (2), ruminal bacterium (1), Salmonella bongori (10), Salmonella enterica (433), Salmonella sp. (27), Salmonella subterranea (1), selenate-reducing bacterium (1), Serratia entomophila (1), Serratia marcescens (230), Serratia nematodiphila (8), Serratia sp. (212), Serratia symbiont (various) (4), Serratia ureilytica (4), Shigella boydii (74), Shigella dysenteriae (37), Shigella flexneri (188), Shigella sonnei (47), Shigella sp. (28), Streptomyces sp. (1), Strongylocentrotus purpuratus (1), Strongyloides ratti (1), swine fecal bacterium (9), swine manure bacterium (2), synthetic construct (14), uncultured Azoarcus sp. (1), uncultured Bacillus sp. (1), uncultured bacterium (4909), uncultured Citrobacter sp. (383), uncultured Cronobacter sp. (1), uncultured endophytic bacterium (1), uncultured Enterobacter sp. (228), uncultured Enterobacteriaceae bacterium (27), uncultured Erwinia sp. (1), uncultured Escherichia sp. (20), uncultured Firmicutes bacterium (2), uncultured gamma proteobacterium (353), uncultured Klebsiella sp. (129), uncultured marine bacterium (6), uncultured microorganism (1), uncultured organism (1702), uncultured Pantoea sp. (15), uncultured Parabacteroides sp. (4), uncultured Pectobacterium sp. (1), uncultured prokaryote (4), uncultured proteobacterium (4), uncultured Pseudomonas sp. (1), uncultured Psychrobacter sp. (1), uncultured Salmonella sp. (15), uncultured Serratia sp. (129), uncultured sheep mite bacterium (6), uncultured Shigella sp. (66), uncultured soil bacterium (41), uncultured Stenotrophomonas sp. (2), uncultured Streptomyces sp. (1), uncultured Tolumonas sp. (1), uncultured Verrucomicrobia bacterium (1), uncultured Yersinia sp. (1), unidentified (63), Yersinia sp. (1), Yokenella regensburgei (6)
	NCA AGA CCA AAG AGG GGG	Citrobacter sp. (1), Enterobacter sp. (2), Enterobacteriaceae bacterium (1), Pantoea agglomerans (1), uncultured bacterium (1)

	G**N**A AGA CCA AAG AGG GGG	Citrobacter sedlakii (1), Escherichia coli (1), Pantoea agglomerans (1)
	GC**N** AGA CCA AAG AGG GGG	Pantoea endophytica (1)
	GCA **N**GA CCA AAG AGG GGG	Enterobacteriaceae bacterium (1)
	GCA AGA CC**N** AAG AGG GGG	swine fecal bacterium (1)
	GCA AGA CCA AA**N** AGG GGG	Serratia marcescens (1)
	GCA AGA CCA AAG **N**GG GGG	Klebsiella pneumoniae (1)
	GCA AGA CCA AAG A**N**G GGG	Escherichia coli (1), Pseudomonas fluorescens (1)
	GCA AGA CCA AAG AGG **N**GG	uncultured bacterium (2)
	GCA AGA CCA AAG AGG G**N**G	Escherichia coli (1)
	NNA AGA CCA AAG AGG GGG	uncultured soil bacterium (1)
	NC**N** AGA CCA AAG AGG GGG	uncultured Enterobacter sp. (1)
	GCA AG**N** **N**CA AAG AGG GGG	Escherichia coli (1)
1 mm	**A**CA AGA CCA AAG AGG GGG	Citrobacter sp. (1), Enterobacter sp. (2), Enterobacteriaceae bacterium (1), Serratia sp. (1), uncultured bacterium (6), uncultured Klebsiella sp. (4), uncultured organism (9), uncultured Pantoea sp. (1)
	CCA AGA CCA AAG AGG GGG	Achromobacter xylosoxidans (1), Citrobacter freundii (1), endophytic bacterium (1), Enterobacter sp. (1), gamma proteobacterium (1), Pantoea agglomerans (1), rape rhizosphere bacterium (1), uncultured bacterium (2), uncultured gamma proteobacterium (1), uncultured organism (4), Xenorhabdus nematophila (1)
	UCA AGA CCA AAG AGG GGG	Enterobacter sp. (4), gamma proteobacterium (1), Pantoea agglomerans (4), Pantoea sp. (5), selenate-reducing bacterium (1), uncultured bacterium (2), uncultured organism (2), unidentified (3), Yokenella sp. (1)
	G**A**A AGA CCA AAG AGG GGG	Escherichia coli (6), Pantoea sp. (1), uncultured bacterium (3), uncultured Citrobacter sp. (3), uncultured organism (25), uncultured Pantoea sp. (1), uncultured Salmonella sp. (1)
	G**G**A AGA CCA AAG AGG GGG	Pantoea sp. (1), uncultured bacterium (1)
	G**U**A AGA CCA AAG AGG GGG	Escherichia coli (1), Shigella sp. (2), uncultured bacterium (6), uncultured Enterobacter sp. (5), uncultured Klebsiella sp. (2), uncultured organism (2)
	GC**C** AGA CCA AAG AGG GGG	Bacterium (1), uncultured bacterium (1), uncultured organism (1)
	GC**G** AGA CCA AAG AGG GGG	Enterobacter sp. (2), Pantoea endophytica (1), Pseudomonas sp. (1), uncultured bacterium (7), uncultured Citrobacter sp. (2), uncultured sheep mite bacterium (1)
	GCA **C**GA CCA AAG AGG GGG	Pantoea agglomerans (1), Pantoea sp. (1), uncultured organism (2)
	GCA **G**GA CCA AAG AGG GGG	Enterobacter nickellidurans (1), Escherichia coli (1), Pantoea agglomerans (1), Salmonella enterica (4), uncultured bacterium (8), uncultured Serratia sp. (1)

	GCA **U**GA CCA AAG AGG GGG	uncultured bacterium (1)
	GCA A**A**A CCA AAG AGG GGG	Escherichia coli (2), Pantoea sp. (1), Shigella dysenteriae (5), uncultured bacterium (3), uncultured beta proteobacterium (2), uncultured gamma proteobacterium (3), uncultured Shigella sp. (1)
	GCA AG**C** CCA AAG AGG GGG	uncultured bacterium (2)
	GCA AG**G** CCA AAG AGG GGG	Citrobacter sp. (1), Enterobacter cloacae (1), Pseudomonas sp. (1), uncultured bacterium (5), uncultured Citrobacter sp. (1)
	GCA AG**U** CCA AAG AGG GGG	uncultured bacterium (2)
	GCA AGA **G**CA AAG AGG GGG	bacterium (3), Enterobacteriaceae bacterium (1), Erwinia chrysanthemi (2), Erwinia tracheiphila (1), Erwinia sp. (7), Listonella anguillarum (1), Nevskia ramosa (1), Nevskia sp. (7), Oryza sativa Indica Group (1), Pantoea cedenensis (6), Pantoea sp. (1), Pectobacterium atrosepticum (1), Pectobacterium carotovorum (124), Pectobacterium sp. (4), uncultured bacterium (19), uncultured Erwinia sp. (11), uncultured gamma proteobacterium (2)
	GCA AGA **U**CA AAG AGG GGG	uncultured bacterium (1)
	GCA AGA C**A**A AAG AGG GGG	Pantoea agglomerans (2), uncultured bacterium (1)
	GCA AGA C**G**A AAG AGG GGG	Enterobacteriaceae bacterium (1)
	GCA AGA C**U**A AAG AGG GGG	Escherichia coli (3), Shigella sonnei (4), uncultured bacterium (2), uncultured Serratia sp. (1)
	GCA AGA CC**C** AAG AGG GGG	Shigella sonnei (1)
	GCA AGA CC**G** AAG AGG GGG	Enterobacter aerogenes (1), Enterobacter sp. (2), Serratia marcescens (1), uncultured bacterium (2), uncultured organism (6)
	GCA AGA CC**U** AAG AGG GGG	Serratia marcescens (2)
	GCA AGA CCA **C**AG AGG GGG	uncultured bacterium (1)
	GCA AGA CCA **G**AG AGG GGG	Escherichia albertii (1), uncultured bacterium (6), uncultured Citrobacter sp. (1), uncultured organism (3), uncultured sheep mite bacterium (1)
	GCA AGA CCA A**C**G AGG GGG	uncultured bacterium (1)
	GCA AGA CCA A**G**G AGG GGG	Pantoea sp. (1), uncultured bacterium (2), uncultured gamma proteobacterium (1), uncultured organism (4)
	GCA AGA CCA A**U**G AGG GGG	uncultured bacterium (4), Vestimentiferan symbiont (1)
	GCA AGA CCA AA**A** AGG GGG	bacterium (6), endosymbiont (1), Enterobacter sp. (1), Escherichia coli (2), Pantoea sp. (1), Serratia marcescens (1), Shigella boydii (2), Shigella sp. (1), uncultured bacterium (59), uncultured Escherichia sp. (1), uncultured Shigella sp. (4)
	GCA AGA CCA AA**U** AGG GGG	uncultured bacterium (1)
	GCA AGA CCA AAG **C**GG GGG	Aquamonas haywardensis (1), Budvicia sp. (1), Enterobacteriaceae bacterium (25), Pantoea agglomerans (1), Sodalis glossinidius (2), Tatumella ptyseos (5), Tatumella punctata (4), Tatumella sp. (3), uncultured bacterium (53), uncultured Enterobacteriaceae bacterium (13),

		uncultured gamma proteobacterium (4), uncultured Pseudomonas sp. (1)
	GCA AGA CCA AAG **G**GG GGG	Pantoea sp. (1), Serratia marcescens (1), uncultured bacterium (6), uncultured Citrobacter sp. (1), uncultured gamma proteobacterium (1), uncultured Klebsiella sp. (1), uncultured Shigella sp. (1), uncultured Verrucomicrobiales bacterium (1)
	GCA AGA CCA AAG **U**GG GGG	Bacillus megaterium (1), Bacillus sp. (4), Bacillus subtilis (1), bacterium (50), BEV proteobacterium (1), Biostraticola tofi (1), Brenneria goodwinii (3), Brenneria rubrifaciens (7), Brenneria salicis (1), Burkholderia cepacia (1), Candidatus Regiella insecticola (22), Candidatus Rohrkolberia cinguli (1), Candidatus Stammerula sp. (1), Cenchrus americanus (3), Cimex lectularius endosymbiont (4), Citrobacter sp. (1), Cronobacter dublinensis (2), Cronobacter muytjensii (21), Cronobacter sakazakii (1), Cronobacter sp. (1), Dickeya dadantii (8), Dickeya dianthicola (1), Dickeya dieffenbachiae (1), Dickeya sp. (8), Edwardsiella hoshinae (2), Edwardsiella ictaluri (29), Edwardsiella sp. (7), Edwardsiella tarda (76), endophytic bacterium (9), endosymbiont (various) (4), Enterobacter aerogenes (51), Enterobacter cloacae (8), Enterobacter helveticus (4), Enterobacter hormaechei (1), Enterobacter ludwigii (4), Enterobacter pulveris (4), Enterobacter sp. (37), Enterobacteriaceae bacterium (24), enterobacterium (1), Erwinia chrysanthemi (30), Erwinia mallotivora (1), Erwinia papayae (1), Erwinia psidii (2), Erwinia sp. (18), Erwinia tracheiphila (1), Escherichia blattae (2), Escherichia sp. (2), gamma proteobacterium (6), Gibbsiella quercinecans (5), Glossina pallidipes S-endosymbiont (1), human gut metagenome (2), Klebsiella alba (2), Klebsiella granulomatis (4), Klebsiella milletis (1), Klebsiella oxytoca (12), Klebsiella pneumoniae (270), Klebsiella singaporensis (2), Klebsiella sp. (337), Klebsiella variicola (17), Kluyvera ascorbata (19), Kluyvera cryocrescens (8), Kluyvera georgiana (3), Kluyvera intermedia (15), Kluyvera sp. (13), Leclercia sp. (5), Lonsdalea quercina (19), Lysinibacillus fusiformis (1), Nannospalax galili (1), nitrogen-fixing bacterium (1), Obesumbacterium sp. (1), Pantoea agglomerans (13), Pantoea ananatis (1), Pantoea calida (1), Pantoea cypripedii (10), Pantoea dispersa (14), Pantoea gaviniae (1), Pantoea sp. (39), Pantoea stewartii (17), Pantoea wallisii (2), Pectobacterium carotovorum (1), Pectobacterium sp. (1), Photorhabdus luminescens (18), Photorhabdus sp. (14), Photorhabdus temperata (37), primary endosymbiont (various) (7), proteobacterium (1), Pseudomonas aeruginosa (1), Pseudomonas sp. (5), Rahnella aquatilis (18), Rahnella sp. (3), rainbow trout intestinal bacterium (1), Raoultella ornithinolytica (28), Raoultella planticola (18), Raoultella sp. (23), Raoultella terrigena (7), Regiella symbiont (5), Salmonella enterica (1), secondary endosymbiont (various) (5), secondary symbiont (various) (16), Serratia fonticola (1), Serratia liquefaciens (1), Serratia rubidaea (8), Serratia sp. (5), Serratia symbiotica (28), Shigella flexneri (1), Shimwellia blattae (2), Sitophilus zeamais (1), Sodalis glossinidius (6), Sodalis secondary endosymbiont (various) (2), Tatumella citrea (3), Tatumella morbirosei (3), Tatumella punctata (1), Tatumella terrea (3), Thorsellia anophelis (1), uncultured actinomycete (1),

		uncultured bacterium (1127), uncultured Citrobacter sp. (2), uncultured compost bacterium (1), uncultured Edwardsiella sp. (1), uncultured Enterobacter sp. (7), uncultured Enterobacteriaceae bacterium (19), uncultured Erwinia sp. (7), uncultured gamma proteobacterium (4), uncultured Klebsiella sp. (449), uncultured Kluyvera sp. (4), uncultured organism (23), uncultured Pantoea sp. (3), uncultured proteobacterium (4), uncultured Rahnella sp. (10), uncultured Raoultella sp. (10), uncultured rumen bacterium (1), uncultured Serratia sp. (1), uncultured soil bacterium (1), uncultured Xanthomonadaceae bacterium (1), uncultured Yersinia sp. (1), unidentified (10), Xenorhabdus poinarii (2), Yersinia sp. (1)
	GCA AGA CCA AAG A**A**G GGG	Enterobacter cloacae (1), uncultured bacterium (2)
	GCA AGA CCA AAG A**U**G GGG	Enterobacter sp. (1)
	GCA AGA CCA AAG AG**A** GGG	Pantoea sp. (1), uncultured bacterium (3), uncultured gamma proteobacterium (1)
	GCA AGA CCA AAG AG**U** GGG	Orbus hercynius (1)
	GCA AGA CCA AAG AGG **A**GG	Salmonella enterica (1), uncultured bacterium (1), uncultured Klebsiella sp. (1), uncultured organism (1)
	GCA AGA CCA AAG AGG **U**GG	uncultured bacterium (1)
	GCA AGA CCA AAG AGG G**A**G	Enterobacter sp. (1), uncultured bacterium (1)
	GCA AGA CCA AAG AGG G**C**G	uncultured bacterium (1)
	GCA AGA CCA AAG AGG G**U**G	Escherichia coli (1), uncultured bacterium (1)
	GCA AGA CCA AAG AGG GG**A**	Escherichia coli (7), Shigella flexneri (2), uncultured bacterium (13), uncultured Citrobacter sp. (2), uncultured organism (1)
	GCA AGA CCA AAG AGG GG**U**	Escherichia coli (8), uncultured bacterium (3), uncultured gamma proteobacterium (1), uncultured organism (1), unidentified (1)
	NCA AGA CCA AAG **U**GG GGG	Raoultella terrigena (1)
	GC**N** AGA CCA AAG **U**GG GGG	Pantoea dispersa (1), Pantoea septica (2), Photorhabdus luminescens (1), Raoultella terrigena (2)
	GCA AG**N** C**A**A AAG AGG GGG	Pantoea agglomerans (1)
	GCA AGA **N**CA AAG **U**GG GGG	Yersinia kristensenii (1)
	GCA AGA CCA AAG **U**GG GG**N**	uncultured bacterium (1)
2 mm	**A**C**G** AGA CCA AAG AGG GGG **A**CA AGA CCA **G**AG AGG GGG **A**CA AGA CCA AA**A** AGG GGG **A**CA AGA CCA AAG **G**GG GGG **A**CA AGA CCA AAG **U**GG GGG	Bacillus cereus (1), Citrobacter freundii (1) Serratia marcescens (1) Enterobacter sp. (1) Enterobacter sp. (1) Enterobacteriaceae bacterium (1), uncultured bacterium (3), uncultured Klebsiella sp. (3)

	ACA AGA CCA AAG AGG GG**C**	Citrobacter freundii (1)
	CAA AGA CCA AAG AGG GGG	uncultured bacterium (2)
	CUA AGA CCA AAG AGG GGG	Escherichia coli (1)
	CCA AGA CC**G** AAG AGG GGG	uncultured bacterium (1)
	CCA AGA CCA AAG **U**GG GGG	Klebsiella pneumoniae (1)
	UC**C** AGA CCA AAG AGG GGG	uncultured bacterium (1)
	UCA AGA **A**CA AAG AGG GGG	uncultured bacterium (1)
	UCA AGA **G**CA AAG AGG GGG	Pantoea agglomerans (1)
	UCA AGA CC**G** AAG AGG GGG	bacterium (1), uncultured bacterium (1)
	UCA AGA CCA A**G**G AGG GGG	Pantoea sp. (1), uncultured bacterium (1)
	UCA AGA CCA AA**A** AGG GGG	Erwinia chrysanthemi (2)
	G**AU** AGA CCA AAG AGG GGG	uncultured Colwellia sp. (1)
	G**A**A **U**GA CCA AAG AGG GGG	uncultured bacterium (1)
	G**A**A AGA CCA AAG **C**GG GGG	Budvicia aquatica (1), Candidatus Baumannia cicadellinicola (2), secondary endosymbiont (1), uncultured bacterium (1)
	G**A**A AGA CCA AAG **U**GG GGG	Candidatus Baumannia cicadellinicola (1), Candidatus Ecksteinia adelgidicola (2), Candidatus Kleidoceria schneideri (6), Candidatus Regiella insecticola (1), secondary endosymbiont (2), Serratia symbiotica (3), uncultured bacterium (5), uncultured organism (2), uncultured Rahnella sp. (1), uncultured Sodalis sp. (1)
	G**U**A AGA CCA AAG **C**GG GGG	Enterobacteriaceae bacterium (2), secondary endosymbiont (1)
	G**U**A AGA CCA AAG **G**GG GGG	uncultured Verrucomicrobia bacterium (1)
	G**U**A AGA CCA AAG **U**GG GGG	Candidatus Baumannia cicadellinicola (1), Candidatus Moranella endobia (1), Candidatus Schneideria nysicola (11), Candidatus Stammerula sp. (5), Candidatus Stammerula tephritidis (14), Enterobacteriaceae bacterium (14), Klebsiella pneumoniae (1), Pantoea sp. (1), Planococcus citri gamma-proteobacterial endosymbiont (1), primary endosymbiont (1), secondary endosymbiont (various (4), secondary symbiont (1), Serratia symbiotica (4), symbiont (11), uncultured bacterium (2), uncultured Pantoea sp. (5), uncultured proteobacterium (1), uncultured Sodalis sp. (1)
	GC**C** **G**GA CCA AAG AGG GGG	Erwinia chrysanthemi (1), Erwinia rhapontici (2)
	GC**C** **U**GA CCA AAG AGG GGG	uncultured bacterium (1)
	GC**G** **G**GA CCA AAG AGG GGG	Photobacterium profundum (14)
	GC**G** AGA CCA AAG **C**GG GGG	Bacteriophage (1), Pseudomonas flectens (2)
	GC**G** AGA CCA AAG **G**GG GGG	Enterobacter sp. (1)

	GC**G** AGA CCA AAG **U**GG GGG	Bacteriophage (2), Candidatus Hamiltonella defensa (17), Enterobacteriaceae bacterium (1), Erwinia sp. (1), Hamiltonella symbiont (6), male-killer in Chilomenes sexmaculatus (1), Pantoea agglomerans (7), Pantoea dispersa (2), Pantoea sp. (2), Pantoea stewartii (1), Photorhabdus asymbiotica (16), Photorhabdus luminescens (70), Photorhabdus sp. (5), Photorhabdus temperata (1), secondary endosymbiont (7), secondary symbiont (various) (10), uncultured bacterium (142), uncultured Enterobacteriaceae bacterium (1), uncultured Erwinia sp. (2), uncultured organism (1), uncultured Photorhabdus sp. (1)
	GC**U** **G**GA CCA AAG AGG GGG	uncultured bacterium (1)
	GC**U** AGA CCA AA**A** AGG GGG	uncultured Shigella sp. (1)
	GC**U** AGA CCA AAG **U**GG GGG	Candidatus Baumannia cicadellinicola (2), Pantoea sp. (1)
	GCA **G**GA CCA AA**A** AGG GGG	uncultured bacterium (1)
	GCA **G**GA CCA AAG **U**GG GGG	Klebsiella pneumoniae (1), Raoultella ornithinolytica (1), uncultured bacterium (3), uncultured Pantoea sp. (1)
	GCA **U**GA CC**G** AAG AGG GGG	Enterobacter sp. (1)
	GCA A**A**A CCA AA**A** AGG GGG	Escherichia coli (7), Salmonella enterica (2)
	GCA A**A**A CCA AAG **U**GG GGG	primary endosymbiont (1), secondary endosymbiont (1)
	GCA AG**C** **A**CA AAG AGG GGG	Escherichia coli (4), unidentified (1)
	GCA AG**G** CCA A**G**G AGG GGG	uncultured organism (1)
	GCA AG**G** CCA AAG **C**GG GGG	uncultured Enterobacteriaceae bacterium (1)
	GCA AG**G** CCA AAG **U**GG GGG	uncultured bacterium (3)
	GCA AGA **G**CA AAG **G**GG GGG	uncultured bacterium (1)
	GCA AGA **G**CA AAG **U**GG GGG	Aranicola sp. (9), bacterium (6), Brenneria nigrifluens (4), Brenneria sp. (7), Enterobacteriaceae bacterium (10), Erwinia persicina (5), Erwinia sp. (1), Erwinia toletana (9), Ewingella americana (4), Hafnia sp. (4), Klebsiella sp. (1), lobster gut bacterium (1), Margalefia venezuelensis (1), Nevskia ramosa (2), Pantoea oleae (3), Pantoea septica (1), Pantoea sp. (1), Rahnella aquatilis (10), Rahnella genomosp. (2), Rahnella sp. (36), Serratia grimesii (1), Tiedjeia arctica (1), uncultured Aeromonas sp. (1), uncultured bacterium (67), uncultured compost bacterium (1), uncultured Ewingella sp. (1), uncultured gamma proteobacterium (6), uncultured marine bacterium (1), uncultured Pantoea sp. (1), uncultured Rahnella sp. (7), uncultured Serratia sp. (7), uncultured Yersinia sp. (1), Yersinia aldovae (3), Yersinia aleksiciae (2), Yersinia enterocolitica (1), Yersinia frederiksenii (7), Yersinia intermedia (6), Yersinia kristensenii (15), Yersinia mollaretii (5), Yersinia pestis (156), Yersinia pseudotuberculosis (55), Yersinia rohdei (7), Yersinia ruckeri (21), Yersinia similis (5), Yersinia sp. (12)
	GCA AGA **G**CA AAG A**A**G GGG	Vibrio porteresiae (3), Vibrio sp. (1)
	GCA AGA **U**CA AAG **U**GG GGG	uncultured bacterium (1)

	GCA AGA C**AU** AAG AGG GGG	Enterobacter cloacae (1), Enterobacter sp. (1)
	GCA AGA C**A**A AAG **U**GG GGG	Klebsiella pneumoniae (1)
	GCA AGA C**U**A AAG **U**GG GGG	Sodalis glossinidius (7), uncultured Klebsiella sp. (1)
	GCA AGA C**U**A AAG A**C**G GGG	uncultured bacterium (2), uncultured Verrucomicrobia bacterium (10), Verrucomicrobiaceae bacterium (1)
	GCA AGA CC**C** **C**AG AGG GGG	Enterobacter sp. (1)
	GCA AGA CC**G** AAG **U**GG GGG	Klebsiella pneumoniae (1), Klebsiella sp. (1)
	GCA AGA CCA **G**AG **G**GG GGG	uncultured sheep mite bacterium (1)
	GCA AGA CCA **G**AG **U**GG GGG	Klebsiella sp. (2), uncultured bacterium (1), uncultured Klebsiella sp. (1)
	GCA AGA CCA **UC**G AGG GGG	uncultured bacterium (1)
	GCA AGA CCA A**C**G **C**GG GGG	unidentified thrip gut bacterium (1)
	GCA AGA CCA A**G**G **C**GG GGG	uncultured Enterobacteriaceae bacterium (1)
	GCA AGA CCA A**G**G **U**GG GGG	Klebsiella sp. (2), Rahnella sp. (1)
	GCA AGA CCA A**U**G **U**GG GGG	uncultured bacterium (1)
	GCA AGA CCA AA**A** **U**GG GGG	Candidatus Baumannia cicadellinicola (1)
	GCA AGA CCA AAG **UA**G GGG	uncultured Klebsiella sp. (1)
	GCA AGA CCA AAG **U**G**A** GGG	Edwardsiella tarda (1), endosymbiont (7)
	GCA AGA CCA AAG **U**GG **A**GG	Klebsiella sp. (2), primary endosymbiont (1), uncultured bacterium (2)
	GCA AGA CCA AAG **U**GG G**A**G	uncultured bacterium (2)
	GCA AGA CCA AAG **U**GG GG**A**	Serratia symbiotica (1), uncultured bacterium (4)
	GCA AGA CCA AAG **CA**G GGG	gamma proteobacterium (1), Panacagrimonas perspica (1), uncultured bacterium (3), uncultured soil bacterium (1)
	GCA AGA CCA AAG **CC**G GGG	uncultured Xanthomonadaceae bacterium (6)
	GCA AGA CCA AAG **CU**G GGG	gamma proteobacterium (3), Solimonas flava (1), Solimonas soli (3), Solimonas variicoloris (1), uncultured Acidobacteria bacterium (1), uncultured bacterium (4)
	GCA AGA CCA AAG **GA**G GGG	Enterobacter hormaechei (1)
	GCA AGA CCA AAG AGG **CC**G	uncultured bacterium (1)
	GCA AGA CCA AAG AGG **C**G**C**	Enterobacter cancerogenus (1)
	ANA **U**GA CCA AAG AGG GGG	mucus bacterium (1)
	G**N**A AGA **G**CA AAG **U**GG GGG	Rahnella aquatilis (2), Yersinia aleksiciae (1)
	GC**U** **C**GA CCA **N**AG AGG GGG	gamma proteobacterium (1)
	GCA AG**N** C**G**A A**C**G AGG GGG	uncultured bacterium (1)

Name of the probe: ENF 16S 191

Target organism: *Enterococcus faecalis*

Sequence of the probe: GAA AGC GCC TTT CAC TCT TAT GC

Date of *in-silico* assessment: September 2017

Mismatch count	Ribosomal RNA sequence corresponding to the probe	Matching with known sequences (without italics)
0 mm	GC AUA AGA GUG AAA GGC GCU UUC	bacterium (4), Enterococcus durans (1), Enterococcus faecalis (321), Enterococcus faecium (5), Enterococcus sp. (52), Lactococcus lactis (1), Lactobacillus plantarum (1), Photorhabdus luminescens (1), swine manure bacterium (2), uncultured bacterium (151), uncultured Enterococcus sp. (19), uncultured Firmicutes bacterium (1), uncultured microorganism (4), uncultured organism (112), Vibrio cholerae (1)
	GC AUA A**N**A GUG AAA GGC GCU UUC	Enterococcus faecalis (1)
	GC AUA AGA G**N**G AAA GGC GCU UUC	bacterium (1)
1 mm	G**G** AUA AGA GUG AAA GGC GCU UUC	Enterococcus sp. (1)
	G**U** AUA AGA GUG AAA GGC GCU UUC	uncultured Bacillus sp. (1), uncultured bacterium (3), uncultured Enterococcus sp. (1)
	GC **C**UA AGA GUG AAA GGC GCU UUC	Enterococcus faecalis (1)
	GC **G**UA AGA GUG AAA GGC GCU UUC	uncultured Enterococcus sp. (1)
	GC **U**UA AGA GUG AAA GGC GCU UUC	Enterococcus faecalis (1)
	GC AUA AG**G** GUG AAA GGC GCU UUC	uncultured organism (1)
	GC AUA AGA **A**UG AAA GGC GCU UUC	uncultured bacterium (1)
	GC AUA AGA GUG A**G**A GGC GCU UUC	uncultured bacterium (1)
	GC AUA AGA GUG AA**G** GGC GCU UUC	Enterococcus faecalis (1)
	GC AUA AGA GUG AAA **A**GC GCU UUC	uncultured organism (1)
	GC AUA AGA GUG AAA GGC GCU UU**G**	swine manure bacterium (1)
	GC AUA AGA GUG AAA GGC GCU UU**U**	uncultured bacterium (1)
2 mm	GC AUA AGA GUG A**G**A GGC GCU U**C**C	uncultured bacterium (1)

Name of the probe: ENU 23S 140 Beimfohr

Target organism: *Enterococcus faecium*

Sequence of the probe: TTC ACA CAA TCG TAA CAT CCT A

Date of *in-silico* assessment: August 2017

Mismatch count	**Ribosomal RNA sequence corresponding to the probe**	**Matching with known sequences (without italics)**
0 mm	U AGG AUG UUA CGA UUG UGU GAA	Enterococcus faecium (36), human gut metagenome (1)
1 mm		
2 mm	U AGG AUG UUA CGU UUG GGU GAA	Corynebacterium diphtheriae (1), Enterococcus durans (1), Enterococcus faecium (1), Enterococcus hirae (1)

Name of the probe: EGA 16S 141

Target organism: *Enterococcus gallinarum*

Sequence of the probe: ATT CAC AAC TGT GTA ACA TCC TAT

Date of *in-silico* assessment: August 2017

Mismatch count	Ribosomal RNA sequence corresponding to the probe	Matching with known sequences (without italics)
0 mm	AUA GGA UGU UAC ACA GUU GUG AAU	Enterococcus gallinarum (2), Enterococcus saccharolyticus (1)
1 mm		
2 mm		

Name of the probe: ENC 16S 221

Target organism: *Enterococcus* spp.

Sequence of the probe: CAC CGC GGG TCC ATC CAT CA

Date of *in-silico* assessment: February 2018

Mismatch count	**Ribosomal RNA sequence corresponding to the probe**	**Matching with known sequences (without italics)**
0 mm	UG AUG GAU GGA CCC GCG GUG	Abiotrophia para-adiacens (1), Bacillus sp. (1), bacterium (36), Catellicoccus marimammalium (1), Enterococcaceae bacterium (2), Enterococcus avium (19), Enterococcus azikeevi (1), Enterococcus caccae (2), Enterococcus camelliae (3), Enterococcus canis (4), Enterococcus casseliflavus (42), Enterococcus cecorum (11), Enterococcus columbae (5), Enterococcus devriesei (6), Enterococcus durans (184), Enterococcus faecalis (357), Enterococcus faecium (275), Enterococcus gallinarum (51), Enterococcus gilvus (9), Enterococcus haemoperoxidus (3), Enterococcus hawaiiensis (1), Enterococcus hirae (39), Enterococcus italicus (21), Enterococcus lactis (8), Enterococcus malodoratus (7), Enterococcus moraviensis (3), Enterococcus mundtii (37), Enterococcus pernyi (1), Enterococcus phoeniculicola (3), Enterococcus plantarum (3), Enterococcus pseudoavium (6), Enterococcus quebecensis (1), Enterococcus raffinosus (6), Enterococcus rivorum (5), Enterococcus rottae (1), Enterococcus saccharolyticus (8), Enterococcus silesiacus (6), Enterococcus sp. (178), Enterococcus sulfureus (7), Enterococcus termitis (2), Enterococcus thailandicus (12), Enterococcus ureasiticus (2), Enterococcus viikkiensis (5), Enterococcus villorum (4), Eubacterium sp. (1), Fusobacterium sp. (1), Granulicatella adiacens (10), Granulicatella elegans (7), Granulicatella para-adiacens (3), Granulicatella sp. (5), human gut metagenome (1), intestinal bacterium (2), Lactobacillus casei (3), Lactobacillus fermentum (1), Lactobacillus helveticus (1), Lactobacillus plantarum (1), Lactococcus lactis (3), Leuconostoc mesenteroides (1), marine bacterium (3), Photorhabdus luminescens (1), Rhizobium etli (1), rumen bacterium (9), swine fecal bacterium (9), swine manure bacterium (4), uncultured Abiotrophia sp. (2), uncultured Bacilli bacterium (1), uncultured Bacillus sp. (1), uncultured bacterium (724), uncultured compost bacterium (4), uncultured Enterococcaceae bacterium (1), uncultured Enterococcus sp. (59), uncultured Firmicutes bacterium (2), uncultured Granulicatella sp. (11), uncultured isopod gut bacterium (1), uncultured Lactobacillales bacterium (13), uncultured microorganism (4), uncultured organism (389), uncultured prokaryote (1),

		uncultured soil bacterium (1), uncultured Sphingomonas sp. (1), uncultured Streptococcaceae bacterium (2), uncultured Vibrio sp. (1), unidentified (2), Vibrio cholerae (1), Vibrio fluvialis (1)
	UG **N**UG GAU GGA CCC GCG GUG	Enterococcus casseliflavus (1), Enterococcus raffinosus (1)
	UG A**N**G GAU GGA CCC GCG GUG	bacterium (1)
	UG AUG **N**AU GGA CCC GCG GUG	Enterococcus faecalis (1)
	UG AUG GA**N** GGA CCC GCG GUG	bacterium (1)
	UG AUG GAU GGA CCC **N**CG GUG	bacterium (1)
	UG AUG GAU GGA CCC GCG G**N**G	Enterococcus durans (1)
	UG AUG GAU G**N**A CCC GCG G**N**G	Enterococcus faecalis (1)
	UG AUG GAU G**NN** CCC **N**CG GUG	Enterococcus saccharolyticus (1)
1 mm	**C**G AUG GAU GGA CCC GCG GUG	uncultured bacterium (1), uncultured organism (1)
	U**A** AUG GAU GGA CCC GCG GUG	uncultured Enterococcaceae bacterium (1), uncultured Enterococcus sp. (1)
	U**U** AUG GAU GGA CCC GCG GUG	Carnobacterium divergens (8), Carnobacterium maltaromaticum (1), Carnobacterium sp. (2), Enterococcus faecalis (1), uncultured bacterium (3), uncultured Carnobacterium sp. (1)
	UG **G**UG GAU GGA CCC GCG GUG	Enterococcus avium (1), Enterococcus gallinarum (1), Enterococcus raffinosus (1), Granulicatella (1), Granulicatella sp. (1), uncultured bacterium (14), uncultured Lactobacillales bacterium (1)
	UG **U**UG GAU GGA CCC GCG GUG	Granulicatella balaenopterae (1)
	UG A**A**G GAU GGA CCC GCG GUG	Enterococcus mundtii (1), Eubacterium sp. (1), uncultured bacterium (6), uncultured compost bacterium (2), uncultured Erysipelotrichi bacterium (1), uncultured Lactobacillales bacterium (1), uncultured Lactobacillus sp. (1)
	UG A**C**G GAU GGA CCC GCG GUG	Enterococcus faecalis (3), uncultured bacterium (35), uncultured Lactobacillales bacterium (1), uncultured organism (1)
	UG AU**A** GAU GGA CCC GCG GUG	uncultured bacterium (3)
	UG AUG **U**AU GGA CCC GCG GUG	uncultured bacterium (1)
	UG AUG G**G**U GGA CCC GCG GUG	uncultured bacterium (1)
	UG AUG GA**C** GGA CCC GCG GUG	uncultured bacterium (3)
	UG AUG GAU GG**G** CCC GCG GUG	Enterococcus faecium (1), Melissococcus plutonius (46), uncultured bacterium (3), uncultured organism (2), Vagococcus carniphilus (1), Vagococcus teuberi (3)
	UG AUG GAU GGA **U**CC GCG GUG	Enterococcus sp. (1)
	UG AUG GAU GGA CC**U** GCG GUG	bacterium (1), Enterococcus ratti (3), Enterococcus sp. (1), uncultured bacterium (1),

		uncultured Lactobacillales bacterium (1)
	UG AUG GAU GGA CCC **A**CG GUG	Enterococcus faecalis (1), Enterococcus gallinarum (1)
	UG AUG GAU GGA CCC G**U**G GUG	Enterococcus sp. (1)
	UG AUG GAU GGA CCC GC**C** GUG	Enterococcus faecalis (1)
	UG AUG GAU GGA CCC GCG **A**UG	uncultured bacterium (2), uncultured organism (1)
	UG AUG GAU GGA CCC GCG **C**UG	Enterococcus aquimarinus (2), Enterococcus inusitatus (3), Enterococcus sp. (3), swine manure pit bacterium (2), uncultured anaerobic bacterium (1), uncultured bacterium (29), uncultured Firmicutes bacterium (1), uncultured isopod gut bacterium (1), uncultured Lactobacillales bacterium (1), Vagococcus elongatus (1)
	UG AUG GAU GGA CCC GCG G**C**G	Atopobacter phocae (1), Granulicatella sp. (2), uncultured bacterium (1), uncultured organism (3)
	UG AUG GAU GGA CCC GCG GU**A**	uncultured organism (1)
	U**U** AUG GAU GGA CCC **N**CG GUG	Carnobacterium divergens (1)
	UG AUG G**C**U GG**N** CCC GCG GUG	bacterium (1), Tetragenococcus halophilus (2)
	UG AUG GAU GG**N** **U**CC GCG GUG	Granulicatella sp. (1)
2 mm	**AC** AUG GAU GGA CCC GCG GUG	uncultured bacterium (1)
	CG AUG GAU GGA CC**U** GCG GUG	uncultured bacterium (154)
	U**A** A**A**G GAU GGA CCC GCG GUG	Lactobacillus acetotolerans (3), Lactobacillus amylolyticus (3), Lactobacillus crispatus (1), Lactobacillus fructivorans (1), Lactobacillus hamsteri (3), Lactobacillus helveticus (1), Lactobacillus homohiochii (2), Lactobacillus intestinalis (5), Lactobacillus kalixensis (2), Lactobacillus kefiranofaciens (62), Lactobacillus sp. (3), synthetic construct (15), uncultured bacterium (66), uncultured Lactobacillus sp. (4), uncultured organism (4)
	U**A** AUG GAU GGA CCC GCG **C**UG	Enterococcaceae bacterium (1), uncultured bacterium (4), uncultured Enterococcus sp. (1), Vagococcus salmoninarum (3)
	U**A** AUG GAU GGA CCC GCG G**C**G	Antarctic bacterium (1), Carnobacterium maltaromaticum (32), Carnobacterium sp. (8), rainbow trout intestinal bacterium (1), uncultured bacterium (19), uncultured Carnobacterium sp. (6)
	U**C** AUG GAU GGA CC**U** GCG GUG	uncultured bacterium (1)
	U**C** **U**UG GAU GGA CCC GCG GUG	uncultured bacterium (4), uncultured Lactobacillus sp. (1)
	U**U** **C**UG GAU GGA CCC GCG GUG	Lactobacillus vaccinostercus (15), uncultured bacterium (1)
	U**U** **U**UG GAU GGA CCC GCG GUG	Lactobacillus ceti (1)
	U**U** A**A**G GAU GGA CCC GCG GUG	uncultured bacterium (2), uncultured Lactobacillus sp. (2)
	U**U** AU**A** GAU GGA CCC GCG GUG	bacterium (2), Macrococcus caseolyticus (12), Macrococcus sp. (2), Micrococcus luteus (1),

		uncultured bacterium (2)
	U**U** AUG GAU GGA CC**U** GCG GUG	Paenibacillus septentrionalis (1), Paenibacillus sp. (2), Paenibacillus xinjiangensis (1), uncultured bacterium (9), uncultured Paenibacillus sp. (1)
	U**U** AUG GAU GGA CCC GCG G**C**G	Alkalibacterium psychrotolerans (2), Alkalibacterium sp. (3), Bacillus cereus (1), Bacillus sp. (6), Bacillus subtilis (1), bacterium (5), Carnobacterium alterfunditum (3), Carnobacteriaceae bacterium (2), Carnobacterium funditum (3), Carnobacterium gallinarum (1), Carnobacterium jeotgali (1), Carnobacterium mobile (1), Carnobacterium pleistocenium (1), Carnobacterium sp. (37), Carnobacterium viridans (2), Clostridia bacterium (1), Isobaculum melis (1), Lactobacillus senioris (1), Lactobacillus sp. (1), Marinilactibacillus piezotolerans (4), Marinilactibacillus psychrotolerans (18), Marinilactibacillus sp. (5), Nostocoida limicola (3), Nostocoida sp. (1), Paenibacillus agarexedens (1), Paenibacillus glycanilyticus (13), Paenibacillus sp. (29), Trichococcus collinsii (14), Trichococcus flocculiformis (14), Trichococcus palustris (1), Trichococcus pasteurii (4), Trichococcus patagoniensis (1), Trichococcus sp. (13), uncultured Bacilli bacterium (3), uncultured Bacillus sp. (1), uncultured bacterium (237), uncultured Carnobacterium sp. (4), uncultured Firmicutes bacterium (4), uncultured Lactobacillaceae bacterium (1), uncultured Marinilactibacillus sp. (2), uncultured planctomycete (1), uncultured rumen bacterium (1), uncultured Trichococcus sp. (53), unidentified Hailaer soda lake bacterium (1)
	U**U** AUG GAU GGA CCC GCG GU**C**	Bacillus weihenstephanensis (1)
	UG **CA**G GAU GGA CCC GCG GUG	uncultured Lactobacillus sp. (5)
	UG **C**UG GA**G** GGA CCC GCG GUG	Tetragenococcus muriaticus (1), Tetragenococcus sp. (3)
	UG **C**UG GAU GGA CCC GCG G**C**G	Lactobacillus florum (3), uncultured Lactobacillus sp. (2)
	UG **G**UG GAU GG**G** CCC GCG GUG	Vagococcus carniphilus (1), Vagococcus penaei (1), Vagococcus teuberi (2)
	UG **G**UG GAU GGA CCC GCG **C**UG	Vagococcus sp. (1)
	UG **G**UG GAU GGA CCC GCG G**C**G	Bavariicoccus seileri (1), uncultured bacterium (3)
	UG **U**UG GAU GGA CCC GCG G**C**G	Lactobacillus rhamnosus (1)
	UG A**AA** GAU GGA CCC GCG GUG	uncultured bacterium (7)
	UG A**A**G GAU GG**U** CCC GCG GUG	Aerosphaera taetra (2), Facklamia ignava (1), Facklamia sp. (2), Globicatella sp. canine oral taxon (1), uncultured Aerosphaera sp. (1), uncultured bacterium (15), uncultured organism (2)
	UG A**A**G GAU GGA CCC GCG G**C**G	Lactobacillus brevis (1), Lactobacillus harbinensis (6), Lactobacillus perolens (1), Lactobacillus sp. (2), uncultured bacterium (2)
	UG A**A**G GAU GGA CCC GCG GU**C**	uncultured bacterium (4)
	UG A**CA** GAU GGA CCC GCG GUG	Sporolactobacillus sp. (3)
	UG A**C**G GA**C** GGA CCC GCG GUG	Enterococcus faecalis (1)

	UG A**G**G GAU GG**C** CCC GCG GUG	uncultured bacterium (1)
	UG A**G**G GAU GGA CCC GCG G**C**G	Lactobacillus perolens (3), Lactobacillus rhamnosus (1), swine effluent bacterium (1), Trichococcus sp. (1), uncultured bacterium (68)
	UG AU**A** GAU GG**G** CCC GCG GUG	Listeria sp. (4), uncultured bacterium (1)
	UG AU**A** GAU GGA CCC GCG G**A**G	uncultured bacterium (1)
	UG AUG G**C**U GG**C** CCC GCG GUG	Tetragenococcus halophilus (15)
	UG AUG G**C**U GG**U** CCC GCG GUG	bacterium (1), Tetragenococcus halophilus (28), Tetragenococcus koreensis (2), Tetragenococcus solitarius (4), Tetragenococcus sp. (17), uncultured bacterium (11), uncultured Tetragenococcus sp. (1)
	UG AUG G**G**U GGA CC**A** GCG GUG	uncultured bacterium (1)
	UG AUG GAU GG**G** CCC GCG **C**UG	swine fecal bacterium (1), uncultured bacterium (5), Vagococcus lutrae (8), Vagococcus sp. (4)
	UG AUG GAU GG**G** CCC GCG **U**UG	Bradyrhizobiaceae bacterium (1)
	UG AUG GAU GG**U** CC**G** GCG GUG	Enterococcus faecium (1)
	UG AUG GAU GGA **U**C**U** GCG GUG	uncultured bacterium (3)
	UG AUG GAU GGA CC**U** GCG G**C**G	Jeotgalicoccus sp. (1), uncultured bacterium (12), uncultured Jeotgalibacillus sp. (2)
	UG AUG GAU GGA CCC GCG **UC**G	uncultured bacterium (4)
	UG AUG GAU GGA CCC GCG G**GC**	Enterococcus faecalis (1)
	UG AUG GAU GGA CCC GCG G**GU**	bacterium (1)
	NC AUG GAU GGA CC**U** GCG GUG	uncultured bacterium (1)
	U**A** A**A**G GAU GGA CCC **N**CG GUG	Lactobacillus acetotolerans (1)
	U**A** AUG GAU GGA CCC **N**CG G**C**G	Carnobacterium maltaromaticum (2)
	U**U** **N**UG GAU GGA CCC GCG G**C**G	unidentified (1)
	U**U** A**N**G GAU GGA CC**U** GCG GUG	Paenibacillus sp. (1)
	U**U** AUG GAU GGA CCC GCG **NC**G	Bacillus cereus (2), Bacillus sp. (1)
	UG **C**UG GA**G** GG**N** CCC GCG GUG	Tetragenococcus muriaticus (1)
	UG AUG G**C**U GG**U** CCC GC**N** GUG	Tetragenococcus halophilus (1)

Name of the probe: ENC 176 23S kurz

Target organism: *Enterococcus* spp.

Sequence of the probe: CAG TTC TCT GCG TCT ACC TC

Date of *in-silico* assessment: October 2017

Mismatch count	**Ribosomal RNA sequence corresponding to the probe**	**Matching with known sequences (without italics)**
0 mm	GA GGU AGA CGC AGA GAA CUG	Carnobacterium maltaromaticum (1), Carnobacterium sp. (14), Catonella morbi (1), Corynebacterium diphtheria (1), Enterococcus asini (1), Enterococcus avium (2), Enterococcus casseliflavus (5), Enterococcus cecorum (1), Enterococcus columbae (1), Enterococcus dispar (1), Enterococcus durans (1), Enterococcus faecalis (62), Enterococcus faecium (38), Enterococcus gallinarum (2), Enterococcus hirae (1), Enterococcus italicus (1), Enterococcus malodoratus (1), Enterococcus mundtii (2), Enterococcus pseudoavium (1), Enterococcus raffinosus (1), Enterococcus saccharolyticus (2), Enterococcus sp. (1), Enterococcus sulfureus (1), human gut metagenome (2), Vibrio cholerae (1)
1 mm	AA GGU AGA CGC AGA GAA CUG GA GGA AGA CGC AGA GAA CUG GA GGU AAA CGC AGA GAA CUG GA GGU AGA CGC AGU GAA CUG	Facklamia languida (3) Melissococcus plutonius (9) Eremococcus coleocola (1) Lactobacillus fermentum (12), Lactobacillus reuteri (33), Lactobacillus suebicus (1)
2 mm	AA GGU AGA CGC GGA GAA CUG AA GGU AGA CGC AGG GAA CUG GC GGU AGA CGC AGU GAA CUG GA GGA AGA CGC AGG GAA CUG GA GGA AGA CGC AGU GAA CUG	Staphylococcus xylosus (1) Candidatus Arthromitus sp. (13) Lactobacillus coleohominis (1), Lactobacillus mucosae (1), Lactobacillus vaginalis (1) Aerococcus viridans (1), Heterocephalus glaber (1), Lactobacillus mali (1) human gut metagenome (1), Lactobacillus antri (1), Lactobacillus iners (13), Lactobacillus sp. (1), Streptococcus anginosus (3), Streptococcus australis (4), Streptococcus bovis (1), Streptococcus cristatus (4), Streptococcus equinus (4), Streptococcus gallolyticus (13), Streptococcus gordonii (4), Streptococcus infantarius (8), Streptococcus infantis (17), Streptococcus intermedius (2), Streptococcus macedonicus (6), Streptococcus mitis (33), Streptococcus oralis (15), Streptococcus parasanguinis (17), Streptococcus pasteurianus (5), Streptococcus peroris (1),

		Streptococcus phage (4), Streptococcus pneumoniae (649), Streptococcus pseudopneumoniae (1), Streptococcus sanguinis (25), Streptococcus salivarius (26), Streptococcus sp. (11), Streptococcus suis (56), Streptococcus thermophiles (30), Streptococcus vestibularis (9)
	GA GG**C** A**A**A CGC AGA GAA CUG	marine metagenome (1), uncultured gamma proteobacterium (1), uncultured proteobacterium (1)
	GA GG**G** AGA CGC AG**U** GAA CUG	Streptococcus cristatus (1)
	GA GGU A**C**A CGC AG**G** GAA CUG	Granulicatella adiacens (1)
	GA GGU AGA CGC **G**G**G** GAA CUG	Granulicatella elegans (1), Pediococcus cellicola (1), Pediococcus parvulus (1)
	GA GG**A** A**N**A CGC AG**U** GAA CUG	Streptococcus gallolyticus (7)

Name of the probe: ESC 16S 468

Target organism: *Escherichia coli*

Sequence of the probe: GCG GGT AAC GTC AAT GAG CAA AGG

Date of *in-silico* assessment: March 2018

Mismatch count	**Ribosomal RNA sequence corresponding to the probe**	**Matching with known sequences (without italics)**
0 mm	CCU UUG CUC AUU GAC GUU ACC CGC	Acinetobacter sp. (1), Ajellomyces capsulatus (1), bacterium (41), Brenneria alni (1), Brenneria nigrifluens (3), Capra hircus (1), Citrobacter sp. (1), Cloning vector (1), Clonorchis sinensis (1), Cronobacter sakazakii (12), Desulfovibrio sp. (2), endosymbiont of Sphenophorus levis (1), Enterobacter sp. (3), Enterobacteriaceae bacterium (4), Erwinia psidii (2), Erwinia rhapontici (1), Escherichia (1), Escherichia albertii (21), Escherichia coli (1978), Escherichia fergusonii (25), Escherichia sp. (44), Escherichia vulneris (2), estrogen-degrading bacterium (1), gamma proteobacterium (1), Hafnia alvei (1), human gut metagenome (1), iron-reducing enrichment clone (1), Lonsdalea quercina (2), marine metagenome (1), Oryza sativa Indica Group (1), Pantoea cypripedii (2), Paracoccus sp. (1), Pectobacterium carotovorum (3), Pectobacterium wasabiae (1), Photorhabdus luminescens (1), rumen bacterium enrichment culture clone (2), Shigella boydii (29), Shigella dysenteriae (40), Shigella flexneri (160), Shigella sonnei (49), Shigella sp. (30), Strongylocentrotus purpuratus (1), swine fecal bacterium (10), synthetic construct (11), uncultured bacterium (2864), uncultured beta proteobacterium (2), uncultured Enterobacteriaceae bacterium (17), uncultured Escherichia sp. (17), uncultured Firmicutes bacterium (2), uncultured gamma proteobacterium (30), uncultured Klebsiella sp. (1), uncultured marine bacterium (4), uncultured organism (1438), uncultured Parabacteroides sp. (2), uncultured prokaryote (3), uncultured proteobacterium (1), uncultured Shigella sp. (65), uncultured soil bacterium (2), unidentified (56), Vibrio sp. (1)
	C**N**U UUG CUC AUU GAC GUU ACC CGC	uncultured bacterium (1)
	CCU UU**N** CUC AUU GAC GUU ACC CGC	Escherichia coli (3), Shigella flexneri (1)
	CCU UUG CUC A**N**U GAC GUU ACC CGC	Escherichia coli (1)
	CCU UUG CUC AUU GAC GUU **N**CC CGC	Escherichia coli (1)

	CCU UUG CUC AUU GAC GUU ACC C**N**C	swine fecal bacterium (1)
1 mm	**A**CU UUG CUC AUU GAC GUU ACC CGC	uncultured gamma proteobacterium (1)
	GCU UUG CUC AUU GAC GUU ACC CGC	Shigella boydii (13)
	UCU UUG CUC AUU GAC GUU ACC CGC	Escherichia coli (2), uncultured bacterium (2)
	C**A**U UUG CUC AUU GAC GUU ACC CGC	uncultured bacterium (1)
	C**G**U UUG CUC AUU GAC GUU ACC CGC	uncultured bacterium (1)
	C**U**U UUG CUC AUU GAC GUU ACC CGC	Escherichia coli (2), Shigella sonnei (1), uncultured bacterium (2), uncultured organism (1)
	CC**A** UUG CUC AUU GAC GUU ACC CGC	uncultured bacterium (1)
	CC**C** UUG CUC AUU GAC GUU ACC CGC	uncultured bacterium (2), uncultured marine bacterium (1), uncultured organism (1)
	CCU **C**UG CUC AUU GAC GUU ACC CGC	uncultured bacterium (4), uncultured organism (2)
	CCU U**C**G CUC AUU GAC GUU ACC CGC	uncultured organism (2)
	CCU U**G**G CUC AUU GAC GUU ACC CGC	uncultured bacterium (3)
	CCU UU**A** CUC AUU GAC GUU ACC CGC	Desulfovibrio sp. (1), Escherichia coli (151), Escherichia fergusonii (1), Shigella dysenteriae (1), Shigella flexneri (28), Shigella sonnei (3), uncultured bacterium (114), uncultured Enterobacteriaceae bacterium (1), uncultured gamma proteobacterium (1), uncultured organism (33), uncultured Shigella sp. (1), unidentified (1)
	CCU UU**C** CUC AUU GAC GUU ACC CGC	uncultured bacterium (1)
	CCU UU**U** CUC AUU GAC GUU ACC CGC	Escherichia coli (1)
	CCU UUG **A**UC AUU GAC GUU ACC CGC	uncultured bacterium (1)
	CCU UUG **G**UC AUU GAC GUU ACC CGC	uncultured bacterium (2)
	CCU UUG **U**UC AUU GAC GUU ACC CGC	Escherichia albertii (1), Erwinia chrysanthemi (3), uncultured bacterium (5), uncultured organism (2)
	CCU UUG C**C**C AUU GAC GUU ACC CGC	uncultured bacterium (3), uncultured organism (4), uncultured Shigella sp. (1)
	CCU UUG CU**G** AUU GAC GUU ACC CGC	uncultured organism (1)
	CCU UUG CU**U** AUU GAC GUU ACC CGC	uncultured bacterium (5)
	CCU UUG CUC **C**UU GAC GUU ACC CGC	uncultured bacterium (1)
	CCU UUG CUC **G**UU GAC GUU ACC CGC	uncultured bacterium (2), uncultured organism (3)
	CCU UUG CUC A**A**U GAC GUU ACC CGC	uncultured bacterium (2)
	CCU UUG CUC A**C**U GAC GUU ACC CGC	uncultured bacterium (1), uncultured organism (2)
	CCU UUG CUC AU**A** GAC GUU ACC CGC	uncultured bacterium (1)
	CCU UUG CUC AU**C** GAC GUU ACC CGC	Escherichia coli (1), uncultured bacterium (5), uncultured organism (4)
	CCU UUG CUC AUU **A**AC GUU ACC CGC	Escherichia coli (2), uncultured bacterium (2), uncultured organism (3)
	CCU UUG CUC AUU G**G**C GUU ACC CGC	uncultured bacterium (5), uncultured organism (6)

	CCU UUG CUC AUU G**U**C GUU ACC CGC	uncultured bacterium (1)
	CCU UUG CUC AUU GA**U** GUU ACC CGC	uncultured bacterium (2), uncultured organism (1)
	CCU UUG CUC AUU GAC **A**UU ACC CGC	uncultured bacterium (1), uncultured organism (3)
	CCU UUG CUC AUU GAC **C**UU ACC CGC	uncultured organism (2)
	CCU UUG CUC AUU GAC **U**UU ACC CGC	uncultured bacterium (1), uncultured organism (2)
	CCU UUG CUC AUU GAC G**A**U ACC CGC	Escherichia coli (1)
	CCU UUG CUC AUU GAC G**C**U ACC CGC	uncultured Shigella sp. (2), uncultured organism (4), uncultured bacterium (1)
	CCU UUG CUC AUU GAC GU**A** ACC CGC	uncultured bacterium (1)
	CCU UUG CUC AUU GAC GU**C** ACC CGC	Shigella dysenteriae (1), uncultured bacterium (3)
	CCU UUG CUC AUU GAC GU**G** ACC CGC	uncultured organism (1)
	CCU UUG CUC AUU GAC GUU **C**CC CGC	uncultured bacterium (2), uncultured organism (1)
	CCU UUG CUC AUU GAC GUU **G**CC CGC	Strongyloides ratti (1), uncultured bacterium (2), uncultured organism (1)
	CCU UUG CUC AUU GAC GUU **U**CC CGC	uncultured bacterium (1)
	CCU UUG CUC AUU GAC GUU A**A**C CGC	uncultured bacterium (1), uncultured organism (1)
	CCU UUG CUC AUU GAC GUU A**U**C CGC	Shigella boydii (34), Shigella dysenteriae (1), Shigella Flexneri (1), uncultured bacterium (2), uncultured organism (1), uncultured Shigella sp. (1)
	CCU UUG CUC AUU GAC GUU AC**G** CGC	uncultured bacterium (1)
	CCU UUG CUC AUU GAC GUU AC**U** CGC	uncultured bacterium (6), uncultured organism (2)
	CCU UUG CUC AUU GAC GUU ACC **G**GC	uncultured bacterium (1)
	CCU UUG CUC AUU GAC GUU ACC **U**GC	Escherichia coli (1), uncultured bacterium (1), uncultured organism (1)
	CCU UUG CUC AUU GAC GUU ACC C**A**C	uncultured organism (5), uncultured bacterium (5)
	CCU UUG CUC AUU GAC GUU ACC C**C**C	Escherichia coli (4), uncultured bacterium (1), uncultured organism (1)
	CCU UUG CUC AUU GAC GUU ACC C**U**C	uncultured bacterium (1)
	CCU UUG CUC AUU GAC GUU ACC CG**U**	uncultured organism (1), Variovorax paradoxus (1)
	CCU U**GN** CUC AUU GAC GUU ACC CGC	uncultured bacterium (1)
	CCU UUG CUC AU**G** **N**AC GUU ACC CGC	uncultured bacterium (1)
2 mm	**AU**U UUG CUC AUU GAC GUU ACC CGC	uncultured bacterium (1)
	AC**C** UUG CUC AUU GAC GUU ACC CGC	bacterium (1), Enterobacter cloacae (2), Enterobacter sp. (1), Klebsiella oxytoca (1), uncultured bacterium (1), uncultured Klebsiella sp. (1)
	UCU UUG CUC AUU GAC GUU A**U**C CGC	Shigella boydii (1)
	CCU **C**UG **U**UC AUU GAC GUU ACC CGC	Erwinia chrysanthemi (1)

	CCU **C**UG CUC AUU GAC GUU **C**CC CGC	uncultured bacterium (1)
	CCU **C**UG CUC AUU GAC GUU AC**U** CGC	uncultured bacterium (1)
	CCU UU**A** C**C**C AUU GAC GUU ACC CGC	Dickeya zeae (1)
	CCU UU**A** CU**U** AUU GAC GUU ACC CGC	Shigella sp. (1)
	CCU UU**A** CUC AUU **A**AC GUU ACC CGC	Escherichia coli (1)
	CCU UU**A** CUC AUU GAC GUU ACC **U**GC	Escherichia sp. (3)
	CCU UU**A** CUC AUU GAC GUU ACC C**A**C	uncultured bacterium (1)
	CCU UU**A** CUC AUU GAC GUU ACC CG**U**	Escherichia coli (1)
	CCU UU**C** C**A**C AUU GAC GUU ACC CGC	uncultured bacterium (1)
	CCU UUG **G**UC AUU GAC GUU **C**CC CGC	uncultured bacterium (1)
	CCU UUG CU**G** AUU GAC GUU AC**U** CGC	Ewingella americana (1), uncultured Ewingella sp. (1)
	CCU UUG CUC **C**UU GAC **A**UU ACC CGC	uncultured organism (1)
	CCU UUG CUC **C**UU GAC GUU ACC C**C**C	uncultured bacterium (1)
	CCU UUG CUC A**C**U GAC GUU ACC C**A**C	uncultured organism (1)
	CCU UUG CUC AUU G**G**C **C**UU ACC CGC	uncultured bacterium (1)
	CCU UUG CUC AUU GA**G** GUU AC**U** CGC	uncultured bacterium (1)
	CCU UUG CUC AUU GA**U** GUU A**A**C CGC	uncultured organism (1)
	CCU UUG CUC AUU GAC **A**U**C** ACC CGC	uncultured bacterium (1)
	CCU UUG CUC AUU GAC **C**UU **G**CC CGC	uncultured bacterium (1)
	CCU UUG CUC AUU GAC GUU **G**CC C**A**C	uncultured organism (1)
	CCU UUG CUC AUU GAC GUU **UA**C CGC	uncultured bacterium (1)
	CCU UUG CUC AUU GAC GUU ACC C**CG**	uncultured bacterium (2)
	CCU UUG CUC AUU GAC GUU ACC C**UG**	Escherichia coli (1)
	CCU UUG CUC AU**G** **A**AC GUU A**N**C CGC	uncultured bacterium (1)

Name of the probe: Klpn23S

Target organism: *Klebsiella pneumoniae*

Sequence of the probe: CCT ACA CAC CAG CGT GCC

Date of *in-silico* assessment: January 2018

Mismatch count	Ribosomal RNA sequence corresponding to the probe	Matching with known sequences (without italics)
0 mm	GGC ACG CUG GUG UGU AGG	Enterobacter aerogenes (1), human gut metagenome (1), Klebsiella pneumoniae (55), Klebsiella sp. (2), Klebsiella variicola (8)
1 mm	GGC ACG CUG AUG UGU AGG	Enterobacter cloacae (2), Enterobacter mori (2), unidentified (1)
	GGC ACG CUG GUA UGU AGG	secondary endosymbiont (various) (1)
	GGC ACG CUG GUG CGU AGG	Citrobacter rodentium (1)
2 mm	GGC ACA CUG GUA UGU AGG	secondary endosymbiont (various) (1)
	GGC ACG CCG GUG UGU ACG	Marinobacter aquaeolei (3)
	GGC ACG CUG AUA UGU AGG	Ajellomyces capsulatus (1), Citrobacter freundii (2), Citrobacter koseri (7), Citrobacter sp. (1), Citrobacter youngae (1), Cloning vector (1), Clonorchis sinensis (1), Dermacentor variabilis (2), Enterobacter aerogenes (9), Escherichia albertii (6), Enterobacter asburiae (7), Enterobacter cloacae (27), Escherichia coli (1949), Escherichia fergusonii (9), Enterobacter hormaechei (1), Escherichia sp. (2), human gut metagenome (6), Klebsiella oxytoca (2), Mus musculus (2), Oryza sativa (2), Phyllostachys edulis (1), Shigella boydii (47), Shigella dysenteriae (37), Shigella flexneri (7), Shigella sonnei (33), Shigella sp. (1), Strongyloides ratti (3), synthetic construct (5), unidentified (26)
	GGC ACG CUG AUC UGU AGG	Escherichia coli (1)
	GGC ACG CUG GCA UGU AGG	Candidatus Moranella endobia (2), Candidatus Steffania adelgidicola (1), Edwardsiella ictaluri (18), Edwardsiella tarda (3), Oryza sativa (1), secondary endosymbiont (various) (4), Serratia symbiotica (6), Sodalis glossinidius (9)
	GGC ACG CUG GCG CGU AGG	Cenchrus americanus (2), Citrobacter rodentium (6), Enterobacteriaceae bacterium (1), Erwinia amylovora (7), Erwinia billingiae (7), Erwinia pyrifoliae (14), Erwinia sp. (6), Erwinia tasmaniensis (7), Oryza sativa (3), Pantoea ananatis (29), Pantoea stewartii (7), Pantoea sp. (2), Pantoea vagans (7), Pectobacterium wasabiae (7), Rahnella aquatilis (7), Rahnella sp. (7), Serratia odorifera (1),

	GGC ACG CUG GUG **A**GU A**A**G	Serratia proteamaculans (7), Serratia sp. (21), unidentified phage (7) secondary endosymbiont (various) (1)

Name of the probe: Psae Ulm 16S 182

Target organism: *Pseudomonas aeruginosa*

Sequence of the probe: CCA CTT TCT CCC TCA GGA CG

Date of *in-silico* assessment: April 2018

Mismatch count	Ribosomal RNA sequence corresponding to the probe	Matching with known sequences (without italics)
0 mm	CG UCC UGA GGG AGA AAG UGG	Bacillus sp. (1), bacterium (14), Bordetella sp. (1), Enterobacter sp. (3), Klebsiella pneumoniae (1), Klebsiella sp. (1), marine bacterium (1), Pseudomonas aeruginosa (746), Pseudomonas fluorescens (2), Pseudomonas mosselii (1), Pseudomonas otitidis (2), Pseudomonas putida (1), Pseudomonas sp. (182), Pseudomonas tropicalis (4), Rhodococcus erythropolis (1), Rhodococcus sp. (2), Shigella sp. (1), Streptomyces sp. (1), uncultured bacterium (3317), uncultured beta proteobacterium (3), uncultured gamma proteobacterium (10), uncultured microorganism (10), uncultured Pseudomonas sp. (91), unidentified (3)
	CG UC**N** UGA GGG AGA AAG UGG	uncultured bacterium (4)
	CG UCC UGA GG**N** AGA AAG UGG	uncultured bacterium (2)
	C**N** UCC UGA GGG A**N**A AAG UGG	Pseudomonas aeruginosa (1)
1 mm	**A**G UCC UGA GGG AGA AAG UGG	Pseudomonas aeruginosa (1)
	UG UCC UGA GGG AGA AAG UGG	uncultured bacterium (1)
	C**A** UCC UGA GGG AGA AAG UGG	uncultured bacterium (2)
	C**U** UCC UGA GGG AGA AAG UGG	Pseudomonas aeruginosa (1), uncultured bacterium (1)
	CG **A**CC UGA GGG AGA AAG UGG	uncultured bacterium (1)
	CG **C**CC UGA GGG AGA AAG UGG	uncultured bacterium (9), uncultured Rhodocyclaceae bacterium (1)
	CG U**A**C UGA GGG AGA AAG UGG	uncultured bacterium (1)
	CG U**U**C UGA GGG AGA AAG UGG	uncultured bacterium (2)
	CG UC**U** UGA GGG AGA AAG UGG	Pseudomonas aeruginosa (1), uncultured bacterium (1)
	CG UCC **C**GA GGG AGA AAG UGG	uncultured bacterium (8)
	CG UCC **G**GA GGG AGA AAG UGG	uncultured bacterium (3)
	CG UCC U**A**A GGG AGA AAG UGG	actinobacterium (1), Burkholderia sp. (1), Duganella sp. (3), endosymbiont (1), gamma proteobacterium (1),

		Herbaspirillum sp. (1), Janthinobacterium sp. (1), Oxalicibacterium sp. (1), Paederus fuscipes endosymbiont (1), Paederus melanurus endosymbiont (1), Paederus riparius endosymbiont (1), Paederidus ruficollis endosymbiont (1), Paederus sabaeus endosymbiont (1), Pseudomonas citronellolis (2), Pseudoxanthomonas icgebensis (1), Teredinibacter turnerae (9), uncultured bacterium (9), uncultured beta proteobacterium (1)
	CG UCC UG**C** GGG AGA AAG UGG	Pseudomonas sp. (3)
	CG UCC UG**G** GGG AGA AAG UGG	uncultured bacterium (10)
	CG UCC UGA G**A**G AGA AAG UGG	uncultured bacterium (2)
	CG UCC UGA GG**A** AGA AAG UGG	uncultured bacterium (2)
	CG UCC UGA GG**U** AGA AAG UGG	Pseudomonas sp. (1)
	CG UCC UGA GGG **G**GA AAG UGG	Pseudomonas aeruginosa (2), Pseudomonas sp. (1), uncultured bacterium (5), uncultured Pseudomonas sp. (3)
	CG UCC UGA GGG AG**C** AAG UGG	uncultured bacterium (1)
	CG UCC UGA GGG AG**G** AAG UGG	uncultured bacterium (4)
	CG UCC UGA GGG AG**U** AAG UGG	uncultured bacterium (1)
	CG UCC UGA GGG AGA **C**AG UGG	uncultured bacterium (1)
	CG UCC UGA GGG AGA **G**AG UGG	uncultured bacterium (7)
	CG UCC UGA GGG AGA **U**AG UGG	Pseudomonas aeruginosa (1)
	CG UCC UGA GGG AGA A**C**G UGG	uncultured bacterium (2)
	CG UCC UGA GGG AGA A**G**G UGG	uncultured bacterium (4)
	CG UCC UGA GGG AGA AAG **A**GG	uncultured bacterium (1)
	CG UCC UGA GGG AGA AAG **C**GG	Acidithiobacillus sp. (3), Acidithiobacillus thiooxidans (2), Azoarcus indigens (3), Azoarcus sp. (2), bacterium (4), Bergeriella denitrificans (4), beta proteobacterium (5), Candidatus Dactylopiibacterium carminicum (2), Denitratisoma sp. (2), denitrifying bacterium (9), Eikenella corrodens (2), Eikenella sp. (1), iron-reducing bacterium enrichment culture clone (2), Methylocystis sp. (1), Methyloversatilis sp. (2), Methyloversatilis universalis (4), Rhodocyclaceae bacterium (5), Simonsiella muelleri (5), Sphingomonas sp. (1), Thauera (3), Thauera aromatica (9), Thauera butanivorans (3), Thauera chlorobenzoica (4), Thauera linaloolentis (2), Thauera mechernichensis (1), Thauera selenatis (2), Thauera sp. (5), Thiobacter sp. (3), Uliginosibacterium gangwonense (2), Ultramicrobacter hongkongensis (1), uncultured Acidithiobacillus sp. (2), uncultured anaerobic bacterium (7), uncultured Azoarcus sp. (3), uncultured bacterium (501), uncultured beta proteobacterium (73), uncultured compost bacterium (1), uncultured Eikenella sp. (1) uncultured gamma proteobacterium (2), uncultured marine bacterium (3),

		uncultured Methyloversatilis sp. (3), uncultured organism (2), uncultured prokaryote (2), uncultured Rhodocyclaceae bacterium (55), uncultured Rubrobacteridae bacterium (1), uncultured rumen bacterium (1), uncultured sludge bacterium (12), uncultured soil bacterium (91), uncultured Thauera sp. (3), uncultured Zoogloea sp. (14), unidentified (81), unidentified proteobacterium (1), Zoogloea caeni (2), Zoogloea sp. (2)
	CG UCC UGA GGG AGA AAG **G**GG	Pseudomonas aeruginosa (1)
	CG UCC UGA GGG AGA AAG U**A**G	uncultured bacterium (1)
	CG UCC UGA GGG AGA AAG U**C**G	Pseudomonas aeruginosa (1), uncultured Pseudomonas sp. (3)
	CG UCC UGA GGG AGA AAG UG**A**	uncultured bacterium (1)
	CG **N**CC UGA GGG **G**GA AAG UGG	Thiobacillus thioparus (2)
	CG UCC U**NC** GGG AGA AAG UGG	Pseudomonas stutzeri (1)
2 mm	**A**G UCC UGA GGG AGA AAG **C**GG	Acidiphilium sp. (1), Acidithiobacillus caldus (1), Acidithiobacillus sp. (6), bacterium (1), Georgfuchsia toluolica (1), Sutterella parvirubra (3), uncultured Acidithiobacillus sp. (8), uncultured bacterium (12), uncultured beta proteobacterium (4)
	UG UCC UGA GGG AGA AAG **C**GG	uncultured bacterium (2)
	C**A** UCC UGA GGG AGA AAG **C**GG	uncultured bacterium (2)
	C**U** UCC UGA GGG **U**GA AAG UGG	uncultured bacterium (1)
	CG **A**CC UGA GGG **C**GA AAG UGG	uncultured bacterium (1), uncultured proteobacterium (1), uncultured Ralstonia sp. (3)
	CG **A**CC UGA GGG **G**GA AAG UGG	uncultured bacterium (2)
	CG **A**CC UGA GGG **U**GA AAG UGG	Bacterium (19), beta proteobacterium (4), blood disease bacterium (6), Burkholderia sp. (4), Cupriavidus metallidurans (19), Cupriavidus necator (1), Cupriavidus sp. (7), Formivibrio citricus (1), iron-reducing bacterium enrichment culture clone (1), iron-reducing enrichment clone (3), Kingella sp. (1), Pseudomonas sp. (2), Ralstonia detusculanense (1), Ralstonia insidiosa (3), Ralstonia mannitolilytica (12), Ralstonia pickettii (32), Ralstonia solanacearum (146), Ralstonia sp. (90), Ralstonia syzygii (6), uncultured Acinetobacter sp. (4), uncultured bacterium (338), uncultured beta proteobacterium (63), uncultured Bradyrhizobiaceae bacterium (1), uncultured Bradyrhizobium sp. (1), uncultured Brevundimonas sp. (1), uncultured Burkholderia sp. (5), uncultured Burkholderiaceae bacterium (31), uncultured Burkholderiales bacterium (4), uncultured Cupriavidus sp. (8), uncultured gamma proteobacterium (3), uncultured Mycoplana sp. (1), uncultured Nitrosomonadaceae bacterium (1), uncultured organism (1), uncultured prokaryote (1), uncultured Propionibacterium sp. (1), uncultured proteobacterium (29), uncultured Ralstonia sp. (1010),

		uncultured Rhodocyclaceae bacterium (2), uncultured soil bacterium (7), uncultured Sphingomonas sp. (2), uncultured Xanthomonadaceae bacterium (2)
	CG **A**CC UGA GGG AGA AAG **C**GG	Burkholderia sp. (9), Sterolibacterium denitrificans (1), uncultured bacterium (2), uncultured beta proteobacterium (1), uncultured Burkholderia sp. (7), uncultured Thiobacillus sp. (6)
	CG **C**CC UGA GGG **G**GA AAG UGG	Aminomonas aminovorus (1), Andreprevotia chitinilytica (2), Azoarcus communis (1), Azoarcus sp. (15), bacterium (6), beta proteobacterium (8), Burkholderia sp. (3), Chitiniphilus sp. (2), Chitinolyticbacter meiyuanensis (1), Chromobacterium aquaticum (1), Chromobacterium haemolyticum (1), Chromobacterium piscinae (1), Chromobacterium sp. (87), Chromobacterium subtsugae (1), Chromobacterium violaceum (3), Deefgea chitinilytica (1), Deefgea rivuli (1), Deefgea sp. (1), drinking water bacterium (1), Herbaspirillum sp. (1), iron-reducing bacterium enrichment culture clone (3), Jeongeupia naejangsanensis (1), Jeongeupia sp. (2), Laribacter sp. (1), Leeia oryzae (1), Limnobacter litoralis (6), Limnobacter sp. (9), Limnobacter thiooxidans (3), Methylobacillus flagellatus (4), Methylobacillus glycogenes (1), Methylobacillus sp. (3), Methylomonas sp. (1), Microvirgula aerodenitrificans (5), Neisseriaceae bacterium (1), Nitrincola sp. (1), Polynucleobacter rarus (1), Polynucleobacter sp. (2), Pseudoburkholderia malthae (1), Silvimonas terrae (2), Thiobacillus denitrificans (5), Thiobacillus sp. (6), Thiobacillus thioparus (10), Thiomonas sp. (1), uncultured Aminomonas sp. (1), uncultured Azoarcus sp. (3), uncultured bacterium (356), uncultured beta proteobacterium (75), uncultured Burkholderia sp. (1), uncultured compost bacterium (1), uncultured gamma proteobacterium (1), uncultured Hydrogenophilaceae bacterium (3), uncultured Hydrogenophilales bacterium (2), uncultured Limnobacter sp. (10), uncultured marine bacterium (4), uncultured Microvirgula sp. (2), uncultured organism (174), uncultured prokaryote (13), uncultured proteobacterium (2), uncultured Pseudomonadales bacterium (1), uncultured rape rhizosphere bacterium (1), uncultured Rhodocyclaceae bacterium (6), uncultured Silvimonas sp. (1), uncultured soil bacterium (124), uncultured Thiobacillus sp. (18), uncultured Thiothrix sp. (1), uncultured Zoogloea sp. (2), unidentified (1), Vibrio sp. (1), Vogesella sp. (1), Zoogloea ramigera (4), Zoogloea resiniphila (1), Zoogloea sp. (5)
	CG **C**CC UGA GGG **U**GA AAG UGG	uncultured beta proteobacterium (1)
	CG **C**CC UGA GGG AG**G** AAG UGG	uncultured bacterium (1)
	CG **C**CC UGA GGG AGA AAG **C**GG	uncultured Bordetella sp. (1), uncultured soil bacterium (1), unidentified (3)
	CG **G**CC UGA GGG **U**GA AAG UGG	uncultured proteobacterium (1), uncultured Ralstonia sp. (3)
	CG U**A**C UGA GG**U** AGA AAG UGG	bacterium (1), freshwater bacterium (2), Pseudogulbenkiania sp. (1), uncultured bacterium (21), uncultured beta proteobacterium (1), Vogesella indigofera (1), Vogesella perlucida (2), Vogesella sp. (4)

	CG UC**G** **C**GA GGG AGA AAG UGG	Pseudomonas aeruginosa (1)
	CG UC**U** UGA G**A**G AGA AAG UGG	Stenoxybacter acetivorans (7), uncultured bacterium (1)
	CG UCC **C**GA GGG AGA AAG **A**GG	uncultured gamma proteobacterium (10)
	CG UCC **C**GA GGG AGA AAG **C**GG	uncultured gamma proteobacterium (1)
	CG UCC U**AC** GGG AGA AAG UGG	Azomonas agilis (2), Azomonas macrocytogenes (3), Azomonas sp. (1), Azorhizophilus paspali (4), Azotobacter beijerinckii (5), Azotobacter chroococcum (31), Azotobacter salinestris (5), Azotobacter sp. (4), Azotobacter vinelandii (34), Bacillus sp. (1), bacterium (38), Beijerinckia indica (1), fenthion-degrading bacterium (1), Flavobacterium lutescens (1), gamma proteobacterium (12), glacial ice bacterium (1), Gram-negative bacterium (1), Halomonadaceae bacterium (1), Halomonas sp. (8), Lysobacter niabensis (1), Lysobacter sp. (12), Lysobacter ximonensis (2), marine bacterium (2), Marinospirillum celere (1), Marinospirillum sp. (1), mucus bacterium (2), nitrogen-fixing bacterium (1), Oceanospirillaceae bacterium (1), proteobacterium (1), Pseudomonas (1), Pseudomonas abietaniphila (1), Pseudomonas acetoxians (2), Pseudomonas aeruginosa (4), Pseudomonas alcaligenes (1), Pseudomonas alcaliphila (1), Pseudomonas andersonii (6), Pseudomonas azotifigens (1), Pseudomonas benzenivorans (1), Pseudomonas citronellolis (16), Pseudomonas delhiensis (1), Pseudomonas duriflava (1), Pseudomonas ficuserectae (1), Pseudomonas fluorescens (48), Pseudomonas fragi (1), Pseudomonas fulva (1), Pseudomonas graminis (1), Pseudomonas guezennei (2), Pseudomonas indica (3), Pseudomonas knackmussii (1), Pseudomonas luteola (6), Pseudomonas marincola (4), Pseudomonas mendocina (4), Pseudomonas monteilii (5), Pseudomonas mosselii (1), Pseudomonas oleovorans (5), Pseudomonas oryzihabitans (19), Pseudomonas otitidis (5), Pseudomonas pachastrellae (6), Pseudomonas panipatensis (2), Pseudomonas plecoglossicida (15), Pseudomonas pohangensis (1), Pseudomonas protegens (4), Pseudomonas pseudoalcaligenes (4), Pseudomonas psychrotolerans (4), Pseudomonas putida (22), Pseudomonas resinovorans (3), Pseudomonas salinarum (1), Pseudomonas saponiphila (2), Pseudomonas segetis (1), Pseudomonas sp. (529), Pseudomonas stutzeri (154), Pseudomonas syringae (1), Pseudomonas thermotolerans (1), Rhizobium sp. (1), Silanimonas lenta (2), uncultured alpha proteobacterium (1), uncultured Azoarcus sp. (1), uncultured bacterium (349), uncultured beta proteobacterium (4), uncultured Burkholderia sp. (1), uncultured compost bacterium (1), uncultured deep-sea bacterium (8), uncultured gamma proteobacterium (39), uncultured Gram-negative bacterium (1), uncultured Lysobacter sp. (18), uncultured Marinobacterium sp. (1), uncultured organism (1), uncultured proteobacterium (2), uncultured Pseudomonadaceae bacterium (7), uncultured Pseudomonas sp. (57), uncultured sediment bacterium (3), uncultured soil bacterium (9),

		uncultured Xanthomonadaceae bacterium (1), uncultured Xanthomonas sp. (3), unidentified (20), Xanthomonadaceae bacterium (2), Xanthomonas sp. (1)
	CG UCC U**AU** GGG AGA AAG UGG	Pseudomonas aeruginosa (1), uncultured bacterium (5)
	CG UCC U**A**A GGG AGA AAG **A**GG	uncultured bacterium (2)
	CG UCC U**A**A GGG AGA AAG **C**GG	Chitinibacter sp. (1), Congregibacter litoralis (2), Duganella violaceinigra (1), Eikenella corrodens (2), gamma proteobacterium (22), Pseudomonas sp. (1), uncultured bacterium (14), uncultured Ectothiorhodospiraceae bacterium (8), uncultured Eikenella sp. (2), uncultured gamma proteobacterium (2), uncultured Xanthomonadaceae bacterium (1)
	CG UCC U**A**A GGG AGA AAG **G**GG	Halochromatium sp. (2), Lamprobacter modestohalophilus (1), uncultured bacterium (4)
	CG UCC U**CC** GGG AGA AAG UGG	Unidentified (1)
	CG UCC U**U**A GGG AGA AAG **A**GG	marine metagenome (2), uncultured bacterium (55), uncultured gamma proteobacterium (8), uncultured marine bacterium (5), uncultured marine microorganism (1), uncultured SAR86 cluster bacterium (1)
	CG UCC U**U**A GGG AGA AAG **C**GG	uncultured soil bacterium (1)
	CG UCC UG**G** GGG AGA AAG **C**GG	uncultured bacterium (2), uncultured beta proteobacterium (1)
	CG UCC UG**U** GGG AGA AAG **A**GG	gamma proteobacterium endosymbiont (1)
	CG UCC UG**U** GGG AGA AAG **C**GG	uncultured bacterium (6), uncultured beta proteobacterium (1)
	CG UCC UG**U** GGG AGA AAG UG**C**	Pseudomonas stutzeri (2)
	CG UCC UGA **A**GG AGA AAG **C**GG	uncultured bacterium (1)
	CG UCC UGA **C**G**U** AGA AAG UGG	uncultured bacterium (1)
	CG UCC UGA G**A**G AGA AAG **C**GG	uncultured bacterium (1)
	CG UCC UGA GGG **G**GA AAG **C**GG	Neisseria sp. (2), Thiobacter subterraneus (1), uncultured bacterium (21), uncultured prokaryote (1), uncultured soil bacterium (3), unidentified beta proteobacterium (1)
	CG UCC UGA GGG **UC**A AAG UGG	Pseudomonas sp. (1)
	CG UCC UGA GGG A**A**A AAG **C**GG	uncultured soil bacterium (1)
	CG UCC UGA GGG A**U**A AAG **C**GG	uncultured beta proteobacterium (1)
	CG UCC UGA GGG AG**C** **C**AG UGG	Pseudomonas sp. (1)
	CG UCC UGA GGG AG**G** AAG **C**GG	uncultured bacterium (1)
	CG UCC UGA GGG AGA **G**AG **C**GG	unidentified (3)
	CG UCC UGA GGG AGA A**G**G **C**GG	denitrifying bacterium (1), uncultured bacterium (1)
	CG UCC UGA GGG AGA AA**C** **C**GG	Acidithiobacillus thiooxidans (1)
	CG UCC UGA GGG AGA AAG **CA**G	Azoarcus sp. (1), Azovibrio restrictus (2), Azovibrio sp. (5), beta proteobacterium (2), Neisseria sp. (1), Rhodocyclales bacterium (2), uncultured Azovibrio sp. (2), uncultured bacterium (43),

		uncultured beta proteobacterium (1), uncultured gamma proteobacterium (2), uncultured marine bacterium (4), uncultured marine microorganism (1), uncultured Pseudomonadaceae bacterium (1), uncultured Rhodocyclaceae bacterium (1), uncultured soil bacterium (2), uncultured Stenotrophomonas sp. (1), uncultured Thiobacillus sp. (4)
	CG **A**CC UGA GGG **N**GA AAG **C**GG	Cupriavidus taiwanensis (1)
	CG **A**CC UGA GGG **U**GA AAG U**N**G	Ralstonia syzygii (1)
	CG **C**CC **C**GA GGG **N**GA AAG UGG	uncultured Rhodocyclaceae bacterium (1)
	CG **N**CC U**AC** GGG AGA AAG UGG	uncultured bacterium (1)
	CG **N**CC UGA GGG **G**GA AAG **G**GG	uncultured Rhodocyclaceae bacterium (1)
	CG UCC U**AC** GG**N** AGA AAG UGG	Pseudomonas sp. (1)
	CG UCC U**AC** GGG AGA AAG **N**GG	Pseudomonas sp. (1)
	CG UCC U**AN** GGG AGA AAG **C**GG	Chromohalobacter israelensis (1), Chromohalobacter marismortui (1), Fulvimonas soli (1)

Name of the probe: Sal 23S 331

Target organism: *Salmonella* spp.

Sequence of the probe: TGC GCT TTT GTG TAC GGG GCT

Date of *in-silico* assessment: January 2018

Mismatch count	Ribosomal RNA sequence corresponding to the probe	Matching with known sequences (without italics)
0 mm	AGC CCC GUA CAC AAA AGC GCA	Enterobacteria phage (7), Phage Gifsy (7), Salmonella enterica (273)
1 mm	AGC CCC GUA CAC AAA AG**U** GCA	Escherichia coli (1)
	AGC CCC GUA CAC AAA AGC G**U**A	Salmonella enterica (3)
2 mm	AG**U** CCC GUA CAC AAA AG**U** GCA	Citrobacter freundii (1), Citrobacter sp. (1)
	AGC CCC GUA CAC **G**AA A**A**C GCA	Lutiella nitroferrum (1), Pseudogulbenkiania sp. (8)
	AGC CCC GUA CAC **G**AA AG**G** GCA	Carnimonas nigrificans (1)
	AGC CCC GUA CAC **G**AA AGC **A**CA	Enterobacter asburiae (2)
	AGC CCC GUA CAC **G**AA AGC G**A**A	Kangiella koreensis (2)
	AGC CCC GUA CAC AAA A**AG** GCA	Erwinia amylovora (7), Erwinia pyrifoliae (14), Erwinia sp. (7), unidentified phage (7)
	AGC CCC GUA CAC AAA A**AU** GCA	Ajellomyces capsulatus (1), Cloning vector (1), Clonorchis sinensis (1), Escherichia albertii (6), Escherichia coli (1835), Escherichia fergusonii (9), Escherichia sp. (3), Erwinia tasmaniensis (7), human gut metagenome (3), Oryza sativa (1), Phyllostachys edulis (1), Serratia symbiotica (6), Shigella boydii (48), Shigella dysenteriae (37), Shigella flexneri (164), Shigella sonnei (25), Shigella sp. (1), Strongyloides ratti (1), synthetic construct (5), unidentified (26)
	AGC CCC GUA CAC AAA A**C**C GC**U**	Oceanimonas sp. (1)
	AGC CCC GUA CAC AAA A**UA** GCA	Escherichia coli (2)
	AGC CCC GUA CAC AAA A**UU** GCA	Escherichia coli (1)

Name of the probe: Sal Yer 23S 1705 Komp

Target organism: none, prevention of cross-reaction with organisms other than *Salmonella* spp.

Sequence of the probe: T CAC CTA CAT ATC AGC GTG C

Date of *in-silico* assessment: January 2018

Mismatch count	**Ribosomal RNA sequence corresponding to the probe**	**Matching with known sequences (without italics)**
0 mm	G CAC GCU GAU AUG UAG GUG A	Ajellomyces capsulatus (1), Citrobacter freundii (2), Citrobacter koseri (7), Citrobacter sp. (1), Citrobacter youngae (1), Cloning vector (1), Clonorchis sinensis (1), Dermacentor variabilis (2), Enterobacter aerogenes (9), Enterobacter asburiae (7), Enterobacter cloacae (27), Enterobacter hormaechei (1), Escherichia albertii (6), Escherichia coli (1949), Escherichia fergusonii (9), Escherichia sp. (2), human gut metagenome (6), Klebsiella oxytoca (2), Mus musculus (2), Oryza sativa (2), Phyllostachys edulis (1), Shigella boydii (47), Shigella dysenteriae (37), Shigella flexneri (7), Shigella sonnei (33), Shigella sp. (1), Strongyloides ratti (3), synthetic construct (5), unidentified (26)
1 mm	G C**G**C GCU GAU AUG UAG GUG A	Escherichia coli (1)
	G C**U**C GCU GAU AUG UAG GUG A	Escherichia coli (1)
	G CA**U** GCU GAU AUG UAG GUG A	Shigella dysenteriae (1)
	G CAC GC**C** GAU AUG UAG GUG A	Escherichia coli (1)
	G CAC GCU **A**AU AUG UAG GUG A	Candidatus Blochmannia vafer (1), Escherichia coli (1)
	G CAC GCU **U**AU AUG UAG GUG A	Escherichia coli (1)
	G CAC GCU G**G**U AUG UAG GUG A	secondary endosymbiont (various) (1)
	G CAC GCU GA**C** AUG UAG GUG A	Cronobacter sakazakii (7), Cronobacter turicensis (4), Salmonella bongori (8), Salmonella enterica (26)
	G CAC GCU GAU **C**UG UAG GUG A	Escherichia coli (1)
	G CAC GCU GAU **G**UG UAG GUG A	Enterobacter cloacae (2), Enterobacter mori (2), unidentified (1)
	G CAC GCU GAU A**C**G UAG GUG A	Escherichia coli (33), Klebsiella oxytoca (1), Shigella boydii (1), Shigella flexneri (173), Shigella sonnei (1)
	G CAC GCU GAU A**G**G UAG GUG A	Cenchrus americanus (1)
	G CAC GCU GAU AUG UA**A** GUG A	Escherichia coli (1)
	G CAC GCU GAU AUG UAG **A**UG A	Escherichia coli (3)
2 mm	G CA**U** GCU GAU A**C**G UAG GUG A	Shigella flexneri (1)

	G CAC GCU G**GC** AUG UAG GUG A	Candidatus Steffania adelgidicola (1), Edwardsiella ictaluri (18), Edwardsiella tarda (3), Oryza sativa (1), secondary endosymbiont (various) (2), Serratia symbiotica (6)
	G CAC GCU G**G**U **G**UG UAG GUG A	Enterobacter aerogenes (1), human gut metagenome (1), Klebsiella pneumoniae (55), Klebsiella sp. (2), Klebsiella variicola (7)
	G CAC GCU GA**C** A**C**G UAG GUG A	Enterobacteria phage (7), Phage Gifsy (7), Salmonella bongori (1), Salmonella enterica (280), Yersinia enterocolitica (1)
	G CAC GCU GA**C** AUG UA**A** GUG A	Cronobacter turicensis (3)
	G CAC GCU GAU A**A**G UA**A** GUG A	Klebsiella oxytoca (2)
	G CAC GCU GAU AUG UA**A** GU**A** A	secondary endosymbiont (various) (2)

Name of the probe: SalYer 23S 1705

Target organism: *Salmonella* spp.

Sequence of the probe: CTT CAC CTA CGT GTC AGC G

Date of *in-silico* assessment: January 2018

Mismatch count	Ribosomal RNA sequence corresponding to the probe	Matching with known sequences (without italics)
0 mm	C GCU GAC ACG UAG GUG AAG	Enterobacteria phage (7), Phage Gifsy (7), Salmonella bongori (1), Salmonella enterica (280), Yersinia enterocolitica (1)
1 mm	C GCU G**G**C ACG UAG GUG AAG	Escherichia hermannii (1), Edwardsiella tarda (16)
	C GCU GA**U** ACG UAG GUG AAG	Escherichia coli (33), Klebsiella oxytoca (1), Shigella boydii (1), Shigella flexneri (173), Shigella sonnei (1)
	C GCU GAC A**U**G UAG GUG AAG	Cronobacter sakazakii (7), Cronobacter turicensis (4), Salmonella bongori (8), Salmonella enterica (26)
2 mm	**U** GCU GA**U** ACG UAG GUG AAG	Shigella flexneri (1)
	C GCU G**G**C **G**CG UAG GUG AAG	Cenchrus americanus (1), Citrobacter rodentium (6), Enterobacteriaceae bacterium (1), Erwinia amylovora (7), Erwinia billingiae (7), Erwinia pyrifoliae (14), Erwinia sp. (6), Erwinia tasmaniensis (7), Oryza sativa (3), Pantoea ananatis (29), Pectobacterium wasabiae (7), Rahnella aquatilis (7), Rahnella sp. (7), Serratia odorifera (1), Serratia proteamaculans (7), Serratia sp. (21), unidentified phage (7)
	C GCU G**G**C A**U**G UAG GUG AAG	Edwardsiella ictaluri (18), Edwardsiella tarda (3), Oryza sativa (1), secondary endosymbiont (various) (2)
	C GCU G**G**C ACG UAG GUG **G**AG	primary endosymbiont (various) (5)
	C GCU GA**U** A**G**G UAG GUG AAG	Cenchrus americanus (1)
	C GCU GA**U** A**U**G UAG GUG AAG	Ajellomyces capsulatus (1), Citrobacter freundii (2), Citrobacter koseri (7), Citrobacter sp. (1), Citrobacter youngae (1), Clonorchis sinensis (1), Dermacentor variabilis (2), Enterobacter aerogenes (9), Enterobacter asburiae (7), Enterobacter cloacae (27), Enterobacter hormaechei (1), Escherichia albertii (6), Escherichia coli (1846), Escherichia fergusonii (9), Escherichia sp. (2), human gut metagenome (6), Klebsiella oxytoca (2), Mus musculus (2), Oryza sativa (2), Phyllostachys edulis (1), Shigella boydii (47), Shigella dysenteriae (37), Shigella flexneri (7), Shigella sonnei (33), Shigella sp. (1), Strongyloides ratti (3), unidentified (8)
	C GCU GA**U** ACG UA**A** GUG AAG	Klebsiella oxytoca (2)
	C GCU GAC A**U**G UA**A** GUG AAG	Cronobacter turicensis (3)

	C GCU GA**U** A**U**G UAG GUG A**N**G	Escherichia coli (1)

Name of the probe: Komp Sal 23S 331

Target organism: none, prevention of cross-reaction with organisms other than *Salmonella* spp.

Sequence of the probe: G TGC ATT TTT GTG TAC GGG GC

Date of *in-silico* assessment: January 2018

Mismatch count	**Ribosomal RNA sequence corresponding to the probe**	**Matching with known sequences (without italics)**
0 mm	GC CCC GUA CAC AAA AAU GCA C	Ajellomyces capsulatus (1), Cloning vector (1), Clonorchis sinensis (1), Erwinia tasmaniensis (7), Escherichia albertii (6), Escherichia coli (1835), Escherichia fergusonii (9), Escherichia sp. (3), human gut metagenome (3), Oryza sativa (1), Phyllostachys edulis (1), Serratia symbiotica (6), Shigella boydii (48), Shigella dysenteriae (37), Shigella flexneri (164), Shigella sonnei (25), Shigella sp. (1), Strongyloides ratti (1), synthetic construct (5), unidentified (26)
1 mm	**C**C CCC GUA CAC AAA AAU GCA C	Escherichia coli (2)
	G**U** CCC GUA CAC AAA AAU GCA C	Citrobacter freundii (1), Dickeya dadantii (7), Escherichia coli (1), Pectobacterium atrosepticum (7), Pectobacterium carotovorum (8), Pectobacterium wasabiae (7), Rahnella aquatilis (7), Rahnella sp. (7)
	GC **U**CC GUA CAC AAA AAU GCA C	Escherichia coli (2)
	GC CCC **A**UA CAC AAA AAU GCA C	Escherichia coli (2)
	GC CCC G**C**A CAC AAA AAU GCA C	Escherichia coli (1)
	GC CCC GU**C** CAC AAA AAU GCA C	Escherichia coli (2)
	GC CCC GUA C**G**C AAA AAU GCA C	Escherichia coli (1)
	GC CCC GUA CAC **G**AA AAU GCA C	Enterobacter cloacae (7), Escherichia coli (3), Salmonella bongori (9)
	GC CCC GUA CAC **U**AA AAU GCA C	human gut metagenome (3), Klebsiella oxytoca (4), Oryza sativa (2)
	GC CCC GUA CAC A**G**A AAU GCA C	Escherichia coli (2)
	GC CCC GUA CAC AA**G** AAU GCA C	Escherichia coli (1)
	GC CCC GUA CAC AA**U** AAU GCA C	Escherichia coli (1)
	GC CCC GUA CAC AAA **G**AU GCA C	Escherichia coli (1)
	GC CCC GUA CAC AAA A**G**U GCA C	Escherichia coli (1)
	GC CCC GUA CAC AAA A**U**U GCA C	Escherichia coli (1)
	GC CCC GUA CAC AAA AA**G** GCA C	Erwinia amylovora (7), Erwinia pyrifoliae (14), Erwinia sp. (7), unidentified phage (7)
	GC CCC GUA CAC AAA AAU **A**CA C	Escherichia coli (28), Shigella dysenteriae (1), Shigella flexneri (8), Shigella sonnei (8)

	GC CCC GUA CAC AAA AAU G**U**A C	Shigella flexneri (1)
	GC CCC GUA CAC AAA AAU GC**G** C	Escherichia coli (2)
	GC CCC GUA CAC AAA AAU GC**U** C	Escherichia coli (1)
2 mm	**AG** CCC GUA CAC AAA AAU GCA C	Escherichia coli (4), Shigella flexneri (1)
	CU CCC GUA CAC AAA AAU GCA C	Erwinia billingiae (7)
	CC CC**G** GUA CAC AAA AAU GCA C	Escherichia coli (1)
	G**U** CCC GUA CAC **C**AA AAU GCA C	Enterobacter aerogenes (11), human gut metagenome (2), Klebsiella pneumoniae (55), Klebsiella sp. (1), Klebsiella variicola (7), Yersinia pestis (141), Yersinia pseudotuberculosis (30)
	G**U** CCC GUA CAC **G**AA AAU GCA C	Citrobacter rodentium (1), Enterobacter cloacae (2), Enterobacter hormaechei (1), Oryza sativa (1)
	G**U** CCC GUA CAC **U**AA AAU GCA C	Serratia sp. (17)
	G**U** CCC GUA CAC AAA AAU GCA **U**	Yersinia enterocolitica (21)
	GC CCC GUA CAC **U**AA AAU GCA **U**	Serratia odorifera (1)
	GC CCC GUA CAC AAA A**C**U **A**CA C	Shigella flexneri (1)
	GC CCC GUA CAC AAA A**GC** GCA C	Salmonella enterica (2)
	GC CCC GUA CAC AAA A**UA** GCA C	Escherichia coli (2)
	CC CC**G** **N**UA CAC AAA AAU GCA C	Strongyloides ratti (1)
	GC CCC GUA CAC AAA A**GC** GCA **N**	Salmonella enterica (1)

Name of the probe: Stalle 16S

Target organism: *Staphylococcus* spp.

Sequence of the probe: TCC TCC ATA TCT CTG CGC

Date of *in-silico* assessment: April 2018

Mismatch count	Ribosomal RNA sequence corresponding to the probe	Matching with known sequences (without italics)
0 mm	GCG CAG AGA UAU GGA GGA	Acinetobacter johnsonii (1), Arctic sea ice bacterum (1), Arthrobacter nitroguajacolicus (1), Bacillales bacterium (3), Bacillus cereus (1), Bacillus pumilus (1), Bacillus sp. (5), bacterium (41), Brevibacterium sp. (1), Deinococcus sp. (1), endophytic bacterium (1), Firmicutes bacterium (1), Geobacillus stearothermophilus (1), haloalkaliphilic bacterium (1), human oral bacterium (1), Jeotgalicoccus (1), Jeotgalicoccus aerolatus (2), Jeotgalicoccus coquinae (2), Jeotgalicoccus halophilus (2), Jeotgalicoccus halotolerans (3), Jeotgalicoccus huakuii (1), Jeotgalicoccus marinus (1), Jeotgalicoccus nanhaiensis (1), Jeotgalicoccus pinnipedialis (1), Jeotgalicoccus psychrophilus (4), Jeotgalicoccus sp. (5), low G+C Gram-positive bacterium (1), Macrococcus bovicus (1), Macrococcus brunensis (4), Macrococcus carouselicus (1), Macrococcus caseolyticus (12), Macrococcus equipercicus (3), Macrococcus hajekii (1), Macrococcus lamae (1), Macrococcus sp. (5), marine bacterium (1), marine sediment bacterium (1), Micrococcus luteus (2), Micrococcus sp. (1), Nosocomiicoccus ampullae (2), Planomicrobium okeanokoites (1), Prevotella dentalis (1), Pseudomonas sp. (1), Psychrobacter pulmonis (1), psychrophilic marine bacterium (1), rainbow trout intestinal bacterium (1), rumen bacterium (1), Salinicoccus albus (1), Salinicoccus alkaliphilus (3), Salinicoccus carnicancri (1), Salinicoccus halodurans (3), Salinicoccus hispanicus (1), Salinicoccus iranensis (1), Salinicoccus jeotgali (1), Salinicoccus kekensis (1), Salinicoccus kunmingensis (1), Salinicoccus roseus (13), Salinicoccus salitudinis (1), Salinicoccus salsiraiae (1), Salinicoccus siamensis (2), Salinicoccus sp. (18), Serratia sp. (1), soil bacterium (1), Spirochaeta sp. (1), Staphylococcaceae bacterium (5), Staphylococcus agnetis (13), Staphylococcus arlettae (22), Staphylococcus aureus (504), Staphylococcus auricularis (5), Staphylococcus capitis (20), Staphylococcus caprae (8), Staphylococcus carnosus (12), Staphylococcus chromogenes (2), Staphylococcus cohnii (28), Staphylococcus condimenti (2), Staphylococcus croceolyticus (1), Staphylococcus delphini (18), Staphylococcus devriesei (9), Staphylococcus epidermidis (259), Staphylococcus equorum (29), Staphylococcus felis (2), Staphylococcus fleurettii (1), Staphylococcus gallinarum (8), Staphylococcus haemolyticus (49),

		Staphylococcus hominis (39), Staphylococcus hyicus (1), Staphylococcus intermedius (3), Staphylococcus kloosii (5), Staphylococcus lentus (7), Staphylococcus lugdunensis (18), Staphylococcus lutrae (1), Staphylococcus massiliensis (1), Staphylococcus microti (2), Staphylococcus muscae (1), Staphylococcus nepalensis (4), Staphylococcus pasteuri (71), Staphylococcus pettenkoferi (8), Staphylococcus phage (5), Staphylococcus piscifermentans (5), Staphylococcus pseudintermedius (22), Staphylococcus pseudolugdunensis (3), Staphylococcus rostri (2), Staphylococcus saccharolyticus (2), Staphylococcus saprophyticus (82), Staphylococcus schleiferi (5), Staphylococcus sciuri (34), Staphylococcus simiae (2), Staphylococcus simulans (2), Staphylococcus sp. (474), Staphylococcus succinus (13), Staphylococcus vitulinus (3), Staphylococcus warneri (33), Staphylococcus xylosus (17), Streptomyces brasiliensis (1), swine fecal bacterium (3), swine manure bacterium (1), synthetic construct (10), uncultured Bacilli bacterium (1), uncultured Bacillus sp. (5), uncultured bacterium (2866), uncultured Clostridium sp. (1), uncultured Firmicutes bacterium (5), uncultured Gram-positive bacterium (2), uncultured Jeotgalibacillus sp. (2), uncultured Jeotgalicoccus sp. (2), uncultured Macrococcus sp. (1), uncultured microorganism (15), uncultured organism (274), uncultured prokaryote (1), uncultured rumen bacterium (2), uncultured Salinicoccus sp. (1), uncultured soil bacterium (2), uncultured Staphylococcaceae bacterium (5), uncultured Staphylococcus sp. (286), unidentified (21), unidentified Hailaer soda lake bacterium (1)
	GCG CA**N** AGA UAU GGA GGA	bacterium (1), Salinicoccus sp. (1), Staphylococcus aureus (1), Staphylococcus epidermidis (1), Staphylococcus pasteuri (1), uncultured bacterium (1), uncultured Staphylococcus sp. (5)
	GCG CAG AGA U**N**U GGA GGA	Staphylococcus hominis (1), Staphylococcus sp. (2)
	GCG CAG AGA UA**N** GGA GGA	uncultured Staphylococcus sp. (1)
	GCG CAG AGA UAU G**N**A GGA	uncultured Staphylococcus sp. (3)
	GCG CAG AGA UAU GGA **N**GA	Salinicoccus sp. (1)
	GCG CAG AGA UAU GGA GG**N**	Staphylococcus hominis (1)
	GC**N** **N**AG AGA UAU GGA GGA	Bacillus cereus (1)
	GC**N** CA**N** AGA UAU GG**N** GGA	Salinicoccus marinus (1)
	GCG CAG AGA U**NN** **N**GA GGA	uncultured bacterium (1)
1 mm	**A**CG CAG AGA UAU GGA GGA	uncultured bacterium (1), uncultured Staphylococcus sp. (1)
	CCG CAG AGA UAU GGA GGA	Staphylococcus succinus (1), uncultured Firmicutes bacterium (1)
	GC**A** CAG AGA UAU GGA GGA	Staphylococcus aureus (2), uncultured bacterium (4), uncultured organism (1)

	GC**C** CAG AGA UAU GGA GGA	Bacterium (1)
	GCG **U**AG AGA UAU GGA GGA	Acetobacter pasteurianus (6), Acinetobacter sp. (1), Alicyclobacillus pohliae (4), Anoxybacillus toebii (1), ant fungus garden metagenome (1), Arsenophonus endosymbiont (1), Arthrobacter sp. (1), Bacillaceae bacterium (38), Bacillus aeolius (2), Bacillus amyloliquefaciens (1), Bacillus anthracis (316), Bacillus cereus (1239), Bacillus coagulans (2), Bacillus cytotoxicus (16), Bacillus gaemokensis (1), Bacillus licheniformis (1), Bacillus marcorestinctum (1), Bacillus megaterium (1), Bacillus mycoides (70), Bacillus nealsonii (1), Bacillus phage (24), Bacillus pseudomycoides (19), Bacillus pumilus (4), Bacillus samanii (5), Bacillus sp. (1442), Bacillus subtilis (20), Bacillus thermocloaceae (1), Bacillus thuringiensis (528), Bacillus weihenstephanensis (50), bacterium (62), Brevibacillus brevis (9), bromate-reducing bacterium (1), Budvicia sp. (1), Burkholderia cepacia (1), Burkholderia gladioli (1), Candidatus Riesia pediculicola (13), Candidatus Tremblaya phenacola (1), Cerasibacillus quisquiliarum (2), Chlamydomonas reinhardtii (12), Clostridium acetobutylicum (1), Clostridium sp. (2), Enterobacter cloacae (1), Geobacillus stearothermophilus (2), glacial ice bacterium (4), groundwater biofilm bacterium (1), Halomonas sp. (1), intestinal bacterium (1), Klebsiella pneumoniae (1), low G+C Gram-positive bacterium (6), Lysinibacillus fusiformis (1), marine bacterium (1), Nitrosomonas cryotolerans (2), Oceanobacillus caeni (3), Oceanobacillus sp. (3), Paenibacillus larvae (1), Pseudomonas sp. (1), rumen bacterium (1), Serratia marcescens (1), Staphylococcus epidermidis (1), Streptococcus agalactiae (1), Streptomyces sp. (1), swine manure bacterium (1), Thermobacillus composti (3), Thermobacillus sp. (9), Thermobacillus xylanilyticus (1), Turicibacter sanguinis (3), uncultured anaerobic bacterium (1), uncultured Bacillaceae bacterium (4), uncultured Bacillus sp. (74), uncultured bacterium (682), uncultured Bacteroidetes bacterium (1), uncultured beta proteobacterium (2), uncultured compost bacterium (42), uncultured Firmicutes bacterium (4), uncultured Geobacillus sp. (2), uncultured low G+C Gram-positive bacterium (1), uncultured marine bacterium (1), uncultured microorganism (1), uncultured Nitrosomonas sp. (2), uncultured organism (25), uncultured Paenibacillaceae bacterium (1), uncultured rumen bacterium (6), uncultured soil bacterium (1), uncultured Staphylococcus sp. (5), uncultured Turicibacter sp. (5), uncultured Ureibacillus sp. (2), unidentified (2), unidentified eubacterium clone (1), Ureibacillus composti (2), Ureibacillus sp. (6), Ureibacillus suwonensis (6), Ureibacillus terrenus (1), Ureibacillus thermophilus (4), Ureibacillus thermosphaericus (31), Virgibacillus halophilus (2), Virgibacillus sp. (4)
	GCG C**C**G AGA UAU GGA GGA	Staphylococcus epidermidis (1), uncultured bacterium (1)
	GCG C**G**G AGA UAU GGA GGA	uncultured bacterium (6)
	GCG C**U**G AGA UAU GGA GGA	Staphylococcus aureus (1), uncultured bacterium (1), uncultured organism (1)
	GCG CA**A** AGA UAU GGA GGA	Staphylococcus aureus (1), Staphylococcus epidermidis (1), Staphylococcus sp. (2), uncultured bacterium (5),

		uncultured Staphylococcus sp. (14)
	GCG CA**C** AGA UAU GGA GGA	Staphylococcus arlettae (1), Staphylococcus aureus (1), Staphylococcus capitis (1), Staphylococcus sp. (1)
	GCG CA**U** AGA UAU GGA GGA	Staphylococcus sp. (1), uncultured bacterium (2)
	GCG CAG **G**GA UAU GGA GGA	Staphylococcus sp. (1), uncultured bacterium (4), uncultured Staphylococcus sp. (2)
	GCG CAG **U**GA UAU GGA GGA	uncultured bacterium (1)
	GCG CAG A**A**A UAU GGA GGA	uncultured bacterium (2), uncultured Staphylococcus sp. (1)
	GCG CAG A**U**A UAU GGA GGA	uncultured bacterium (238), uncultured delta proteobacterium (1), uncultured Erysipelotrichaceae bacterium (1)
	GCG CAG AG**G** UAU GGA GGA	uncultured bacterium (5)
	GCG CAG AG**U** UAU GGA GGA	uncultured bacterium (2)
	GCG CAG AGA **C**AU GGA GGA	bacterium (1), Staphylococcus sp. (1), uncultured bacterium (1), uncultured Staphylococcus sp. (1)
	GCG CAG AGA U**C**U GGA GGA	Acinetobacter radioresistens (1), Acinetobacter sp. (1), uncultured bacterium (6), uncultured Enterobacter sp. (2), uncultured gamma proteobacterium (1), uncultured Staphylococcus sp. (1)
	GCG CAG AGA U**G**U GGA GGA	Bacillus flexus (1), Burkholderia tropica (1), denitrifying bacterium (1), Pandoraea sp. (1), SMC proteobacterium (2), uncultured Bacillus sp. (2), uncultured bacterium (17), uncultured organism (5), uncultured soil bacterium (1)
	GCG CAG AGA U**U**U GGA GGA	Bacillales bacterium (1), uncultured bacterium (1)
	GCG CAG AGA UA**C** GGA GGA	uncultured bacterium (3)
	GCG CAG AGA UA**G** GGA GGA	uncultured bacterium (1), uncultured rumen bacterium (1)
	GCG CAG AGA UAU G**A**A GGA	uncultured bacterium (4)
	GCG CAG AGA UAU GG**C** GGA	Bacterium (1)
	GCG CAG AGA UAU GG**G** GGA	uncultured bacterium (4), uncultured Staphylococcus sp. (1)
	GCG CAG AGA UAU GGA **A**GA	uncultured bacterium (157), uncultured organism (2), uncultured Staphylococcus sp. (2)
	GCG CAG AGA UAU GGA G**A**A	Staphylococcus sp. (1), uncultured bacterium (6)
	GCG CAG AGA UAU GGA GG**C**	uncultured bacterium (1), uncultured Staphylococcus sp. (1)
	GCG CAG AGA UAU GGA GG**G**	Staphylococcus aureus (1), uncultured bacterium (8), uncultured Staphylococcus sp. (1)
	NCG **U**AG AGA UAU GGA GGA	Bacillus thuringiensis (1)
	G**N**G **U**AG AGA UAU GGA GGA	uncultured soil bacterium (1)
	GCG **N**AG A**U**A UAU GGA GGA	Lactococcus lactis (1)
	GCG **N**AG AGA U**C**U GGA GGA	Acinetobacter lwoffii (1), uncultured Acinetobacter sp. (1)
	GCG **N**AG AGA U**G**U GGA GGA	uncultured soil bacterium (2)
	GCG **U**A**N** AGA UAU GGA GGA	Bacillus cereus (1), Bacillus sp. (6), uncultured Bacillus sp. (3), uncultured Firmicutes bacterium (1)

	GCG UAG ANA UAU GGA GGA	uncultured bacterium (1)
	GCG UAG AGA UNU GGA GGA	Acinetobacter sp. (2), Bacillus cereus (1), Bacillus sp. (5), Cronobacter turicensis (1), Enhydrobacter sp. (1), uncultured Acinetobacter sp. (5), uncultured Exiguobacterium sp. (1)
	GCG CAG ANA UCU GGA GGA	uncultured bacterium (1)
	GNG UAG AGA UNU GGA GGA	Acinetobacter calcoaceticus (2), uncultured soil bacterium (1)
	GCN NAG AGA UGU GGA GGA	uncultured soil bacterium (2)
	GCN UAN AGA UAU GGA GGA	Bacillus cereus (1)
	GCN CAA ANA UAU GGA GGA	uncultured Staphylococcus sp. (1)
	GCG NNG AGA UGU GGA GGA	uncultured soil bacterium (2)
	GCG UAN AGA UNU GGA GGA	bacterium (1)
	GCG UAG ANA UNU GGA GGA	uncultured Acinetobacter sp. (1)
	GCG UAG AGA UNU GGA NGA	uncultured Paenibacillus sp. (1)
	GCG UAG AGA UNU GGA GGN	uncultured Acinetobacter sp. (1)
	GCG CAA AGA UAU GGA NGN	uncultured Staphylococcus sp. (1)
	GCG CAG AUA UNN GGA GGA	uncultured bacterium (2)
	GCG CAG AGU UNN GGA GGA	uncultured bacterium (1)
	GCG CAG AGA UCN NGA GGA	uncultured bacterium (1)
2 mm	ACG UAG AGA UAU GGA GGA	uncultured bacterium (1)
	ACG CAG AGA UAG GGA GGA	Halomonas halophila (1)
	GAU CAG AGA UAU GGA GGA	Bacillus cereus (1)
	GAG UAG AGA UAU GGA GGA	Bacillus sp. (1)
	GCA UAG AGA UAU GGA GGA	Bacillus sp. (1), uncultured bacterium (4)
	GCA CAG AUA UAU GGA GGA	uncultured bacterium (1)
	GCA CAG AGA UCU GGA GGA	uncultured bacterium (1)
	GCC CAA AGA UAU GGA GGA	Staphylococcus xylosus (1), uncultured Staphylococcus sp. (1)
	GCC CAU AGA UAU GGA GGA	Staphylococcus aureus (1)
	GCG AGG AGA UAU GGA GGA	uncultured bacterium (1)
	GCG AAG AUA UAU GGA GGA	uncultured bacterium (3)
	GCG AAG AGA UCU GGA GGA	Erwinia chrysanthemi (1), uncultured bacterium (2)
	GCG AAG AGA UGU GGA GGA	Burkholderia tropica (1), uncultured bacterium (2), uncultured Burkholderia sp. (1), uncultured organism (2)
	GCG AAG AGA UUU GGA GGA	uncultured bacterium (2)
	GCG GAG AUA UAU GGA GGA	uncultured bacterium (2)

	GCG **G**AG AGA U**G**U GGA GGA	Methyloversatilis universalis (1)
	GCG **G**AG AGA U**U**U GGA GGA	uncultured bacterium (1)
	GCG **G**AG AGA UAU GGA GG**G**	uncultured bacterium (1)
	GCG **U**A**A** AGA UAU GGA GGA	Bacillus alkalitolerans (1), Bacillus cereus (6), Bacillus sp. (5), Candidatus Phytoplasma mali (1), Candidatus Phytoplasma pyri (8), Chinaberry yellows phytoplasma (3), Peach yellow leafroll phytoplasma (1), Phytoplasma sp. (1), uncultured Bacillus sp. (10), uncultured bacterium (1), unidentified mollicute (2)
	GCG **U**A**C** AGA UAU GGA GGA	Bacillus cereus (3), Bacillus sp. (1), uncultured bacterium (1)
	GCG **U**AG A**A**A UAU GGA GGA	Bacillus sp. (1), Bacillus thuringiensis (1), Enterococcus faecium (1), uncultured bacterium (1), uncultured organism (1)
	GCG **U**AG A**C**A UAU GGA GGA	Bacillus sp. (1), Granulicatella sp. (2), uncultured bacterium (7), uncultured organism (2)
	GCG **U**AG A**U**A UAU GGA GGA	Abiotrophia defectiva (4), Abiotrophia para-adiacens (1), Abiotrophia sp. (2), Aerococcaceae bacterium (1), Aerococcus suis (1), Aerococcus urinaehominis (1), Aerosphaera taetra (2), Agrobacterium tumefaciens (1), Alkalibacterium iburiense (3), Alkalibacterium indicireducens (3), Alkalibacterium kapii (8), Alkalibacterium olivapovliticus (4), Alkalibacterium pelagium (2), Alkalibacterium psychrotolerans (2), Alkalibacterium putridalgicola (9), Alkalibacterium sp. (11), Alkalibacterium subtropicum (2), Alkalibacterium thalassium (2), Alloiococcus otitis (3), Anaerobacillus alkalidiazotrophicus (1), Anaerobacillus alkalilacustre (1), Anaerobacillus arseniciselenatis (2), Anaerorhabdus furcosa (2), ant fungus garden metagenome (2), Atopobacter phocae (1), Atopococcus tabaci (1), Atopostipes sp. (1), Atopostipes suicloacalis (1), Bacillaceae bacterium (1), Bacillus decolorationis (1), Bacillus macyae (1), Bacillus sp. (22), bacterium (86), Bavariicoccus seileri (1), bovine rumen bacterium (14), Bulleidia extructa (4), Candidatus Bacilloplasma mollicute (1), Candidatus Lumbricincola sp. (5), Candidatus Mycoplasma haematoparvum (1), Carnobacteriaceae bacterium (3), Carnobacterium divergens (9), Carnobacterium funditum (3), Carnobacterium maltaromaticum (1), Carnobacterium sp. (5), Carnococcus allantoicus (1), Catenibacterium mitsuokai (10), Catonella morbi (1), Citrobacter sp. (1), Clostridiaceae bacterium (1), Clostridiales bacterium (2), Clostridium aff. innocuum (1), Clostridium cocleatum (2), Clostridium innocuum (5), Clostridium ramosum (7), Clostridium saccharogumia (1), Clostridium sp. (6), Clostridium spiroforme (4), Coprobacillus cateniformis (4), Coprobacillus sp. (3), Corynebacterium jeikeium (1), Desemzia incerta (6), Desemzia sp. (1), Desulfosporosinus orientis (1), Dolosicoccus paucivorans (1), Drosophila bipectinata (1), Drosophila kikkawai (4), Edwardsiella tarda (1), Eggerthia catenaformis (2), endosymbiont (various) (3), Enterococcaceae bacterium (3), Enterococcus aquimarinus (2), Enterococcus asini (3), Enterococcus avium (19), Enterococcus azikeevi (1), Enterococcus caccae (2), Enterococcus camelliae (3), Enterococcus canintestini (3), Enterococcus canis (4), Enterococcus casseliflavus (43), Enterococcus cecorum (11), Enterococcus columbae (5),

		Enterococcus devriesei (6), Enterococcus dispar (5), Enterococcus durans (186), Enterococcus faecalis (361), Enterococcus faecium (275), Enterococcus gallinarum (52), Enterococcus gilvus (9), Enterococcus haemoperoxidus (2), Enterococcus hawaiiensis (1), Enterococcus hermanniensis (4), Enterococcus hirae (38), Enterococcus inusitatus (3), Enterococcus italicus (20), Enterococcus lactis (8), Enterococcus malodoratus (7), Enterococcus moraviensis (3), Enterococcus mundtii (38), Enterococcus pallens (3), Enterococcus pernyi (1), Enterococcus phoeniculicola (3), Enterococcus plantarum (3), Enterococcus pseudoavium (6), Enterococcus quebecensis (1), Enterococcus raffinosus (8), Enterococcus ratti (3), Enterococcus rivorum (5), Enterococcus rottae (1), Enterococcus saccharolyticus (9), Enterococcus silesiacus (6), Enterococcus sp. (185), Enterococcus sulfureus (7), Enterococcus termitis (2), Enterococcus thailandicus (12), Enterococcus ureasiticus (2), Enterococcus viikkiensis (5), Enterococcus villorum (4), Entomoplasma melaleucae (1), Eremococcus coleocola (2), Erysipelothrix inopinata (1), Erysipelothrix muris (1), Erysipelothrix rhusiopathiae (28), Erysipelothrix sp. (4), Erysipelothrix tonsillarum (4), Erysipelotrichaceae bacterium (14), Eubacterium cylindroides (2), Eubacterium dolichum (2), Eubacterium sp. (3), Eubacterium tortuosum (1), Facklamia hominis (1), Facklamia ignava (1), Facklamia languida (4), Facklamia miroungae (1), Facklamia sourekii (2), Facklamia sp. (3), Facklamia tabacinasalis (1), Firmicutes bacterium enrichment culture clone (1), Firmicutes oral clone (1), Globicatella sanguinis (1), Globicatella sp. (2), Globicatella sulfidifaciens (2), Granulicatella (1), Granulicatella adiacens (10), Granulicatella balaenopterae (1), Granulicatella elegans (7), Granulicatella para-adiacens (3), Granulicatella sp. (7), gut bacterium (1), haloalkaliphilic bacterium (1), Halolactibacillus alkaliphilus (2), Halolactibacillus halophilus (11), Halolactibacillus miurensis (8), Halolactibacillus sp. (3), Helcococcus kunzii (5), Helcococcus ovis (14), Helcococcus sueciensis (2), Holdemania filiformis (2), human gut metagenome (4), human oral bacterium (2), Ignavigranum ruoffiae (1), intestinal bacterium (2), Isobaculum melis (1), Kandleria vitulina (3), Lachnospiraceae bacterium (2), Lacticigenium naphtae (1), Lactobacillales bacterium (2), Lactobacillus amylolyticus (3), Lactobacillus casei (3), Lactobacillus fermentum (1), Lactobacillus fructivorans (5), Lactobacillus hamsteri (1), Lactobacillus helveticus (1), Lactobacillus homohiochii (3), Lactobacillus plantarum (1), Lactobacillus sp. (3), Lactococcus chungangensis (1), Lactococcus fujiensis (1), Lactococcus garvieae (86), Lactococcus lactis (583), Lactococcus piscium (3), Lactococcus plantarum (2), Lactococcus raffinolactis (27), Lactococcus sp. (73), Leuconostoc mesenteroides (1), Leuconostoc pseudomesenteroides (1), Listeria grayi (6), Listeria sp. (4), marine bacterium (8), Marinilactibacillus piezotolerans (4), Marinilactibacillus psychrotolerans (18), Marinilactibacillus sp. (7), Melissococcus plutonius (46), Mesoplasma chauliocola (1), Mesoplasma photuris (1), metagenome sequence (2), Microaerobacter geothermalis (1), Mollicutes bacterium (1),

		Nostocoida limicola (1), Nostocoida sp. (1), Okadaella gastrococcus (1), Paenibacillus abekawaensis (1), Paenibacillus sp. (1), Pediococcus acidilactici (1), Pilibacter termitis (1), primary endosymbiont (1), proteobacterium symbiont (1), rumen bacterium (27), secondary endosymbiont (1), Sharpea azabuensis (5), Solobacterium moorei (16), Spiroplasma apis (1), Spiroplasma atrichopogonis (1), Spiroplasma chinense (1), Spiroplasma chrysopicola (1), Spiroplasma citri (9), Spiroplasma clarkii (1), Spiroplasma corruscae (1), Spiroplasma culicicola (1), Spiroplasma diabroticae (1), Spiroplasma endosymbiont (63), Spiroplasma eriocheiris (1), Spiroplasma floricola (1), Spiroplasma gladiatoris (1), Spiroplasma helicoides (1), Spiroplasma insolitum (1), Spiroplasma kunkelii (1), Spiroplasma leptinotarsae (1), Spiroplasma leucomae (1), Spiroplasma lineolae (1), Spiroplasma litorale (1), Spiroplasma melliferum (2), Spiroplasma mirum (1), Spiroplasma monobiae (1), Spiroplasma montanense (1), Spiroplasma penaei (1), Spiroplasma phoeniceum (1), Spiroplasma poulsonii (1), Spiroplasma sp. (64), Spiroplasma syrphidicola (1), Spiroplasma tabanidicola (1), Spiroplasma taiwanense (1), Spiroplasma turonicum (1), Spiroplasma velocicrescens (1), Staphylococcus aureus (1), Streptococcus agalactiae (175), Streptococcus alactolyticus (4), Streptococcus anginosus (98), Streptococcus australis (9), Streptococcus bovis (1), Streptococcus caballi (1), Streptococcus canis (43), Streptococcus castoreus (1), Streptococcus constellatus (53), Streptococcus criceti (14), Streptococcus cristatus (16), Streptococcus dentapri (1), Streptococcus dentirousetti (1), Streptococcus devriesei (3), Streptococcus didelphis (9), Streptococcus downei (13), Streptococcus dysgalactiae (208), Streptococcus entericus (1), Streptococcus equi (85), Streptococcus equinus (93), Streptococcus ferus (6), Streptococcus fryi (4), Streptococcus gallinaceus (1), Streptococcus gallolyticus (134), Streptococcus genomosp. (8), Streptococcus gordonii (18), Streptococcus halichoeri (1), Streptococcus henryi (1), Streptococcus hyointestinalis (4), Streptococcus ictaluri (6), Streptococcus infantarius (23), Streptococcus infantis (25), Streptococcus iniae (23), Streptococcus intermedius (22), Streptococcus lactarius (1), Streptococcus luteciae (3), Streptococcus lutetiensis (23), Streptococcus macacae (7), Streptococcus macedonicus (6), Streptococcus marimammalium (1), Streptococcus massiliensis (1), Streptococcus merionis (1), Streptococcus milleri (1), Streptococcus minor (20), Streptococcus mitis (94), Streptococcus mutans (116), Streptococcus oligofermentans (3), Streptococcus oralis (49), Streptococcus orisratti (2), Streptococcus orisuis (2), Streptococcus ovis (1), Streptococcus parasanguinis (33), Streptococcus parauberis (19), Streptococcus pasteuri (2), Streptococcus pasteurianus (5), Streptococcus peroris (3), Streptococcus phage (40), Streptococcus phocae (5), Streptococcus pluranimalium (7), Streptococcus plurextorum (2), Streptococcus pneumoniae (714), Streptococcus porci (2), Streptococcus porcinus (17), Streptococcus pseudopneumoniae (11), Streptococcus pseudoporcinus (15), Streptococcus pyogenes (156), Streptococcus ratti (2),

		Streptococcus salivarius (435), Streptococcus sanguinis (51), Streptococcus seminale (3), Streptococcus sinensis (4), Streptococcus sobrinus (22), Streptococcus sp. (205), Streptococcus suis (136), Streptococcus thermophilus (18), Streptococcus thoraltensis (1), Streptococcus tigurinus (1), Streptococcus uberis (13), Streptococcus urinalis (7), Streptococcus ursoris (1), Streptococcus vestibularis (12), swine effluent bacterium (1), swine fecal bacterium (12), swine manure bacterium (6), swine manure pit bacterium (3), Synergistetes oral clone (1), Tetragenococcus doogicus (1), Tetragenococcus halophilus (43), Tetragenococcus koreensis (2), Tetragenococcus muriaticus (4), Tetragenococcus solitarius (4), Tetragenococcus sp. (20), Trichococcus collinsii (14), Trichococcus flocculiformis (14), Trichococcus palustris (1), Trichococcus pasteurii (4), Trichococcus patagoniensis (1), Trichococcus sp. (15), uncultured Abiotrophia sp. (5), uncultured actinobacterium (2), uncultured Aerococcaceae bacterium (6), uncultured Aerosphaera sp. (1), uncultured Alkalibacterium sp. (2), uncultured anaerobic bacterium (9), uncultured Anaerorhabdus sp. (1), uncultured Atopostipes sp. (1), uncultured Bacilli bacterium (5), uncultured Bacillus sp. (5), uncultured bacterium (7092), uncultured beta proteobacterium (1), uncultured Bulleidia sp. (4), uncultured Carnobacteriaceae bacterium (47), uncultured Carnobacterium sp. (5), uncultured Clostridiaceae bacterium (3), uncultured Clostridiales bacterium (2), uncultured Clostridium sp. (6), uncultured compost bacterium (8), uncultured Coprobacillus sp. (2), uncultured Enterococcaceae bacterium (6), uncultured Enterococcus sp. (64), uncultured Entomoplasma sp. (1), uncultured Erysipelothrix sp. (2), uncultured Erysipelotrichaceae bacterium (14), uncultured Erysipelotrichi bacterium (4), uncultured Facklamia sp. (5), uncultured feedlot manure bacterium (3), uncultured Firmicutes bacterium (54), uncultured gamma proteobacterium (1), uncultured Gram-positive bacterium (3), uncultured Granulicatella sp. (11), uncultured isopod gut bacterium (1), uncultured Lachnospiraceae bacterium (1), uncultured Lactobacillales bacterium (22), uncultured Lactobacillus sp. (1), uncultured Lactococcus sp. (17), uncultured Leuconostoc sp. (1), uncultured low G+C Gram-positive bacterium (3), uncultured Marinilactibacillus sp. (3), uncultured microorganism (6), uncultured Mollicutes bacterium (21), uncultured organism (1292), uncultured Peptostreptococcaceae bacterium (2), uncultured Polynucleobacter sp. (1), uncultured prokaryote (21), uncultured rumen bacterium (25), uncultured Ruminococcaceae bacterium (1), uncultured sheep mite bacterium Welshpool (1), uncultured soil bacterium (2), uncultured Solobacterium sp. (1), uncultured Sphingomonas sp. (1), uncultured Spiroplasma sp. (6), uncultured Streptococcaceae bacterium (37), uncultured streptococcus (1), uncultured Streptococcus sp. (391), uncultured Tetragenococcus sp. (1), uncultured Trichococcus sp. (53), uncultured Ureaplasma sp. (1),

		uncultured Vagococcus sp. (3), uncultured Vibrio sp. (1), uncultured Weissella sp. (5), uncultured zeta proteobacterium (1), unidentified (139), unidentified eubacterium (4), unidentified Hailaer soda lake bacterium (4), unidentified rumen bacterium (1), Vagococcus carniphilus (4), Vagococcus elongatus (1), Vagococcus fessus (1), Vagococcus fluvialis (9), Vagococcus lutrae (8), Vagococcus penaei (1), Vagococcus salmoninarum (3), Vagococcus sp. (13), Vagococcus teuberi (5), Vibrio cholerae (1), Vibrio fluvialis (1), Vulcanibacillus modesticaldus (1), Weissella sp. (7)
	GCG UAG AGA CAU GGA GGA	uncultured bacterium (1)
	GCG UAG AGA GAU GGA GGA	Jeotgalibacillus sp. (1)
	GCG UAG AGA UCU GGA GGA	Achromobacter xylosoxidans (1), Acidithiobacillus albertensis (7), Acidithiobacillus caldus (22), Acidithiobacillus ferrivorans (6), Acidithiobacillus ferrooxidans (154), Acidithiobacillus sp. (29), Acidithiobacillus thiooxidans (53), Acinetobacter antiviralis (1), Acinetobacter baumannii (435), Acinetobacter baylyi (15), Acinetobacter beijerinckii (8), Acinetobacter bereziniae (4), Acinetobacter bouvetii (4), Acinetobacter brisouii (1), Acinetobacter calcoaceticus (147), Acinetobacter genomosp. (5), Acinetobacter gerneri (2), Acinetobacter guillouiae (9), Acinetobacter gyllenbergii (3), Acinetobacter haemolyticus (14), Acinetobacter indicus (1), Acinetobacter johnsonii (90), Acinetobacter junii (44), Acinetobacter kyonggiensis (1), Acinetobacter lwoffii (63), Acinetobacter marinus (1), Acinetobacter nosocomialis (7), Acinetobacter oleivorans (6), Acinetobacter parvus (4), Acinetobacter pittii (17), Acinetobacter psychrotolerans (1), Acinetobacter radioresistens (53), Acinetobacter rhizosphaerae (5), Acinetobacter schindleri (14), Acinetobacter seohaensis (2), Acinetobacter septicus (5), Acinetobacter soli (8), Acinetobacter sp. (1005), Acinetobacter tandoii (3), Acinetobacter tjernbergiae (4), Acinetobacter towneri (4), Acinetobacter ursingii (5), Acinetobacter venetianus (11), Acinetobacter xiamenensis (2), Actinomycetales bacterium (1), Aeromonadaceae bacterium (3), Aeromonadales bacterium (1), Aeromonas allosaccharophila (12), Aeromonas aquariorum (15), Aeromonas bestiarum (11), Aeromonas bivalvium (2), Aeromonas caviae (104), Aeromonas encheleia (7), Aeromonas enteropelogenes (13), Aeromonas eucrenophila (3), Aeromonas fluvialis (1), Aeromonas guangheii (1), Aeromonas hydrophila (269), Aeromonas jandaei (21), Aeromonas media (61), Aeromonas molluscorum (6), Aeromonas piscicola (6), Aeromonas popoffii (16), Aeromonas rivuli (2), Aeromonas salmonicida (76), Aeromonas sanarellii (3), Aeromonas schubertii (12), Aeromonas sharmana (2), Aeromonas simiae (4), Aeromonas sobria (78), Aeromonas sp. (316), Aeromonas taiwanensis (2), Aeromonas tecta (1), Aeromonas veronii (231), Aestuariibacter halophilus (1), Aestuariibacter sp. (3), Agitococcus lubricus (1), Ajellomyces capsulatus (1), Alcanivorax indicus (1), Alkanindiges hongkongensis (3), Alkanindiges illinoisensis (1), Alkanindiges sp. (1), Allochromatium minutissimum (2),

		Allochromatium palmeri (2), Allochromatium phaeobacterium (3), Allochromatium renukae (2), Allochromatium sp. (8), Allochromatium truperi (1), Allochromatium vinosum (10), Allochromatium warmingii (1), Alteromonadaceae bacterium (6), Alteromonas halophila (1), Alteromonas sp. (8), Alvinella pompejana symbiont (1), ant fungus garden metagenome (1), Antarctic bacterium (4), Antarctic seawater bacterium (2), Aquamonas haywardensis (1), Aranicola proteolyticus (1), Aranicola sp. (12), Arcobacter sp. (2), Arctic sea ice bacterium (4), Arctic seawater bacterium (1), Arthrobacter sp. (2), Averyella dalhousiensis (4), Bacillus megaterium (1), Bacillus sp. (8), Bacillus subtilis (3), bacterium (319), beta-symbiont (1), BEV proteobacterium (1), Biostraticola tofi (1), Blochmannia endosymbiont (various) (2), Bowmanella denitrificans (2), Bowmanella pacifica (1), Bowmanella sp. (1), Brenneria alni (3), Brenneria goodwinii (3), Brenneria lupinicola (1), Brenneria nigrifluens (6), Brenneria rubrifaciens (8), Brenneria salicis (3), Brenneria sp. (7), Burkholderia cepacia (1), Buttiauxella agrestis (7), Buttiauxella brennerae (1), Buttiauxella ferragutiae (1), Buttiauxella gaviniae (1), Buttiauxella izardii (1), Buttiauxella noackiae (4), Buttiauxella sp. (6), Buttiauxella warmboldiae (1), Caenorhabditis remanei (1), Candidatus Blochmannia americanus (1), Candidatus Blochmannia castaneus (2), Candidatus Blochmannia chromaiodes (1), Candidatus Blochmannia fellah (1), Candidatus Blochmannia festinatus (1), Candidatus Blochmannia floridanus (3), Candidatus Blochmannia herculeanus (2), Candidatus Blochmannia laevigatus (1), Candidatus Blochmannia novaeboracensis (1), Candidatus Blochmannia ocreatus (1), Candidatus Blochmannia pennsylvanicus (4), Candidatus Blochmannia rufipes (1), Candidatus Blochmannia sansabeanus (1), Candidatus Blochmannia sayi (1), Candidatus Blochmannia schaefferi (1), Candidatus Blochmannia ulcerosus (1), Candidatus Blochmannia vafer (2), Candidatus Blochmannia vicinus (1), Candidatus Curculioniphilus endosymbiont (19), Candidatus Cuticobacterium kirbyi (1), Candidatus Kleidoceria schneideri (6), Candidatus Regiella insecticola (21), Candidatus Rohrkolberia cinguli (1), Candidatus Schneideria nysicola (16), Candidatus Steffania adelgidicola (2), Candidatus Tremblaya princeps (9), Capra hircus (1), Cedecea davisae (4), Cedecea lapagei (1), Cedecea neteri (2), Cedecea sp. (1), Cenchrus americanus (3), Chromatiaceae bacterium (2), Chromatium okenii (2), Chromatium sp. (1), Cimex lectularius endosymbiont (4), Citrobacter amalonaticus (10), Citrobacter braakii (5), Citrobacter farmeri (9), Citrobacter freundii (91), Citrobacter gillenii (3), Citrobacter koseri (7), Citrobacter murliniae (7), Citrobacter rodentium (11), Citrobacter sedlakii (5), Citrobacter sp. (96), Citrobacter werkmanii (3), Citrobacter youngae (2), Cloning vector (1), Clonorchis sinensis (1), Clostridium sp. (1), Cronobacter dublinensis (18), Cronobacter malonaticus (12), Cronobacter muytjensii (22),

		Cronobacter sakazakii (418), Cronobacter sp. (5), Cronobacter turicensis (27), cucurbit yellow vine disease bacterium (1), Curtobacterium plantarum (1), Dickeya dadantii (22), Dickeya dianthicola (1), Dickeya dieffenbachiae (2), Dickeya paradisiaca (2), Dickeya sp. (15), Dickeya zeae (9), ectosymbiont (1), Edwardsiella hoshinae (2), Edwardsiella ictaluri (29), Edwardsiella sp. (6), Edwardsiella tarda (74), Elbe River snow isolate (2), endophytic bacterium (51), endosymbiont (various) (16), Enhydrobacter aerosaccus (6), Enhydrobacter sp. (5), Enteric Group (1), Enterobacter aerogenes (76), Enterobacter amnigenus (18), Enterobacter arachidis (1), Enterobacter asburiae (37), Enterobacter cancerogenus (24), Enterobacter cloacae (187), Enterobacter cowanii (7), Enterobacter endosymbiont (2), Enterobacter gergoviae (4), Enterobacter helveticus (4), Enterobacter hormaechei (42), Enterobacter kobei (2), Enterobacter ludwigii (31), Enterobacter mori (4), Enterobacter nickellidurans (1), Enterobacter oryzae (9), Enterobacter pulveris (5), Enterobacter pyrinus (2), Enterobacter radicincitans (2), Enterobacter sp. (633), Enterobacter turicensis (2), Enterobacteria phage (7), Enterobacteriaceae bacterium (134), Enterobacterial endosymbiont (4), Enterobacteriales bacterium (4), enterobacterium (1), Erwinia (1), Erwinia amylovora (44), Erwinia aphidicola (3), Erwinia billingiae (20), Erwinia chrysanthemi (56), Erwinia mallotivora (5), Erwinia papayae (1), Erwinia persicina (15), Erwinia piriflorinigrans (2), Erwinia psidii (3), Erwinia pyrifoliae (33), Erwinia rhapontici (15), Erwinia soli (4), Erwinia sp. (69), Erwinia tasmaniensis (13), Erwinia toletana (10), Erwinia tracheiphila (1), Escherichia (1), Escherichia albertii (22), Escherichia blattae (2), Escherichia coli (2158), Escherichia fergusonii (26), Escherichia hermannii (13), Escherichia senegalensis (1), Escherichia sp. (50), Escherichia vulneris (4), estrogen-degrading bacterium (1), Ewingella americana (21), Flavobacterium sp. (1), gamma proteobacterium (70), Gibbsiella quercinecans (6), glacial ice bacterium (3), Glaciecola sp. (3), Glossina pallidipes S-endosymbiont (1), Gordonia sp. (2), Gram-negative bacterium (1), Grimontella senegalensis (1), Grimontella sp. (2), Haemophilus piscium (2), Haemophilus sp. (2), Hafnia alvei (28), Hafnia paralvei (3), Hafnia sp. (10), Hahella chejuensis (7), Hahella ganghwensis (1), Hahella sp. (2), Halomonas sp. (1), human gut metagenome (8), Hyphomicrobium sp. (1), iron-reducing enrichment clone (1), Isochromatium buderi (1), Kangiella aquimarina (1), Kangiella sp. (3), Kartchner Caverns bacterium (1), Klebsiella alba (2), Klebsiella granulomatis (4), Klebsiella milletis (1), Klebsiella oxytoca (131), Klebsiella pneumoniae (262), Klebsiella singaporensis (2), Klebsiella sp. (376), Klebsiella variicola (17), Kluyvera ascorbata (19), Kluyvera cryocrescens (9), Kluyvera georgiana (3), Kluyvera intermedia (16), Kluyvera sp. (13), Leclercia adecarboxylata (15), Leclercia sp. (10), Listonella anguillarum (1), lobster gut bacterium (1), Lonsdalea quercina (23), Lysinibacillus fusiformis (1), Mangrovibacter plantisponsor (1), Mangrovibacter sp. (1), Margalefia venezuelensis (1), Marichromatium sp. (1), marine bacterium (10), marine metagenome (7), marine psychrotrophic bacterium (1),

		Marinobacter lipolyticus (1), Marinomonas sp. (1), Methylophaga sp. (1), midgut symbiont (1), mine drainage metagenome (1), Moraxella atlantae (5), Moraxella boevrei (1), Moraxella bovis (22), Moraxella bovoculi (46), Moraxella canis (1), Moraxella caprae (1), Moraxella catarrhalis (17), Moraxella Branhamella caviae (1), Moraxella cuniculi (2), Moraxella equi (1), Moraxella lacunata (15), Moraxella lincolnii (2), Moraxella nonliquefaciens (17), Moraxella oblonga (2), Moraxella osloensis (18), Moraxella ovis (2), Moraxella pluranimalium (1), Moraxella sp. (43), Moraxellaceae bacterium (5), Morganella morganii (1), Nannospalax galili (1), Nephila clavata (1), nitrogen-fixing bacterium (3), Obesumbacterium proteus (5), Obesumbacterium sp. (1), Ophthalmotilapia ventralis (1), Oryza sativa Indica Group (5), Paenibacillus durus (1), Pantoea agglomerans (311), Pantoea ananatis (107), Pantoea anthophila (5), Pantoea brenneri (2), Pantoea calida (1), Pantoea cedenensis (6), Pantoea conspicua (3), Pantoea cypripedii (13), Pantoea deleyi (1), Pantoea dispersa (18), Pantoea endophytica (10), Pantoea eucalypti (5), Pantoea eucrina (4), Pantoea gaviniae (1), Pantoea oleae (3), Pantoea rodasii (3), Pantoea rwandensis (2), Pantoea septica (3), Pantoea sp. (206), Pantoea stewartii (19), Pantoea vagans (11), Pantoea wallisii (2), Paracoccus sp. (1), Pasteurella multocida (1), Pectobacterium atrosepticum (18), Pectobacterium betavasculorum (3), Pectobacterium cacticida (3), Pectobacterium carotovorum (206), Pectobacterium sp. (9), Pectobacterium wasabiae (18), Phage Gifsy (7), Photorhabdus luminescens (1), Plesiomonas shigelloides (8), Plesiomonas sp. (3), primary endosymbiont (various) (9), Prolinoborus fasciculus (1), proteobacterium (9), Providencia sp. (2), Pseudoalteromonas sp. (2), Pseudomonas aeruginosa (2), Pseudomonas flectens (2), Pseudomonas fluorescens (13), Pseudomonas putida (3), Pseudomonas sp. (13), Psychrobacter alimentarius (5), Psychrobacter aquaticus (6), Psychrobacter arcticus (6), Psychrobacter celer (14), Psychrobacter cibarius (5), Psychrobacter cryohalolentis (6), Psychrobacter faecalis (35), Psychrobacter fozii (2), Psychrobacter frigidicola (2), Psychrobacter fulvigenes (2), Psychrobacter glacialis (1), Psychrobacter glacincola (7), Psychrobacter halophilus (1), Psychrobacter immobilis (6), Psychrobacter jeotgali (2), Psychrobacter luti (1), Psychrobacter marincola (8), Psychrobacter maritimus (10), Psychrobacter meningitidis (1), Psychrobacter namhaensis (3), Psychrobacter okhotskensis (1), Psychrobacter phenylpyruvicus (1), Psychrobacter psychrophilus (8), Psychrobacter pulmonis (25), Psychrobacter salsus (1), Psychrobacter sp. (257), Psychrobacter submarinus (1), Psychrobacter urativorans (1), Psychrobacter vallis (1), psychrophilic marine bacterium (1), Rahnella aquatilis (51), Rahnella genomosp. (3), Rahnella sp. (104), rainbow trout intestinal bacterium (5), Raoultella ornithinolytica (28), Raoultella planticola (19), Raoultella sp. (23), Raoultella terrigena (12), rape rhizosphere bacterium (1), Regiella symbiont (3), Rhabdochromatium marinum (1), Rhodobacter capsulatus (2), Rhodococcus sp. (1), Rhodopseudomonas palustris (1),

		Rhodopseudomonas sp. (1), rumen bacterium enrichment culture clone (2), Salmonella bongori (10), Salmonella enterica (440), Salmonella sp. (29), Salmonella subterranea (1), Samsonia erythrinae (1), secondary endosymbiont (various) (9), secondary symbiont (various) (18), selenate-reducing bacterium (2), Serratia entomophila (4), Serratia ficaria (5), Serratia fonticola (9), Serratia grimesii (11), Serratia liquefaciens (14), Serratia marcescens (228), Serratia nematodiphila (8), Serratia odorifera (5), Serratia plymuthica (28), Serratia proteamaculans (46), Serratia quinivorans (11), Serratia rubidaea (8), Serratia sp. (346), Serratia symbiont (various) (4), Serratia symbiotica (27), Serratia ureilytica (5), Shewanella algae (38), Shewanella amazonensis (9), Shewanella arctica (1), Shewanella baltica (91), Shewanella chilikensis (4), Shewanella decolorationis (5), Shewanella fodinae (3), Shewanella gaetbuli (2), Shewanella glacialipiscicola (3), Shewanella hafniensis (4), Shewanella haliotis (7), Shewanella massilia (1), Shewanella morhuae (5), Shewanella oneidensis (17), Shewanella profunda (2), Shewanella putrefaciens (64), Shewanella saccharophilus (1), Shewanella sp. (182), Shewanella upenei (1), Shewanella woodyi (1), Shewanella xiamenensis (3), Shigella boydii (77), Shigella dysenteriae (42), Shigella flexneri (192), Shigella sonnei (53), Shigella sp. (31), Shimwellia blattae (2), Sitophilus zeamais (1), Sodalis glossinidius (15), Sodalis secondary endosymbiont (various) (2), Sporolactobacillus dextrus (1), Staphylococcus pasteuri (1), Stenotrophomonas sp. (1), Strongylocentrotus purpuratus (1), Strongyloides ratti (1), sulfur-oxidizing bacterium (1), Sulfur-oxidizing endosymbiont (1), swine fecal bacterium (12), swine manure bacterium (1), symbiont (various) (17), synthetic construct (14), Tatumella citrea (3), Tatumella morbirosei (3), Tatumella ptyseos (5), Tatumella punctata (5), Tatumella saanichensis (1), Tatumella sp. (1), Tatumella terrea (3), Theobroma cacao (1), thermophilic bacterium (1), Thioalkalicoccus limnaeus (1), Thioalkalispira microaerophila (1), Thiobaca sp. (1), Thiobaca trueperi (2), Thiobacillus sp. (3), Thiocapsa bogorovii (1), Thiocapsa imhoffii (1), Thiocapsa litoralis (1), Thiocapsa pendens (1), Thiocapsa rosea (3), Thiocapsa roseopersicina (2), Thiocapsa sp. (3), Thiococcus pfennigii (3), Thiococcus sp. (3), Thiocystis gelatinosa (3), Thiocystis minor (1), Thiocystis sp. (3), Thiocystis violacea (3), Thiocystis violascens (2), Thioflavicoccus mobilis (2), Thiohalophilus thiocyanatoxydans (1), Thiolamprovum pedioforme (2), Thiophaeococcus mangrovi (1), Thiophaeococcus sp. (4), Thiorhodococcus bheemlicus (2), Thiorhodococcus mannitoliphagus (2), Thiorhodococcus minor (2), Thiorhodococcus pfennigii (1), Thiorhodococcus sp. (3), Thiorhodovibrio sibirica (1), Thorsellia anophelis (1), Tiedjeia arctica (1), Tolumonas auensis (9), Tolumonas sp. (3), Trabulsiella guamensis (3), Trabulsiella odontotermitis (2), uncultured Acidithiobacillus caldus (1), uncultured Acidithiobacillus ferrooxidans (3), uncultured Acidithiobacillus sp. (49), uncultured Acinetobacter sp. (1261), uncultured Actinobacillus sp. (1), uncultured actinomycete (1), uncultured Aeromonadaceae bacterium (2), uncultured Aeromonas sp. (203),

		uncultured Alkanindiges sp. (2), uncultured alpha proteobacterium (2), uncultured Alteromonadaceae bacterium (4), uncultured Alteromonadales bacterium (3), uncultured Alteromonas sp. (3), uncultured anaerobic bacterium (2), uncultured archaeon (4), uncultured Azoarcus sp. (1), uncultured Bacillus sp. (2), uncultured bacterium (12617), uncultured Bacteroidetes bacterium (1), uncultured beta proteobacterium (90), uncultured Burkholderia sp. (1), uncultured Burkholderiales bacterium (1), uncultured Buttiauxella sp. (1), uncultured Chloroflexi bacterium (1), uncultured Chromatiaceae bacterium (16), uncultured Citrobacter sp. (392), uncultured compost bacterium (5), uncultured Cronobacter sp. (2), uncultured cyanobacterium (1), uncultured deep-sea bacterium (58), uncultured Edwardsiella sp. (1), uncultured endophytic bacterium (1), uncultured Enhydrobacter sp. (8), uncultured Enterobacter sp. (278), uncultured Enterobacteriaceae bacterium (68), uncultured Enterobacteriales bacterium (2), uncultured Erwinia sp. (58), uncultured Escherichia sp. (17), uncultured Ewingella sp. (1), uncultured Firmicutes bacterium (2), uncultured gamma proteobacterium (599), uncultured Glaciecola sp. (13), uncultured Green Bay ferromanganous micronodule bacterium (1), uncultured Hafnia sp. (3), uncultured Kangiella sp. (3), uncultured Klebsiella sp. (580), uncultured Kluyvera sp. (4), uncultured Ktedobacteria bacterium (4), uncultured marine bacterium (29), uncultured marine microorganism (2), uncultured Methylophaga sp. (3), uncultured microorganism (3), uncultured Moraxella sp. (12), uncultured Moraxellaceae bacterium (8), uncultured Nitrosomonadaceae bacterium (4), uncultured organism (1764), uncultured Pantoea sp. (26), uncultured Parabacteroides sp. (3), uncultured Pectobacterium sp. (1), uncultured Plesiomonas sp. (2), uncultured prokaryote (8), uncultured proteobacterium (32), uncultured Pseudomonadales bacterium (1), uncultured Pseudomonas sp. (6), uncultured Psychrobacter sp. (46), uncultured Rahnella sp. (29), uncultured Raoultella sp. (11), uncultured Rhodocyclaceae bacterium (1), uncultured rumen bacterium (2), cultured Salmonella sp. (16), uncultured Serratia sp. (155), uncultured sheep mite bacterium (9), uncultured Shewanella sp. (38), uncultured Shewanellaceae bacterium (4), uncultured Shigella sp. (64), uncultured sludge bacterium (1), uncultured Sodalis sp. (2), uncultured soil bacterium (70), uncultured Staphylococcaceae bacterium (1), uncultured Stenotrophomonas sp. (14), uncultured Streptomyces sp. (1), uncultured Sulfitobacter sp. (1), uncultured Tolumonas sp. (6), uncultured Vibrio sp. (3), uncultured Xanthomonas sp. (3), uncultured Yersinia sp. (2), unidentified (93), unidentified phage (7), unidentified thrip gut bacterium (3), Vestimentiferan symbiont (1), Vibrio parahaemolyticus (2), Vibrio porteresiae (3), Vibrio sp. (3), Xenorhabdus bovienii (3), Xenorhabdus nematophila (2), Xenorhabdus poinarii (2), Xenorhabdus sp. (1), Yersinia aldovae (3), Yersinia aleksiciae (7), Yersinia bercovieri (5), Yersinia enterocolitica (51), Yersinia frederiksenii (8),

		Yersinia intermedia (10), Yersinia kristensenii (16), Yersinia massiliensis (2), Yersinia mollaretii (5), Yersinia pestis (156), Yersinia pseudotuberculosis (56), Yersinia rohdei (7), Yersinia ruckeri (22), Yersinia similis (5), Yersinia sp. (19), Yokenella regensburgei (6), Yokenella sp. (1), Zymobacter palmae (3)
	GCG **U**AG AGA U**G**U GGA GGA	2,4-D-degrading bacterium (6), Achromobacter sp. (1), Acidithiobacillus thiooxidans (1), Acinetobacter junii (1), Actimicrobium antarcticum (1), Actinobacillus arthritidis (5), Actinobacillus capsulatus (22), Actinobacillus cf. Salpingitidis (1), Actinobacillus delphinicola (2), Actinobacillus equuli (21), Actinobacillus genomosp. (4), Actinobacillus hominis (2), Actinobacillus indolicus (12), Actinobacillus lignieresii (5), Actinobacillus minor (23), Actinobacillus muris (2), Actinobacillus pleuropneumoniae (48), Actinobacillus porcinus (19), Actinobacillus porcitonsillarum (14), Actinobacillus rossii (25), Actinobacillus salpingitidis (1), Actinobacillus scotiae (1), Actinobacillus seminis (2), Actinobacillus sp. (8), Actinobacillus succinogenes (13), Actinobacillus suis (6), Actinobacillus ureae (3), actinobacterium (1), activated sludge bacterium (1), Aeribacillus pallidus (31), Aerococcus sp. (1), Aeromonas eucrenophila (2), Aeromonas schubertii (1), Aggregatibacter actinomycetemcomitans (78), Aggregatibacter aphrophilus (20), Aggregatibacter segnis (10), Aggregatibacter sp. (1), Alcaligenaceae bacterium (10), Alcaligenes faecalis (3), Alcaligenes sp. (25), Alicyclobacillaceae bacterium (2), Alicyclobacillus acidocaldarius (35), Alicyclobacillus acidoterrestris (1), Alicyclobacillus aeris (2), Alicyclobacillus contaminans (4), Alicyclobacillus disulfidooxidans (3), Alicyclobacillus ferrooxydans (1), Alicyclobacillus herbarius (2), Alicyclobacillus kakegawensis (3), Alicyclobacillus mali (1), Alicyclobacillus sendaiensis (3), Alicyclobacillus shizuokensis (2), Alicyclobacillus sp. (57), Alicyclobacillus tolerans (3), Alicyclobacillus vulcanalis (2), Alishewanella sp. (1), Alkalimonas amylolytica (1), Alkalimonas collagenimarina (1), Alkalimonas delamerensis (3), Alkalimonas sp. (2), Alysiella crassa (6), Alysiella filiformis (4), Aminomonas aminovorus (1), Amphibacillus haojiensis (1), Amphibacillus sediminis (2), Amphibacillus sp. (19), Amphibacillus xylanus (3), anaerobic thermophile (1), Aneurinibacillus aneurinilyticus (14), Aneurinibacillus danicus (2), Aneurinibacillus migulanus (9), Aneurinibacillus sp. (6), Aneurinibacillus sp. (6), Aneurinibacillus thermoaerophilus (7), Anoxybacillus amylolyticus (1), Anoxybacillus ayderensis (1), Anoxybacillus beppuensis (2), Anoxybacillus bogrovensis (1), Anoxybacillus contaminans (1), Anoxybacillus eryuanensis (1), Anoxybacillus flavithermus (28), Anoxybacillus gonensis (6), Anoxybacillus kamchatkensis (5), Anoxybacillus kestanbolensis (6), Anoxybacillus kualawohkensis (1), Anoxybacillus mongoliensis (1), Anoxybacillus pushchinoensis (3), Anoxybacillus rupiensis (3), Anoxybacillus sp. (61), Anoxybacillus tengchongensis (1), Anoxybacillus thermarum (1), Anoxybacillus tunisiense (1), Anoxybacillus voinovskiensis (3), Antarctic bacterium (9), Apis mellifera (6), Aquaspirillum serpens (4), Aquaspirillum sp. (3), Aquitalea sp. (1), Arctic sea ice bacterium (9), Arenicella xantha (1),

		Aromatoleum aromaticum (5), Arsenophonus endosymbiont (37), Arsenophonus nasoniae (4), Arsenophonus symbiont (4), Avibacterium avium (2), Avibacterium endocarditidis (1), Avibacterium gallinarum (7), Avibacterium paragallinarum (10), Avibacterium sp. (10), Avibacterium volantium (2), Azoarcus indigens (3), Azoarcus sp. (14), Azonexus caeni (1), Azonexus fungiphilus (3), Azonexus hydrophilus (3), Azonexus sp. (4), Azospira oryzae (7), Azospira restricta (1), Azospira sp. (13), Azospirillum sp. (1), Azovibrio restrictus (2), Azovibrio sp. (4), Bacillaceae bacterium (47), Bacillales bacterium (8), Bacilli bacterium (1), Bacillus acidicola (2), Bacillus acidiproducens (1), Bacillus acidovorans (1), Bacillus aeris (1), Bacillus aerius (2), Bacillus aerophilus (11), Bacillus aestuarii (4), Bacillus agaradhaerens (1), Bacillus aidingensis (1), Bacillus alcalophilus (1), Bacillus alkalinitrilicus (1), Bacillus alkalitelluris (10), Bacillus altitudinis (33), Bacillus alveayuensis (3), Bacillus amiliensis (1), Bacillus aminovorans (1), Bacillus amyloliquefaciens (537), Bacillus anthracis (1), Bacillus arbutinivorans (6), Bacillus arsenicus (11), Bacillus aryabhattai (50), Bacillus asahii (5), Bacillus atrophaeus (80), Bacillus axarquiensis (13), Bacillus azotoformans (1), Bacillus badius (20), Bacillus barbaricus (17), Bacillus bataviensis (11), Bacillus beijingensis (8), Bacillus benzoevorans (5), Bacillus beringensis (4), Bacillus boroniphilus (13), Bacillus caldolyticus (5), Bacillus caldotenax (4), Bacillus caldovelox (5), Bacillus carboniphilus (1), Bacillus catenulatus (3), Bacillus cereus (3), Bacillus chandigarhensis (1), Bacillus cibi (11), Bacillus circulans (38), Bacillus clausii (104), Bacillus coagulans (64), Bacillus cohnii (11), Bacillus deserti (1), Bacillus djibelorensis (2), Bacillus drentensis (19), Bacillus endophyticus (63), Bacillus farraginis (4), Bacillus fastidiosus (2), Bacillus firmus (129), Bacillus flexus (104), Bacillus foraminis (11), Bacillus fordii (3), Bacillus fortis (1), Bacillus fucosivorans (1), Bacillus fumarioli (9), Bacillus funiculus (11), Bacillus galactosidilyticus (1), Bacillus gelatini (5), Bacillus ginsenggisoli (1), Bacillus ginsengi (4), Bacillus ginsengihumi (12), Bacillus hackensackii (1), Bacillus halodurans (70), Bacillus hemicellulosilyticus (1), Bacillus herbersteinensis (6), Bacillus horikoshii (2), Bacillus horneckiae (1), Bacillus horti (2), Bacillus humi (13), Bacillus idriensis (9), Bacillus indicus (5), Bacillus infantis (4), Bacillus infernus (2), Bacillus isabeliae (1), Bacillus jeotgali (8), Bacillus koreensis (5), Bacillus korlensis (5), Bacillus kribbensis (1), Bacillus krulwichiae (1), Bacillus lentus (8), Bacillus licheniformis (814), Bacillus litoralis (5), Bacillus longiquaesitum (3), Bacillus macauensis (1), Bacillus malacitensis (5), Bacillus mangrovensis (1), Bacillus mannanilyticus (2), Bacillus megaterium (542), Bacillus methanolicus (4), Bacillus methylotrophicus (107), Bacillus mojavensis (49), Bacillus nealsonii (17), Bacillus nematocida (1), Bacillus niabensis (20), Bacillus niacini (31), Bacillus nitritophilus (1), Bacillus novalis (6), Bacillus oceanisediminis (13), Bacillus okuhidensis (2), Bacillus oleronius (16), Bacillus pallidus (1), Bacillus panaciterrae (5), Bacillus pocheonensis (8), Bacillus polyfermenticus (6), Bacillus pseudomegaterium (1), Bacillus psychrosaccharolyticus (5), Bacillus pumilus (727), Bacillus qingdaonensis (2), Bacillus racemilacticus (1), Bacillus rigui (1), Bacillus ruris (1),

		Bacillus safensis (74), Bacillus salarius (2), Bacillus selenatarsenatis (9), Bacillus senegalensis (5), Bacillus shackletonii (2), Bacillus siamensis (1), Bacillus simplex (4), Bacillus siralis (2), Bacillus smithii (9), Bacillus soli (8), Bacillus sonorensis (29), Bacillus sp. (3633), Bacillus sporothermodurans (9), Bacillus stratosphericus (7), Bacillus subterraneus (2), Bacillus subtilis (1976), Bacillus taeanensis (1), Bacillus tequilensis (71), Bacillus thermantarcticus (3), Bacillus thermoalkalophilus (1), Bacillus thermoamylovorans (23), Bacillus thermoterrestris (2), Bacillus thioparans (4), Bacillus thuringiensis (2), Bacillus tianmuensis (1), Bacillus vallismortis (60), Bacillus vireti (10), Bacillus viscosus (1), Bacillus vitellinus (1), Bacillus zhanjiangensis (1), bacterium (324), benzene mineralizing consortium clone (1), Bergeriella denitrificans (4), beta proteobacterium (142), Bhargavaea cecembensis (3), Bhargavaea sp. (4), Bibersteinia trehalosi (6), Bisgaard Taxon (39), Bisgaardia genomosp. (3), Bisgaardia hudsonensis (6), blackwater bioreactor bacterium (1), blood disease bacterium (6), Bombus terrestris (1), Bordetella sp. (1), Brackiella oedipodis (1), Brevibacillus agri (32), Brevibacillus borstelensis (34), Brevibacillus brevis (102), Brevibacillus centrosporus (8), Brevibacillus choshinensis (8), Brevibacillus formosus (9), Brevibacillus ginsengisoli (1), Brevibacillus invocatus (6), Brevibacillus laterosporus (28), Brevibacillus levickii (7), Brevibacillus limnophilus (2), Brevibacillus panacihumi (4), Brevibacillus parabrevis (30), Brevibacillus reuszeri (8), Brevibacillus sp. (146), Brevibacillus thermoruber (10), Brevibacterium frigoritolerans (2), Brevibacterium halotolerans (4), Brevibacterium sp. (4), Budvicia aquatica (1), Budvicia sp. (1), Burkholderia acidipaludis (4), Burkholderia ambifaria (20), Burkholderia anthina (3), Burkholderia arboris (2), Burkholderia bannensis (2), Burkholderia brasilensis (1), Burkholderia bryophila (3), Burkholderia caledonica (4), Burkholderia caribensis (16), Burkholderia caryophylli (3), Burkholderia cenocepacia (51), Burkholderia cepacia (196), Burkholderia contaminans (1), Burkholderia endofungorum (2), Burkholderia ferrariae (2), Burkholderia fungorum (37), Burkholderia ginsengisoli (2), Burkholderia gladioli (54), Burkholderia glathei (19), Burkholderia glumae (17), Burkholderia graminis (6), Burkholderia heleia (6), Burkholderia hospita (6), Burkholderia kururiensis (11), Burkholderia lata (4), Burkholderia mallei (60), Burkholderia megapolitana (1), Burkholderia mimosarum (13), Burkholderia multivorans (33), Burkholderia nodosa (7), Burkholderia oklahomensis (5), Burkholderia oxyphila (6), Burkholderia phenazinium (20), Burkholderia phenoliruptrix (1), Burkholderia phymatum (16), Burkholderia phytofirmans (16), Burkholderia plantarii (13), Burkholderia pseudomallei (142), Burkholderia pyrrocinia (13), Burkholderia rhizoxinica (11), Burkholderia sabiae (3), Burkholderia sacchari (4), Burkholderia sartisoli (3), Burkholderia sediminicola (2), Burkholderia seminalis (1), Burkholderia silvatlantica (7), Burkholderia soli (1), Burkholderia sordidicola (6), Burkholderia sp. (1241), Burkholderia stabilis (4), Burkholderia symbiont (7), Burkholderia terrae (8), Burkholderia terricola (4), Burkholderia thailandensis (17), Burkholderia tropica (44),

		Burkholderia tuberum (9), Burkholderia ubonensis (4), Burkholderia unamae (20), Burkholderia vietnamiensis (37), Burkholderia xenovorans (12), Burkholderiaceae bacterium (41), Caldalkalibacillus uzonensis (1), Candidatus Accumulibacter phosphatis clade (2), Candidatus Accumulibacter sp. (1), Candidatus Arsenophonus arthropodicus (1), Candidatus Arsenophonus triatominarum (4), Candidatus Burkholderia hispidae (10), Candidatus Burkholderia kirkii (8), Candidatus Burkholderia nigropunctata (1), Candidatus Burkholderia rigidae (10), Candidatus Burkholderia schumannianae (10), Candidatus Burkholderia verschuerenii (2), Candidatus Glomeribacter gigasporarum (11), Candidatus Phlomobacter fragariae (3), Candidatus Procabacter acanthamoebae (1), Candidatus Procabacter sp. (4), Candidimonas humi (1), Candidimonas nitroreducens (1), Castellaniella caeni (2), Castellaniella defragrans (10), Castellaniella denitrificans (3), Castellaniella ginsengisoli (2), Castellaniella sp. (12), CDC Group IVc-2 str. (1), Chelonobacter oris (5), chimeric sequence (1), Chitinibacter sp. (1), Chitinibacter tainanensis (1), Chitinilyticum litopenaei (1), Chitinimonas koreensis (2), Chitiniphilus shinanonensis (2), Chitiniphilus sp. (2), Chitinolyticbacter meiyuanensis (1), Chromobacterium piscinae (1), Chromobacterium pseudoviolaceum (2), Chromobacterium sp. (138), Chromobacterium violaceum (18), Cohnella damuensis (1), Cohnella fontinalis (3), Cohnella ginsengisoli (1), Cohnella hongkongensis (1), Cohnella laeviribosi (2), Cohnella luojiensis (1), Cohnella panacarvi (1), Cohnella soli (1), Cohnella sp. (27), Cohnella terrae (1), Cohnella thailandensis (1), Cohnella thermotolerans (2), Cohnella xylanilytica (1), Cohnella yongneupensis (1), Collimonas arenae (4), Collimonas fungivorans (17), Collimonas pratensis (4), Collimonas sp. (18), Comamonadaceae bacterium (1), Conchiformibius kuhniae (5), Conchiformibius sp. (3), Conchiformibius steedae (9), Corynebacterium sp. (1), Cosenzaea myxofaciens (3), Cronobacter sp. (1), Cucumis sativus (1), Cupriavidus basilensis (20), Cupriavidus campinensis (4), Cupriavidus gilardii (17), Cupriavidus laharis (1), Cupriavidus metallidurans (19), Cupriavidus necator (30), Cupriavidus oxalaticus (4), Cupriavidus pauculus (7), Cupriavidus pinatubonensis (10), Cupriavidus respiraculi (23), Cupriavidus sp. (129), Cupriavidus taiwanensis (28), Dechloromonas agitata (1), Dechloromonas aromatica (5), Dechloromonas denitrificans (1), Dechloromonas hortensis (1), Dechloromonas sp. (20), Dechlorosoma sp. (7), Dechlorosoma suillum (2), Deefgea chitinilytica (1), Dehalobacter restrictus (3), Dehalobacter sp. (8), Delivery vector (1), Denitratisoma sp. (2), denitrifying bacterium (42), Denitrobacter sp. (3), Denitromonas aromaticus (1), Denitromonas indolicum (1), Denitromonas sp. (3), Derxia gummosa (3), Derxia sp. (1), Desulfitobacterium metallireducens (2), Desulfitobacterium sp. (1), diazotroph str. (1), Duganella nigrescens (1), Duganella sp. (14), Duganella violaceinigra (2), Duganella zoogloeoides (2), Eikenella corrodens (6), Eikenella sp. (3), Elbe River snow isolate (1), Empedobacter brevis (1), endophytic bacterium (14), endosymbiont (various) (5),

		Enterobacter cloacae (1), Enterobacter sp. (2), Enterobacteriaceae bacterium (9), enterobacterium (1), Enterococcus sp. (1), eubacterium (1), eubacterium sp. (5), Exiguobacterium (1), Exiguobacterium acetylicum (23), Exiguobacterium aestuarii (6), Exiguobacterium antarcticum (2), Exiguobacterium arabatum (5), Exiguobacterium artemiae (1), Exiguobacterium aurantiacum (14), Exiguobacterium homiense (4), Exiguobacterium indicum (11), Exiguobacterium marinum (4), Exiguobacterium mexicanum (17), Exiguobacterium oxidotolerans (4), Exiguobacterium panipatensis (1), Exiguobacterium profundum (9), Exiguobacterium sibiricum (12), Exiguobacterium soli (1), Exiguobacterium sp. (200), Exiguobacterium taiwanense (1), Exiguobacterium undae (9), Ferribacterium limneticum (1), Ferribacterium sp. (1), Ferrovum myxofaciens (2), Filibacter limicola (2), Filobacillus sp. (2), Firmicutes bacterium (7), Fontibacillus aquaticus (1), Fontibacillus panacisegetis (1), Fontibacillus sp. (1), freshwater sediment metagenome (6), Gallibacterium anatis (63), Gallibacterium genomosp. (14), Gallibacterium group (2), Gallibacterium melopsittaci (12), Gallibacterium salpingitidis (4), Gallibacterium sp. (1), Gallibacterium trehalosifermentans (3), Gallionella sp. (2), Gallionellaceae bacterium (2), gamma proteobacterium (8), Geobacillus (1), Geobacillus anatolicus (1), Geobacillus bogazici (1), Geobacillus caldoproteolyticus (2), Geobacillus caldoxylosilyticus (15), Geobacillus gargensis (3), Geobacillus jurassicus (3), Geobacillus kaue (2), Geobacillus kaustophilus (22), Geobacillus lituanicus (4), Geobacillus sp. (220), Geobacillus stearothermophilus (117), Geobacillus subterraneus (7), Geobacillus tepidamans (3), Geobacillus thermocatenulatus (5), Geobacillus thermodenitrificans (68), Geobacillus thermoglucosidasius (33), Geobacillus thermoleovorans (45), Geobacillus thermoparaffinivorans (4), Geobacillus toebii (28), Geobacillus tropicalis (1), Geobacillus uralicus (1), Geobacillus uzenensis (7), Geobacillus vulcani (3), Geobacillus zalihae (3), Geomicrobium halophilum (2), Georgfuchsia toluolica (1), Georgfuchsia toluolica (14), Gracilibacillus dipsosauri (2), Gracilibacillus halotolerans (1), Gracilibacillus sp. (9), Gram-positive bacterium (2), Gram-positive heterotrophic acidophile (1), Gram-positive iron-oxidizing acidophile (3), groundwater biofilm bacterium (8), groundwater planktonic bacterium (1), Haemophilus aegyptius (2), Haemophilus cf. paragallinarum (1), Haemophilus ducreyi (13), Haemophilus felis (1), Haemophilus genomosp. (2), Haemophilus haemoglobinophilus (2), Haemophilus haemolyticus (116), Haemophilus influenzae (674), Haemophilus paracuniculus (1), Haemophilus parahaemolyticus (14), Haemophilus parainfluenzae (23), Haemophilus paraphrohaemolyticus (2), Haemophilus parasuis (261), Haemophilus phage (6), Haemophilus pittmaniae (9), Haemophilus quentini (2), Haemophilus simiae (1), Haemophilus somnus (10), Haemophilus sp. (69), Haemophilus taxon C (1), Halalkalibacillus halophilus (2), Halalkalibacillus sp. (1), haloalkaliphilic bacterium (13), Halobacillus sp. (5), Halomonas sp. (1), halophilic bacterium (9), Herbaspirillum seropedicae (2), Herbaspirillum sp. (23), Herminiimonas aquatilis (1),

		Herminiimonas arsenicoxydans (3), Herminiimonas fonticola (5), Herminiimonas glaciei (5), Herminiimonas saxobsidens (2), Herminiimonas sp. (4), Histophilus somni (50), Holophaga foetida (2), Iodobacter fluviatilis (1), iron-reducing bacterium enrichment culture clone (13), iron-reducing enrichment clone (4), Janthinobacterium agaricidamnosum (3), Janthinobacterium sp. (38), Jeongeupia sp. (1), Jeotgalibacillus sp. (1), Jeotgalicoccus psychrophilus (1), Kartchner Caverns bacterium (1), Kingella denitrificans (3), Kingella kingae (7), Kingella oralis (4), Kingella potus (1), Kingella sp. (2), Klebsiella sp. (3), Kurthia zopfii (2), Laribacter hongkongensis (65), Laribacter sp. (1), Leeia oryzae (1), Leminorella grimontii (1), Lentibacillus halodurans (1), Lentibacillus halophilus (1), Lentibacillus juripiscarius (1), Lentibacillus kapialis (1), Lentibacillus salarius (1), Lentibacillus salicampi (1), Lentibacillus salinarum (1), Lentibacillus sp. (6), Leptothrix sp. (1), Lonepinella koalarum (3), low G+C Gram-positive bacterium (21), Lutiella nitroferrum (2), Lutiella sp. (1), Lysinibacillus fusiformis (1), Lysinibacillus sp. (1), Lysinibacillus sphaericus (1), Mannheimia caviae (1), Mannheimia glucosida (10), Mannheimia granulomatis (4), Mannheimia haemolytica (14), Mannheimia ruminalis (13), Mannheimia sp. (17), Mannheimia succiniciproducens (7), Mannheimia varigena (5), marine bacillus (1), marine bacterium (6), marine firmicute (1), marine gamma proteobacterium (1), marine metagenome (15), Massila sp. (1), Massilia aerilata (4), Massilia albidiflava (3), Massilia alkalitolerans (3), Massilia aurea (2), Massilia brevitalea (2), Massilia cf. Timonae (1), Massilia consociata (1), Massilia dura (6), Massilia haematophila (4), Massilia jejuensis (1), Massilia lutea (1), Massilia niabensis (3), Massilia niastensis (5), Massilia plicata (3), Massilia sp. (145), Massilia suwonensis (1), Massilia timonae (20), Massilia varians (1), Mesorhizobium sp. (1), metagenome sequence (2), Methylobacillus flagellatus (4), Methylobacillus glycogenes (1), Methylobacillus pratensis (1), Methylobacillus sp. (6), Methylomonas sp. (1), Methylophilus freyburgensis (1), Methylophilus glucoseoxidans (1), Methylophilus leisingeri (2), Methylophilus methylotrophus (3), Methylophilus quaylei (1), Methylophilus rhizosphaerae (2), Methylophilus sp. (14), Methylotenera mobilis (3), Methylotenera versatilis (3), Methyloversatilis sp. (2), Methyloversatilis universalis (4), Methylovorus glucosetrophus (4), Methylovorus mays (1), Methylovorus menthalis (1), Methylovorus sp. (3), Microbacterium sp. (1), Microvirgula aerodenitrificans (5), mine drainage metagenome (1), Moellerella wisconsensis (3), Morganella morganii (50), Morganella psychrotolerans (14), Morganella sp. (8), Morococcus cerebrosus (1), mycetome symbiont (1), Natribacillus halophilus (1), Naxibacter indica (2), Naxibacter intermedius (1), Naxibacter sp. (21), Necropsobacter rosorum (19), Neisseria (1), Neisseria animalis (1), Neisseria animaloris (2), Neisseria bacilliformis (4), Neisseria canis (4), Neisseria cinerea (6), Neisseria dentiae (1), Neisseria elongata (8), Neisseria flava (2), Neisseria flavescens (10), Neisseria genomosp. (1), Neisseria gonorrhoeae (32), Neisseria iguanae (1), Neisseria lactamica (10), Neisseria macacae (1), Neisseria meningitidis (1008),

		Neisseria meningitidis (6), Neisseria perflava (1), Neisseria pharyngis (1), Neisseria polysaccharea (7), Neisseria shayeganii (6), Neisseria sicca (6), Neisseria sp. (43), Neisseria subflava (6), Neisseria wadsworthii (3), Neisseria weaveri (5), Neisseria zoodegmatis (2), Neisseriaceae bacterium (3), Nicoletella semolina (68), Nitrosococcus mobilis (1), Nitrosospira briensis (3), Nitrosospira multiformis (4), Nitrosospira sp. (67), Nitrosospira tenuis (1), Nitrosovibrio sp. (4), Nitrosovibrio tenuis (5), Oceanobacillus chironomi (1), Oceanobacillus cibarius (1), Oceanobacillus iheyensis (17), Oceanobacillus kapialis (1), Oceanobacillus kimchii (1), Oceanobacillus manasiensis (3), Oceanobacillus oncorhynchi (15), Oceanobacillus picturae (31), Oceanobacillus profundus (11), Oceanobacillus sojae (2), Oceanobacillus sp. (83), Ochrobactrum sp. (1), Orbus hercynius (1), Orbus sp. (1), Ornithinibacillus bavariensis (2), Ornithinibacillus californiensis (1), Ornithinibacillus scapharcae (2), Ornithinibacillus sp. (26), Oryza sativa Indica Group (1), Oxalicibacterium faecigallinarum (1), Oxalicibacterium flavum (2), Oxalicibacterium horti (2), Oxalicibacterium solurbis (2), Oxalicibacterium sp. (3), Oxalobacter sp. (5), Oxalobacteraceae bacterium (26), Paenibacillaceae bacterium (6), Paenibacillus agarexedens (3), Paenibacillus agaridevorans (6), Paenibacillus alginolyticus (8), Paenibacillus alkaliterrae (1), Paenibacillus alvei (9), Paenibacillus amylolyticus (3), Paenibacillus apiarius (1), Paenibacillus assamensis (2), Paenibacillus azoreducens (1), Paenibacillus barcinonensis (4), Paenibacillus barengoltzii (21), Paenibacillus brasilensis (2), Paenibacillus camelliae (1), Paenibacillus castaneae (4), Paenibacillus cellulosilyticus (1), Paenibacillus cf. Polymyxa (1), Paenibacillus chinjuensis (1), Paenibacillus chitinolyticus (8), Paenibacillus chondroitinus (5), Paenibacillus contaminans (1), Paenibacillus cookii (6), Paenibacillus curdlanolyticus (19), Paenibacillus daejeonensis (1), Paenibacillus darangshiensis (1), Paenibacillus dendritiformis (7), Paenibacillus durus (6), Paenibacillus edaphicus (3), Paenibacillus ehimensis (15), Paenibacillus elgii (7), Paenibacillus favisporus (2), Paenibacillus filicis (1), Paenibacillus fonticola (2), Paenibacillus forsythiae (1), Paenibacillus fujiensis (2), Paenibacillus fukuinensis (1), Paenibacillus gansuensis (2), Paenibacillus ginsengarvi (1), Paenibacillus ginsengihumi (1), Paenibacillus glebae (1), Paenibacillus glycanilyticus (13), Paenibacillus graminis (4), Paenibacillus granivorans (1), Paenibacillus harenae (2), Paenibacillus hodogayensis (1), Paenibacillus humicus (9), Paenibacillus hunanensis (4), Paenibacillus illinoisensis (12), Paenibacillus jamilae (7), Paenibacillus kobensis (5), Paenibacillus koleovorans (3), Paenibacillus konsidensis (1), Paenibacillus koreensis (1), Paenibacillus kribbensis (5), Paenibacillus larvae (30), Paenibacillus lentimorbus (17), Paenibacillus macerans (13), Paenibacillus massiliensis (3), Paenibacillus mendelii (2), Paenibacillus montaniterrae (1), Paenibacillus motobuensis (1), Paenibacillus mucilaginosus (66), Paenibacillus nanensis (3), Paenibacillus naphthalenovorans (4), Paenibacillus nematophilus (2),

		Paenibacillus ourofinensis (1), Paenibacillus pabuli (6), Paenibacillus panacisoli (1), Paenibacillus panaciterrae (1), Paenibacillus pasadenensis (4), Paenibacillus pectinilyticus (2), Paenibacillus peoriae (8), Paenibacillus phyllosphaerae (1), Paenibacillus pinihumi (1), Paenibacillus pocheonensis (1), Paenibacillus polymyxa (175), Paenibacillus popilliae (15), Paenibacillus prosopidis (1), Paenibacillus provencensis (1), Paenibacillus pueri (2), Paenibacillus residui (2), Paenibacillus riograndensis (2), Paenibacillus ruminocola (2), Paenibacillus sabinae (5), Paenibacillus sanguinis (1), Paenibacillus septentrionalis (1), Paenibacillus sepulcri (1), Paenibacillus siamensis (1), Paenibacillus soli (3), Paenibacillus sonchi (1), Paenibacillus sp. (535), Paenibacillus sputi (1), Paenibacillus stellifer (9), Paenibacillus taiwanensis (1), Paenibacillus tarimensis (1), Paenibacillus telluris (3), Paenibacillus terrigena (4), Paenibacillus thailandensis (1), Paenibacillus thiaminolyticus (11), Paenibacillus timonensis (5), Paenibacillus turicensis (7), Paenibacillus urinalis (1), Paenibacillus validus (12), Paenibacillus woosongensis (1), Paenibacillus xinjiangensis (1), Paenibacillus xylanexedens (1), Paenibacillus xylanilyticus (5), Paenibacillus zanthoxyli (5), Paenisporosarcina macmurdoensis (3), Paenisporosarcina sp. (4), Paludibacterium sp. (3), Paludibacterium yongneupense (2), Pandoraea apista (3), Pandoraea faecigallinarum (1), Pandoraea norimbergensis (6), Pandoraea oxalativorans (3), Pandoraea pnomenusa (10), Pandoraea pulmonicola (3), Pandoraea sp. (50), Pandoraea sputorum (4), Pandoraea vervacti (1), Panicum virgatum (1), Pantoea agglomerans (1), Paralcaligenes ureilyticus (1), Pasteurella (2), Pasteurella aerogenes (21), Pasteurella bettyae (2), Pasteurella caballi (4), Pasteurella canis (7), Pasteurella dagmatis (7), Pasteurella haemolytica (1), Pasteurella langaaensis (2), Pasteurella mairii (7), Pasteurella multocida (115), Pasteurella pneumotropica (27), Pasteurella skyensis (1), Pasteurella sp. (34), Pasteurella stomatis (2), Pasteurella testudinis (2), Pasteurellaceae (1), Pasteurellaceae bacterium (57), Pasteurellaceae gen. sp. (2), Paucisalibacillus globulus (2), P-decomposing bacterium (1), Pectobacterium carotovorum (1), Pelistega europaea (3), Pelistega sp. (1), perchlorate-reducing bacterium (6), phenanthrene-degrading bacterium (1), Phocoenobacter uteri (1), photoautotrophic bacterium (1), Photorhabdus asymbiotica (16), Photorhabdus luminescens (91), Photorhabdus sp. (19), Photorhabdus temperata (37), Piscibacillus salipiscarius (1), Piscibacillus sp. (3), Planococcaceae bacterium (5), Planococcus antarcticus (4), Planococcus citreus (9), Planococcus columbae (1), Planococcus crocinus (1), Planococcus donghaensis (4), Planococcus kazaiensis (1), Planococcus kocurii (2), Planococcus maitriensis (2), Planococcus maritimus (13), Planococcus pelagicus (1), Planococcus psychrotoleratus (3), Planococcus rifietoensis (11), Planococcus salinarum (2), Planococcus sp. (86), Planomicrobium alkanoclasticum (3), Planomicrobium chinense (3), Planomicrobium glaciei (8), Planomicrobium koreense (7), Planomicrobium mcmeekinii (2), Planomicrobium okeanokoites (14),

		Planomicrobium psychrophilum (1), Planomicrobium sp. (28), Planomicrobium stackebrandtii (1), Polynucleobacter cosmopolitanus (180), Pontibacillus chungwhensis (2), Pontibacillus sp. (4), primary endosymbiont (1), Propionibacter sp. (1), Propionivibrio dicarboxylicus (1), Propionivibrio limicola (1), Propionivibrio pelophilus (2), Propionivibrio sp. (5), proteobacterium (3), proteobacterium symbiont (3), Proteus hauseri (13), Proteus mirabilis (83), Proteus penneri (9), Proteus sp. (30), Proteus vulgaris (26), Providencia alcalifaciens (22), Providencia burhodogranariea (1), Providencia heimbachae (3), Providencia rettgeri (24), Providencia rustigianii (4), Providencia sneebia (1), Providencia sp. (35), Providencia stuartii (12), Providencia vermicola (9), Pseudoburkholderia malthae (1), Pseudogulbenkiania sp. (12), Pseudogulbenkiania subflava (1), Pseudomonas aeruginosa (1), Pseudomonas jianii (1), Pseudomonas monteilii (1), Pseudomonas sp. (5), Pseudomonas xanthomarina (1), Pseudoxanthomonas taiwanensis (1), Pullulanibacillus naganoensis (1), Pullulanibacillus sp. (2), Pusillimonas noertemannii (1), Pusillimonas sp. (16), Pusillimonas terrae (2), Quatrionicoccus australiensis (1), rainbow trout intestinal bacterium (2), Ralstonia detusculanense (1), Ralstonia eutropha (13), Ralstonia insidiosa (3), Ralstonia mannitolilytica (12), Ralstonia pickettii (32), Ralstonia solanacearum (147), Ralstonia sp. (179), Ralstonia syzygii (7), Raoultella planticola (1), Rhizobiaceae bacterium (1), Rhizobium sp. (2), rhizosphere bacterium (1), Rhodococcus sp. (1), Rhodocyclaceae bacterium (4), Rhodocyclus purpureus (3), Rhodocyclus sp. (4), Rhodocyclus tenuis (9), rumen bacterium (3), Saccharibacillus kuerlensis (4), Saccharibacillus sacchari (1), Saccharococcus thermophilus (2), Salibacillus sp. (2), Salmonella sp. (1), SBR proteobacterium (1), secondary endosymbiont (various) (8), secondary symbiont (various) (4), Serratia marcescens (1), Sideroxydans lithotrophicus (4), Sideroxydans paludicola (1), Silvimonas amylolytica (1), Silvimonas iriomotensis (1), Silvimonas sp. (1), Silvimonas terrae (3), Simonsiella muelleri (5), SMC proteobacterium (6), Spirillum kriegii (1), Spirillum sp. (1), Spirillum winogradskyi (1), Sporolactobacillaceae bacterium (2), Sporolactobacillus dextrus (1), Sporolactobacillus inulinus (7), Sporolactobacillus kofuensis (3), Sporolactobacillus laevolacticus (2), Sporolactobacillus laevus (4), Sporolactobacillus putidus (1), Sporolactobacillus sp. (4), Sporolactobacillus terrae (1), Sporolactobacillus vineae (3), Sporosarcina aquimarina (8), Sporosarcina contaminans (1), Sporosarcina ginsengisoli (3), Sporosarcina globispora (7), Sporosarcina koreensis (2), Sporosarcina luteola (3), Sporosarcina newyorkensis (10), Sporosarcina pasteurii (2), Sporosarcina psychrophila (4), Sporosarcina saromensis (6), Sporosarcina soli (3), Sporosarcina sp. (57), Sporosarcina thermotolerans (1), Sporosarcina ureae (4), Staphylococcus sciuri (1), Staphylococcus sp. (2), Stenotrophomonas maltophilia (3), Stenotrophomonas rhizophila (1), Stenotrophomonas sp. (2), Sterolibacterium denitrificans (1), Sterolibacterium sp. (1), Streptomyces clavuligerus (1), Streptomyces indiaensis (1), Streptomyces sp. (4), Sulfobacillus sp. (2),

		Sulfuricella denitrificans (1), Sulfuritalea hydrogenivorans (1), swine fecal bacterium (2), swine manure bacterium (11), symbiont (various) (3), synthetic construct (2), Taylorella asinigenitalis (58), Taylorella equigenitalis (34), Telluria chitinolytica (1), Telluria mixta (3), Terrahaemophilus aromaticivorans (1), Thauera aminoaromatica (1), Thauera aromatica (1), Thauera butanivorans (3), Thauera linaloolentis (2), Thauera phenylacetica (2), Thauera sp. (6), thermal soil bacterium (3), Thermobacillus sp. (3), Thermus aquaticus (2), Thiobacillus (1), Thiobacillus aquaesulis (1), Thiobacillus denitrificans (5), Thiobacillus sajanensis (2), Thiobacillus sp. (7), Thiobacillus thioparus (11), Thiobacter sp. (1), Thiobacter subterraneus (1), Trachelomonas grandis (1), Tuberibacillus calidus (2), Tumebacillus ginsengisoli (1), Tumebacillus permanentifrigoris (1), Ultramicrobacter hongkongensis (1), ultramicrobacterium str. (6), uncultured 2,4-D-degrading bacterium (1), uncultured Acidobacteria bacterium (11), uncultured Acidobacteriales bacterium (21), uncultured Acidobacterium sp. (1), uncultured Acidothermus sp. (1), uncultured Actinobacillus sp. (6), uncultured actinobacterium (2), uncultured Aeromonas sp. (1), uncultured Aggregatibacter sp. (1), uncultured Alcaligenaceae bacterium (7), uncultured Alcaligenes sp. (10), uncultured Alicyclobacillaceae bacterium (2), uncultured Alicyclobacillus sp. (6), uncultured alpha proteobacterium (2), uncultured Aminomonas sp. (1), uncultured ammonia-oxidizing bacterium (33), uncultured anaerobic bacterium (1), uncultured Aneurinibacillus sp. (3), uncultured Anoxybacillus sp. (2), uncultured Antarctic bacterium (1), uncultured Antarctic sea ice bacterium (1), uncultured archaeon (2), uncultured Azoarcus sp. (5), uncultured Azospira sp. (35), uncultured Azovibrio sp. (3), uncultured Bacillaceae bacterium (9), uncultured Bacillales bacterium (6), uncultured Bacilli bacterium (11), uncultured Bacillus sp. (545), uncultured bacterium (7721), uncultured Banisveld landfill bacterium (1), uncultured beta proteobacterium (3183), uncultured Bradyrhizobiaceae bacterium (2), uncultured Brevibacillus sp. (9), uncultured Burkholderia sp. (249), uncultured Burkholderiaceae bacterium (75), uncultured Burkholderiales bacterium (16), uncultured Candidatus Accumulibacter sp. (19), uncultured Castellaniella sp. (2), uncultured Cellvibrio sp. (2), uncultured Citrobacter sp. (1), uncultured clade bacterium (5), uncultured Clostridia bacterium (1), uncultured Clostridiales bacterium (1), uncultured Cohnella sp. (1), uncultured Collimonas sp. (4), uncultured Comamonadaceae bacterium (3), uncultured compost bacterium (253), uncultured Cupriavidus sp. (21), uncultured Dechloromonas sp. (27), uncultured Dechlorosoma sp. (2), uncultured deep-sea bacterium (13), uncultured Deferribacteraceae bacterium (1), uncultured Dehalobacter sp. (3), uncultured delta proteobacterium (2), uncultured Denitratisoma sp. (4), uncultured Denitrobacter sp. (1), uncultured Derxia sp. (1), uncultured Duganella sp. (2),

		uncultured Dyella sp. (1), uncultured earthworm intestine bacterium (1), uncultured Eikenella sp. (3), uncultured eubacterium (14), uncultured Exiguobacterium sp. (16), uncultured Firmicutes bacterium (78), uncultured Frateuria sp. (1), uncultured freshwater bacterium (1), uncultured Gallionella sp. (20), uncultured Gallionellaceae bacterium (2), uncultured gamma proteobacterium (232), uncultured Geobacillus sp. (13), uncultured Geobacter sp. (1), uncultured Gram-positive bacterium (2), uncultured Haemophilus sp. (21), uncultured Halobacillus sp. (2), uncultured Halomonadaceae bacterium (1), uncultured halophilic eubacterium (1), uncultured Herbaspirillum sp. (9), uncultured Herminiimonas sp. (1), uncultured Holophaga sp. (2), uncultured Holophagaceae bacterium (4), uncultured hydrocarbon seep bacterium (4), uncultured Hydrogenophilaceae bacterium (5), uncultured Hydrogenophilales bacterium (6), uncultured Hyphomicrobiaceae bacterium (1), uncultured iron-reducing bacterium (1), uncultured Janthinobacterium sp. (16), uncultured Kingella sp. (9), uncultured Klebsiella sp. (1), uncultured Lentibacillus sp. (2), uncultured low G+C Gram-positive bacterium (12), uncultured marine bacterium (83), uncultured marine microorganism (2), uncultured Massilia sp. (132), uncultured Methylobacillus sp. (13), uncultured Methylobacter sp. (2), uncultured Methylocaldum sp. (1), uncultured Methylococcales bacterium (1), uncultured Methylophilaceae bacterium (43), uncultured Methylophilus sp. (8), uncultured Methylotenera sp. (2), uncultured Methyloversatilis sp. (3), uncultured Methylovorus sp. (4), uncultured Microbacterium sp. (1), uncultured microorganism (3), uncultured Microvirgula sp. (2), uncultured Morganella sp. (8), uncultured Naxibacter sp. (4), uncultured Neisseria sp. (24), uncultured Neisseriaceae bacterium (119), uncultured Nitrosomonadaceae bacterium (9), uncultured Nitrosomonadales bacterium (2), uncultured Nitrosospira sp. (6), uncultured Nitrosovibrio sp. (1), uncultured Nitrospira sp. (2), uncultured Oceanobacillus sp. (1), uncultured Oceanospirillales bacterium (9), uncultured organism (3851), uncultured Oxalobacteraceae bacterium (37), uncultured Paenibacillaceae bacterium (4), uncultured Paenibacillus sp. (26), uncultured Pandoraea sp. (3), uncultured Pasteurellaceae bacterium (5), uncultured Peptococcaceae bacterium (1), uncultured Photorhabdus sp. (1), uncultured Pietermaritzburg bacterium (2), uncultured Planococcaceae bacterium (2), uncultured Planococcus sp. (4), uncultured Planomicrobium sp. (16), uncultured Polynucleobacter sp. (6), uncultured Pontibacillus sp. (2), uncultured prokaryote (44), uncultured Propionibacterium sp. (2), uncultured Propionivibrio sp. (1), uncultured proteobacterium (136), uncultured Proteus sp. (1), uncultured Providencia sp. (203), uncultured Pseudomonas sp. (4), uncultured Pusillimonas sp. (2), uncultured Ralstonia sp. (964), uncultured rape rhizosphere bacterium (1), uncultured Rhodanobacter sp. (1), uncultured Rhodococcus sp. (1), uncultured Rhodocyclaceae bacterium (143), uncultured Rhodocyclales bacterium (7), uncultured Rhodocyclus sp. (7), uncultured rumen bacterium (33),

		uncultured Saccharococcus sp. (1), uncultured Salirhabdus sp. (1), uncultured SAR11 cluster alpha proteobacterium (1), uncultured sediment bacterium (7), uncultured Serratia sp. (2), uncultured Silvimonas sp. (1), uncultured Simonsiella sp. (4), uncultured sludge bacterium (3), uncultured soil bacterium (438), uncultured Sphingomonadaceae bacterium (1), uncultured Sporosarcina sp. (4), uncultured Staphylococcus sp. (3), uncultured Sterolibacterium sp. (2), uncultured synthetic wastewater bacterium (6), uncultured Telluria sp. (18), uncultured Thauera sp. (2), uncultured Thiobacillus sp. (32), uncultured Uromyces (1), uncultured Virgibacillus sp. (9), uncultured Vitreoscilla sp. (1), uncultured Vogesella sp. (1), uncultured Zoogloea sp. (2), Undibacterium oligocarboniphilum (1), unidentified (252), unidentified bacterium sp. (1), unidentified beta proteobacterium (3), unidentified eubacterium clone (11), unidentified Hailaer soda lake bacterium (3), unidentified proteobacterium (1), Uruburuella suis (2), Vibrio parahaemolyticus (1), Virgibacillus arcticus (1), Virgibacillus byunsanensis (1), Virgibacillus carmonensis (1), Virgibacillus chiguensis (1), Virgibacillus dokdonensis (8), Virgibacillus halodenitrificans (14), Virgibacillus kekensis (1), Virgibacillus litoralis (1), Virgibacillus marismortui (12), Virgibacillus necropolis (1), Virgibacillus olivae (3), Virgibacillus pantothenticus (12), Virgibacillus proomii (7), Virgibacillus salarius (5), Virgibacillus salinus (1), Virgibacillus sediminis (1), Virgibacillus siamensis (1), Virgibacillus sp. (134), Virgibacillus subterraneus (1), Virgibacillus xinjiangensis (1), Virgibacillus zhanjiangensis (1), Vitreoscilla stercoraria (2), Vogesella sp. (1), Volucribacter amazonae (2), Volucribacter psittacicida (5), Wautersia numazuensis (3), Wautersia sp. (4), Xenorhabdus beddingii (4), Xenorhabdus bovienii (44), Xenorhabdus budapestensis (4), Xenorhabdus cabanillasii (3), Xenorhabdus doucetiae (2), Xenorhabdus ehlersii (5), Xenorhabdus griffiniae (2), Xenorhabdus hominickii (7), Xenorhabdus indica (7), Xenorhabdus innexi (3), Xenorhabdus japonica (4), Xenorhabdus koppenhoeferi (1), Xenorhabdus kozodoii (6), Xenorhabdus mauleonii (1), Xenorhabdus miraniensis (1), Xenorhabdus nematophila (40), Xenorhabdus poinarii (8), Xenorhabdus romanii (1), Xenorhabdus sp. (24), Xenorhabdus stockiae (8), Xenorhabdus szentirmaii (4), Xenorhabdus vietnamensis (1), Zoogloea oryzae (3), Zoogloea sp. (2)
	GCG UAG AGA UUU GGA GGA	Acetobacter estunensis (2), Acetobacter pasteurianus (2), Alishewanella aestuarii (1), Alishewanella agri (1), Alishewanella fetalis (1), Alishewanella jeotgali (2), Alishewanella sp. (26), Antarctic bacterium (1), arsenic resistant soil bacterium (1), Arsukibacterium ikkense (1), Arthrobacter sp. (1), Bacillaceae bacterium (28), Bacillus acidiceler (6), Bacillus anthracis (1), Bacillus bataviensis (2), Bacillus butanolivorans (1), Bacillus cecembensis (1), Bacillus cereus (7), Bacillus coahuilensis (7), Bacillus decisifrondis (1), Bacillus firmus (2), Bacillus flexus (5), Bacillus granadensis (2), Bacillus halmapalus (5),

		Bacillus horikoshii (25), Bacillus horneckiae (10), Bacillus isronensis (2), Bacillus litoralis (3), Bacillus luciferensis (7), Bacillus massiliensis (11), Bacillus megaterium (6), Bacillus muralis (16), Bacillus niabensis (2), Bacillus niacini (1), Bacillus odysseyi (5), Bacillus oryzae (1), Bacillus pichinotyi (7), Bacillus shandongensis (3), Bacillus simplex (143), Bacillus sp. (775), Bacillus subtilis (4), bacterium (36), Brevibacterium frigoritolerans (12), Brevibacterium sp. (19), Caryophanon latum (3), Caryophanon sp. (7), Caryophanon tenue (2), chironomid egg mass bacterium (1), Chromatiaceae bacterium (1), Chryseomicrobium imtechense (3), compost metagenome (1), Corynebacterineae bacterium (2), Crocinobacterium jejui (1), endosymbiont (1), Epulopiscium fishelsoni (2), Epulopiscium sp. (27), Firmicutes bacterium (1), Flavobacterium sp. (1), freshwater bacterium (1), gamma proteobacterium (13), Geobacillus sp. (2), Geobacillus stearothermophilus (1), glacial ice bacterium (4), Gram-positive bacterium (1), groundwater biofilm bacterium (3), iron-reducing enrichment clone (1), Klebsiella pneumoniae (1), Kurthia gibsonii (20), Kurthia sibirica (2), Kurthia sp. (15), Kurthia zopfii (5), Lysinibacillus (1), Lysinibacillus boronitolerans (5), Lysinibacillus fusiformis (117), Lysinibacillus macroides (8), Lysinibacillus parviboronicapiens (2), Lysinibacillus sp. (135), Lysinibacillus sphaericus (165), Lysinibacillus xylanilyticus (8), Lysobacter sp. (1), marine bacterium (3), marine metagenome (1), Mesorhizobium sp. (4), Micrococcineae bacterium (3), Nanobacterium sp. (1), Neisseriaceae bacterium (5), Paenibacillaceae bacterium (10), Paenibacillus polymyxa (1), Paenibacillus sp. (1), Paenisporosarcina quisquiliarum (2), Paenisporosarcina sp. (3), Planococcaceae bacterium (3), Planococcus sp. (1), Pseudomonas sp. (1), Psychrobacillus insolitus (1), Psychrobacillus psychrodurans (8), Psychrobacillus psychrotolerans (2), Renibacterium salmoninarum (1), Rheinheimera aquimaris (5), Rheinheimera baltica (3), Rheinheimera chironomi (2), Rheinheimera pacifica (2), Rheinheimera perlucida (1), Rheinheimera soli (2), Rheinheimera sp. (35), Rheinheimera tangshanensis (1), Rheinheimera texasensis (3), Rhizobium sp. (3), Rummeliibacillus pycnus (6), Rummeliibacillus sp. (5), Rummeliibacillus stabekisii (6), Shewanella sp. (1), Solibacillus silvestris (26), Solibacillus sp. (4), Sporosarcina sp. (12), Staphylococcus sp. (2), swine effluent bacterium (1), uncultured Acinetobacter sp. (1), uncultured Alishewanella sp. (1), uncultured alpha proteobacterium (1), uncultured archaeon (1), uncultured Bacillaceae bacterium (2), uncultured Bacillales bacterium (1), uncultured Bacilli bacterium (1), uncultured Bacillus sp. (44), uncultured bacterium (1133), uncultured beta proteobacterium (44), uncultured Brevibacterium sp. (1), uncultured Caryophanon sp. (1), uncultured Chromatiaceae bacterium (1), uncultured Clostridia bacterium (1), uncultured Clostridiaceae bacterium (1), uncultured compost bacterium (16), uncultured Enterobacteriaceae bacterium (1), uncultured Firmicutes bacterium (8), uncultured gamma proteobacterium (16), uncultured Gram-positive bacterium (1), uncultured Klebsiella sp. (2), uncultured low G+C Gram-positive bacterium (2), uncultured Lysinibacillus sp. (8),

		uncultured marine bacterium (49), uncultured Methylophilaceae bacterium (7), uncultured Nitrospira sp. (1), uncultured organism (6), uncultured Planococcus sp. (2), uncultured prokaryote (3), uncultured Rheinheimera sp. (6), uncultured sheep mite bacterium (1), uncultured Shewanella sp. (1), uncultured soil bacterium (4), unidentified (7), Ureibacillus sp. (2), Variovorax sp. (1), Viridibacillus arenosi (5), Viridibacillus arvi (2), Viridibacillus neidei (3), Viridibacillus sp. (4)
	GCG **U**AG AGA UA**A** GGA GGA	Bacillus cereus (1), uncultured bacterium (5)
	GCG **U**AG AGA UA**C** GGA GGA	Candidatus Tremblaya princeps (1), uncultured bacterium (3)
	GCG **U**AG AGA UA**G** GGA GGA	Bacterium (1), Clostridiaceae bacterium (1), Pseudomonas sp. (1), rumen bacterium (2), Ruminococcus sp. (1), uncultured bacterium (549), uncultured Clostridiaceae bacterium (1), uncultured rumen bacterium (107)
	GCG **U**AG AGA UAU **A**GA GGA	Bacillus thuringiensis (1)
	GCG **U**AG AGA UAU G**A**A GGA	Pseudoalteromonas sp. (1), Psychrobacter sp. (1), uncultured bacterium (1), uncultured Shewanella sp. (1)
	GCG **U**AG AGA UAU G**C**A GGA	Bacillus sp. (1)
	GCG **U**AG AGA UAU GG**G** GGA	uncultured Bacillus sp. (1), uncultured bacterium (2)
	GCG **U**AG AGA UAU GG**U** GGA	uncultured bacterium (3)
	GCG **U**AG AGA UAU GGA **A**GA	Bacillus cereus (1), Bacillus sp. (2), freshwater sediment metagenome (1), Nitrosomonas aestuarii (3), Nitrosomonas marina (5), Nitrosomonas oligotropha (4), Nitrosomonas sp. (22), Nitrosomonas ureae (3), secondary endosymbiont (various) (2), uncultured ammonia-oxidizing bacterium (32), uncultured bacterium (72), uncultured beta proteobacterium (1), uncultured compost bacterium (1), uncultured Nitrosomonas sp. (4), uncultured rumen bacterium (1), uncultured soil bacterium (1), unidentified (31)
	GCG **U**AG AGA UAU GGA **C**GA	Bacillus sp. (1), uncultured bacterium (1)
	GCG **U**AG AGA UAU GGA G**A**A	Bacillus sp. (1), Bacillus thuringiensis serovar graciosensis (1), Paenibacillus assamensis (1), uncultured bacterium (3), Ureibacillus thermosphaericus (1)
	GCG **U**AG AGA UAU GGA GG**G**	Bacillus cereus (2), Bacillus sp. (2), Bacillus thuringiensis (1), uncultured bacterium (5)
	GCG **U**AG AGA UAU GGA GG**U**	Staphylococcus sp. (1), uncultured bacterium (1)
	GCG C**G**G A**U**A UAU GGA GGA	uncultured bacterium (1)
	GCG C**U**G AGA UAU GG**G** GGA	uncultured bacterium (1)
	GCG CA**A** A**A**A UAU GGA GGA	uncultured Staphylococcus sp. (1)
	GCG CA**A** AGA U**U**U GGA GGA	Staphylococcus sp. (1)
	GCG CA**A** AGA UAU GG**G** GGA	Staphylococcus warneri (1)
	GCG CA**C** A**U**A UAU GGA GGA	Paenibacillus abekawaensis (1)
	GCG CA**C** AGA **C**AU GGA GGA	uncultured organism (1)
	GCG CA**C** AGA U**C**U GGA GGA	uncultured organism (2)

	GCG CA**C** AGA UAU GGA **C**GA	uncultured bacterium (2)
	GCG CA**U** AGA U**C**U GGA GGA	uncultured organism (1)
	GCG CAG A**C**A U**C**U GGA GGA	uncultured bacterium (1)
	GCG CAG A**U**A U**C**U GGA GGA	Actinobaculum massiliense (20), Actinobaculum schaalii (19), Actinobaculum sp. (2), Actinobaculum suis (1), Actinobaculum urinale (4), Arthrobacter sp. (1), bacterium enrichment culture clone (2), bacterium (1), Citrus greening disease-associated bacterium (1), Microbacterium sp. (1), Staphylococcaceae bacterium (1), uncultured Acidobacteria bacterium (5), uncultured actinobacterium (3), uncultured anaerobic bacterium (1), uncultured bacterium (852), uncultured Bellilinea sp. (3), uncultured Chloroflexi bacterium (5), uncultured Coriobacteriales bacterium (1), uncultured eubacterium (1), uncultured Longilinea sp. (4), uncultured marine bacterium (1), uncultured microorganism (4), uncultured prokaryote (1), uncultured soil bacterium (2), Y-symbiont (1)
	GCG CAG A**U**A U**G**U GGA GGA	Alcaligenes faecalis (1), Glycomyces algeriensis (1), Glycomyces arizonensis (1), Glycomyces endophyticus (1), Glycomyces harbinensis (5), Glycomyces illinoisensis (1), Glycomyces lechevalierae (2), Glycomyces mayteni (1), Glycomyces mongolensis (2), Glycomyces rutgersensis (2), Glycomyces sambucus (1), Glycomyces scopariae (2), Glycomyces sp. (17), Glycomyces tenuis (1), Haloglycomyces albus (1), Listeria monocytogenes (1), Micromonosporaceae bacterium (1), Stackebrandtia albiflava (1), Stackebrandtia nassauensis (3), uncultured Actinobacteridae bacterium (1), uncultured bacterium (47), uncultured Glycomyces sp. (1)
	GCG CAG A**U**A U**U**U GGA GGA	Arsenophonus endosymbiont (various) (2), secondary endosymbiont (1), uncultured bacterium (7), uncultured rumen bacterium (1)
	GCG CAG A**U**A UA**A** GGA GGA	Brevibacterium sp. (1), marine metagenome (2), uncultured actinobacterium (2), uncultured bacterium (8)
	GCG CAG A**U**A UA**C** GGA GGA	uncultured bacterium (9)
	GCG CAG A**U**A UA**G** GGA GGA	uncultured bacterium (1)
	GCG CAG A**U**A UAU **A**GA GGA	uncultured bacterium (1)
	GCG CAG A**U**A UAU GGA **A**GA	Lactobacillus acidipiscis (1), uncultured bacterium (29)
	GCG CAG A**U**A UAU GGA GG**C**	uncultured bacterium (1)
	GCG CAG A**U**A UAU GGA GG**G**	uncultured bacterium (1)
	GCG CAG AGA U**CA** GGA GGA	Candidatus Cloacamonas acidaminovorans (2), uncultured actinobacterium (1), uncultured anaerobic bacterium (1), uncultured bacterium (793), uncultured Candidatus Cloacamonas sp. (2), uncultured gamma proteobacterium (1), uncultured Geobacillus sp. (1), uncultured organism (19), uncultured planctomycete (1), uncultured prokaryote (11), uncultured proteobacterium (1), uncultured Spirochaetes bacterium (1), unidentified (3)
	GCG CAG AGA U**CC** GGA GGA	uncultured Chloroflexi bacterium (1), uncultured organism (1)

	GCG CAG AGA UCG GGA GGA	uncultured Acidimicrobidae bacterium (4), uncultured Acidimicrobineae bacterium (1), uncultured actinobacterium (6), uncultured archaeon (1), uncultured bacterium (47), uncultured Chloroflexi bacterium (5), uncultured Nitrospira sp. (1), uncultured organism (3), uncultured prokaryote (1), uncultured rumen bacterium (3), uncultured soil bacterium (2), uncultured Termite group 1 bacterium (2)
	GCG CAG AGA UCU GAA GGA	Pseudoalteromonas sp. (1), uncultured bacterium (2), uncultured marine microorganism (1), uncultured proteobacterium (1), Vibrio sp. (1)
	GCG CAG AGA UCU GGA AGA	uncultured bacterium (1)
	GCG CAG AGA UCU GGA CGA	uncultured bacterium (1)
	GCG CAG AGA UGG GGA GGA	uncultured bacterium (1)
	GCG CAG AGA UGU GGA AGA	uncultured bacterium (1)
	GCG CAG AGA UUA GGA GGA	uncultured bacterium (135), uncultured rumen bacterium (1)
	GCG CAG AGA UUC GGA GGA	uncultured bacterium (2)
	GCG CAG AGA UUG GGA GGA	uncultured bacterium (9), uncultured rumen bacterium (1)
	GCG CAG AGA UAA UGA GGA	uncultured bacterium (1)
	GCG CAG AGA UAU GGG GGG	uncultured bacterium (2)
	NCG UAG AGA UCU GGA GGA	Thioalkalicoccus limnaeus (1), uncultured Acinetobacter sp. (1), uncultured bacterium (1)
	NCG UAG AGA UGU GGA GGA	uncultured bacterium (1), uncultured soil bacterium (1)
	GNG UAG AUA UAU GGA GGA	uncultured bacterium (1), uncultured Streptococcus sp. (1)
	GNG UAG AGA UCU GGA GGA	Aeromonas sp. (1), uncultured Acinetobacter sp. (3)
	GNG UAG AGA UGU GGA GGA	Bacillus megaterium (1), Bacillus pumilus (1), Sulfobacillus sp. (1), swine manure bacterium (1), uncultured Ralstonia sp. (2), uncultured soil bacterium (2)
	GCN UAG AGA UCU GGA GGA	Geobacillus thermodenitrificans (1), Psychrobacter sp. (1), uncultured Acinetobacter sp. (1)
	GCN UAG AGA UGU GGA GGA	Bacillus subtilis (1), uncultured beta proteobacterium (1)
	GCG NAG AGA UGC GGA GGA	uncultured bacterium (1)
	GCG UNG AGA UGU GGA GGA	Aggregatibacter aphrophilus (1), Bacillus subtilis (1), Bisgaard Taxon (1), Haemophilus aegyptius (1), Neisseria animalis (1), Paenibacillus apiarius (2), uncultured soil bacterium (2)
	GCG UAN AUA UAU GGA GGA	Enterococcus faecalis (1), Enterococcus hirae (1), Lactococcus lactis (1), Nostocoida limicola (2), Streptococcus anginosus (1), Tetragenococcus halophilus (3), uncultured Catenibacterium sp. (1), uncultured Streptococcus sp. (1)
	GCG UAN AGA UCU GGA GGA	Acinetobacter baumannii (1), Acinetobacter sp. (3), Alteromonadales bacterium (1), bacterium (2), Enterobacter aerogenes (2), Enterobacter nimipressuralis (1), Enterobacter sp. (1), Erwinia chrysanthemi (1),

		Erwinia rhapontici (1), Erwinia tracheiphila (1), Escherichia coli (1), glacial ice bacterium (1), Klebsiella pneumoniae (1), Pantoea stewartii (1), Pectobacterium wasabiae (1), Psychrobacter aff. glacinola (1), Raoultella ornithinolytica (2), Regiella symbiont (1), Salmonella enterica (1), Serratia marcescens (1), Shewanella saccharophilus (1), uncultured Acinetobacter sp. (34), uncultured bacterium (13), uncultured Enterobacteriaceae bacterium (1), uncultured Escherichia sp. (1), uncultured gamma proteobacterium (2), uncultured Shigella sp. (2)
	GCG **U**A**N** AGA U**G**U GGA GGA	Bacillus endophyticus (1), Bacillus licheniformis (1), Bacillus megaterium (1), Bacillus pumilus (1), Bacillus sp. (4), Bacillus subtilis (1), bacterium str. (1), beta proteobacterium (1), Brevibacillus sp. (1), Burkholderia caledonica (1), Denitrobacter permanens (1), glacial ice bacterium (2), Paenibacillus illinoisensis (1), primary endosymbiont (1), Providencia sp. (1), uncultured Bacillus sp. (2), uncultured bacterium (18), uncultured beta proteobacterium (3), uncultured gamma proteobacterium (1), uncultured Herbaspirillum sp. (1), uncultured Ralstonia sp. (10), uncultured soil bacterium (3)
	GCG **U**A**N** AGA U**U**U GGA GGA	Bacillus sp. (1), bacterium (1)
	GCG **U**A**N** AGA UA**G** GGA GGA	uncultured bacterium (3), uncultured rumen bacterium (1)
	GCG **U**AG **NU**A UAU GGA GGA	uncultured Streptococcus sp. (1)
	GCG **U**AG **N**GA U**C**U GGA GGA	uncultured soil bacterium (1)
	GCG **U**AG **N**GA U**G**U GGA GGA	uncultured soil bacterium (1), uncultured Ralstonia sp. (1)
	GCG **U**AG A**N**A U**C**U GGA GGA	Buchnera aphidicola (1), Enterobacter sp. (1), uncultured Acinetobacter sp. (1), uncultured bacterium (2), uncultured Enterobacter sp. (1), uncultured gamma proteobacterium (1)
	GCG **U**AG A**N**A U**G**U GGA GGA	Bacillus amyloliquefaciens (1), Bacillus farraginis (1), Bacillus tipchiralis (1), Brevibacillus brevis (1), Planococcus sp. (1), uncultured Ralstonia sp. (1)
	GCG **U**AG A**UN** UAU GGA GGA	Alkalibacterium iburiense (1), uncultured Streptococcus sp. (2)
	GCG **U**AG A**U**A U**N**U GGA GGA	Alcaligenes faecalis (1), Cellvibrio sp. (1), Proteus mirabilis (1), uncultured bacterium (1)
	GCG **U**AG A**U**A UA**N** GGA GGA	uncultured bacterium (2), uncultured Bulleidia sp. (1)
	GCG **U**AG A**U**A UAU GGA **N**GA	Aerococcus sanguinicola (1), Streptococcus anginosus (1), uncultured Enterococcaceae bacterium (1)
	GCG **U**AG A**U**A UAU GGA GG**N**	Solobacterium sp. (1), uncultured bacterium (1), uncultured Streptococcus sp. (1)
	GCG **U**AG AG**N** U**C**U GGA GGA	Acidithiobacillus ferrooxidans (1)
	GCG **U**AG AGA **NC**U GGA GGA	Escherichia coli (1), Psychrobacter immobilis (1), Psychrobacter sp. (1)
	GCG **U**AG AGA **NG**U GGA GGA	Bacillus sp. (1)
	GCG **U**AG AGA U**CN** GGA GGA	Kyrpidia tusciae (1), Regiella symbiont (1), uncultured proteobacterium (1)
	GCG **U**AG AGA U**C**U G**N**A GGA	Acinetobacter johnsonii (4), Psychrobacter sanguinis (1), Shewanella halifaxensis (1), uncultured bacterium (1), Yersinia enterocolitica (1)
	GCG **U**AG AGA U**C**U GG**N** GGA	uncultured bacterium (1)

	GCG **U**AG AGA U**C**U GGA **N**GA	uncultured Acinetobacter sp. (4)
	GCG **U**AG AGA U**C**U GGA G**N**A	uncultured bacterium (1)
	GCG **U**AG AGA U**GN** GGA GGA	Geobacillus sp. (1), uncultured soil bacterium (1)
	GCG **U**AG AGA U**G**U **N**GA GGA	uncultured soil bacterium (2), uncultured Ralstonia sp. (1)
	GCG **U**AG AGA U**G**U G**N**A GGA	Bacillus flexus (1), Bacillus licheniformis (1), Bacillus sp. (1), uncultured bacterium (1), uncultured Janthinobacterium sp. (1), uncultured Ralstonia sp. (3)
	GCG **U**AG AGA U**G**U GG**N** GGA	Avibacterium volantium (1), uncultured soil bacterium (2)
	GCG **U**AG AGA U**G**U GGA **N**GA	Bacillus subtilis (1), Nitrosospira sp. (1), Photorhabdus luminescens (1), uncultured bacterium (1), uncultured Massilia sp. (1), uncultured Ralstonia sp. (2)
	GCG **U**AG AGA U**G**U GGA G**N**A	Bacillus flexus (1), Herbaspirillum sp. (1), Paenibacillus sp. (1), uncultured bacterium (1), uncultured Massilia sp. (1)
	GCG **U**AG AGA U**G**U GGA GG**N**	Bacillus sp. (1), uncultured Massilia sp. (1), uncultured Ralstonia sp. (3), uncultured soil bacterium (4)
	GCG **U**AG AGA U**NG** GGA GGA	uncultured bacterium (1)
	GCG **U**AG AGA U**N**U G**A**A GGA	uncultured bacterium (1)
	GCG **U**AG AGA U**UN** GGA GGA	Bacillus horneckiae (1), Lysinibacillus sphaericus (1), uncultured bacterium (2)
	GCG **U**AG AGA U**U**U **N**GA GGA	Bacillus horneckiae (1)
	GCG CAG **NU**A U**C**U GGA GGA	uncultured bacterium (1)
	GCG CAG A**N**A U**CA** GGA GGA	Actinomycetales bacterium (1)
	GCG CAG A**U**A U**CN** GGA GGA	Arthrobacter sp. (1), Streptomyces sp. (1)
	GCG CAG A**U**A U**NA** GGA GGA	Corynebacterium renale (1), Micromonospora auratinigra (1), Streptomyces lavendulae (2), Streptomyces virginiae (1)
	GCG CAG A**U**A U**NC** GGA GGA	uncultured bacterium (2)
	GCG CAG A**U**A U**GN** GGA GGA	uncultured soil bacterium (1)
	GCG CAG AG**N** U**CG** GGA GGA	uncultured Firmicutes bacterium (1)
	GCG CAG AGA U**CA** **N**GA GGA	uncultured bacterium (1)

Name of the probe: Stau16S Kempf

Target organism: *Staphylococcus aureus*

Sequence of the probe: GAA GCA AGC TTC TCG TCC G

Date of *in-silico* assessment: November 2017

Mismatch count	Ribosomal RNA sequence corresponding to the probe	Matching with known sequences (without italics)
0 mm	C GGA CGA GAA GCU UGC UUC	bacterium (3), Staphylococcus aureus (449), Staphylococcus epidermidis (1), Staphylococcus equorum (1), Staphylococcus phage (4), Staphylococcus sp. (12), uncultured bacterium (76), uncultured microorganism (11), uncultured organism (65), uncultured Staphylococcus sp. (27), unidentified (11)
	C GGA NGA GAA GCU UGC UUC	Staphylococcus aureus (2)
1 mm	C AGA CGA GAA GCU UGC UUC	Staphylococcus sciuri (1), uncultured bacterium (1)
	C GGG CGA GAA GCU UGC UUC	uncultured bacterium (1), uncultured microorganism (2)
	C GGA AGA GAA GCU UGC UUC	uncultured bacterium (1)
	C GGA UGA GAA GCU UGC UUC	Staphylococcus aureus (8), Staphylococcus phage (1), uncultured bacterium (3), uncultured organism (7), uncultured Staphylococcus sp. (7)
	C GGA CGA GGA GCU UGC UUC	Staphylococcus aureus (1)
	C GGA CGA GAA GUU UGC UUC	Staphylococcus aureus (4)
	C GGA CGA GAA GCC UGC UUC	uncultured organism (1)
	C GGA CGA GAA GCU GGC UUC	uncultured organism (1)
	C GGA CGA GAA GCU UCC UUC	planctomycete (1), Planctomyces sp. (3), uncultured bacterium (7), uncultured Planctomyces sp. (1), uncultured planctomycete (3)
	C GGA CGA GAA GCU UUC UUC	Staphylococcus aureus (1)
	C GNN CGA GAA GCU UCC UUC	uncultured bacterium (1)
2 mm	A UGA CGA GAA GCU UGC UUC	Bacillus sp. (1), Kurthia gibsonii (12), Kurthia sp. (6), Rummeliibacillus pycnus (1), uncultured bacterium (5), uncultured compost bacterium (1)

	A GGA **U**GA GAA GCU UGC UUC	uncultured bacterium (1)
	A GGA C**A**A GAA GCU UGC UUC	uncultured bacterium (1)
	G **A**GA CGA GAA GCU UGC UUC	uncultured Megasphaera sp. (1)
	U **A**GA CGA GAA GCU UGC UUC	uncultured bacterium (1)
	U **U**GA CGA GAA GCU UGC UUC	Paenibacillus sp. (3), Saccharibacillus kuerlensis (4)
	U GGA **A**GA GAA GCU UGC UUC	bacterium canine oral taxon (2), Paenibacillus gansuensis (1)
	U GGA **U**GA GAA GCU UGC UUC	uncultured bacterium (1)
	C **A**GA **A**GA GAA GCU UGC UUC	Jeotgalibacillus salarius (1), uncultured Staphylococcaceae bacterium (1)
	C **A**GA **G**GA GAA GCU UGC UUC	uncultured bacterium (1)
	C **A**GA **U**GA GAA GCU UGC UUC	Staphylococcus fleurettii (1), Staphylococcus lentus (6), Staphylococcus sciuri (27), Staphylococcus simiae (2), Staphylococcus sp. (35), Staphylococcus vitulinus (3), uncultured bacterium (710), uncultured compost bacterium (1), uncultured rumen bacterium (1), uncultured soil bacterium (1), uncultured Staphylococcus sp. (7)
	C **A**GA CGA G**G**A GCU UGC UUC	Staphylococcus epidermidis (2), synthetic construct (1), uncultured Bacillus sp. (1), uncultured bacterium (15), uncultured Staphylococcus sp. (2), unidentified (1)
	C **U**GA **G**GA GAA GCU UGC UUC	uncultured synthetic wastewater bacterium (2)
	C **U**GA **U**GA GAA GCU UGC UUC	Bacillus megaterium (1), Bacillus sp. (5), bacterium (1), Lysinibacillus sphaericus (3), uncultured bacterium (14), uncultured compost bacterium (1)
	C **U**GA C**U**A GAA GCU UGC UUC	uncultured Bacillus sp. (1)
	C G**AG** CGA GAA GCU UGC UUC	uncultured bacterium (3), uncultured planctomycete (7), uncultured Planctomycetacia bacterium (6)
	C G**A**A **G**GA GAA GCU UGC UUC	uncultured bacterium (2)
	C G**A**A CGA G**G**A GCU UGC UUC	uncultured bacterium (1)
	C G**A**A CGA GAA **C**CU UGC UUC	uncultured bacterium (1), uncultured Chloroflexi bacterium (1)
	C G**A**A CGA GAA GCU **C**GC UUC	uncultured bacterium (1)
	C G**A**A CGA GAA GCU **G**GC UUC	uncultured bacterium (3)
	C G**A**A CGA GAA GCU U**A**C UUC	Hyphomonadaceae bacterium (1), uncultured alpha proteobacterium (2), uncultured bacterium (3)
	C G**A**A CGA GAA GCU U**C**C UUC	uncultured alpha proteobacterium (1)
	C G**A**A CGA GAA GCU U**U**C UUC	uncultured bacterium (1)
	C G**A**A CGA GAA GCU UG**G** UUC	marine metagenome (1), uncultured bacterium (3)
	C G**C**A CGA GAA GCU U**C**C UUC	uncultured bacterium (1)
	C GG**G** **A**GA GAA GCU UGC UUC	uncultured bacterium (1)
	C GG**G** **G**GA GAA GCU UGC UUC	bacterium (1), Ralstonia mannitolilytica (1), Ralstonia sp. (5), uncultured bacterium (23), uncultured beta proteobacterium (1)

	C GG**G** **U**GA GAA GCU UGC UUC	Pasteurella sp. (1), Pasteurellaceae bacterium (1)
	C GG**U** **A**GA GAA GCU UGC UUC	uncultured bacterium (3), uncultured beta proteobacterium (3)
	C GGA **AU**A GAA GCU UGC UUC	uncultured gamma proteobacterium (1)
	C GGA **UA**A GAA GCU UGC UUC	uncultured bacterium (1)
	C GGA **UU**A GAA GCU UGC UUC	uncultured bacterium (1)
	C GGA **U**GA GAA **A**CU UGC UUC	uncultured organism (1)
	C GGA C**U**A **U**AA GCU UGC UUC	uncultured microorganism (1)
	C GGA CGA G**G**A GCU UGC U**C**C	Staphylococcus schleiferi (1), uncultured bacterium (4), uncultured organism (1), uncultured Staphylococcus sp. (1)
	C GGA CGA GA**U** **U**CU UGC UUC	uncultured organism (1)
	C GGA CGA GAA **A**CU U**C**C UUC	uncultured planctomycete (2)
	C GGA CGA GAA G**G**U **A**GC UUC	Alphaproteobacteria (1), Kordiimonas sp. (1), Thalassospira sp. (7), uncultured alpha proteobacterium (1), uncultured bacterium (4)
	C GGA CGA GAA G**G**U U**C**C UUC	alpha proteobacterium (3), bacterium (2), marine proteobacterium (1), Rhodospirillaceae bacterium (2), Thalassospira profundimaris (2), Thalassospira sp. (23), uncultured alphaproteobacterium (1), uncultured bacterium (5), unidentified (1)
	C GGA CGA GAA G**U**U U**C**C UUC	Planctomyces maris (2), uncultured bacterium (1), uncultured Planctomyces sp. (1)
	C GGA CGA GAA GCU **GA**C UUC	uncultured bacterium (1)
	A **U**GA **N**GA GAA GCU UGC UUC	Kurthia sp. (1)
	U **U**GA **N**GA GAA GCU UGC UUC	Paenibacillus amylolyticus (1), Paenibacillus barcinonensis (1), Paenibacillus daejeonensis (1), Paenibacillus illinoisensis (1), Paenibacillus sp. (1), Paenibacillus taichungensis (1)
	N G**C**A CG**G** GAA GCU UGC UUC	uncultured bacterium (1)
	C **CN**A **G**GA GAA GCU UGC UUC	Paenibacillus sp. (1)
	C **N**GA **UU**A GAA GCU UGC UUC	Bacillus sp. (1), uncultured Bacillus sp. (1)
	C GG**N** **AA**A GAA GCU UGC UUC	secondary endosymbiont (various) (1)

Name of the probe: Stemal Hogardt

Target organism: *Stenotrophomonas maltophilila*

Sequence of the probe: GTC GTC CAG TAT CCA CTG C

Date of *in-silico* assessment: February 2018

Mismatch count	**Ribosomal RNA sequence corresponding to the probe**	**Matching with known sequences (without italics)**
0 mm	G CAG UGG AUA CUG GAC GAC	gamma proteobacterium (4), nitrogen-fixing bacterium (1), Pseudomonas geniculata (1), Stenotrophomonas maltophilia (73), Stenotrophomonas sp. (18), uncultured bacterium (160), uncultured gamma proteobacterium (1), uncultured organism (1), uncultured Pseudomonas sp. (1), uncultured Stenotrophomonas bacterium (1), uncultured Stenotrophomonas sp. (13), uncultured Xanthomonadales bacterium (1)
	G CAG UGG AUA CUG **N**AC GAC	uncultured bacterium (2)
	G CAG UGG AUA CUG G**N**C GAC	Stenotrophomonas maltophilia (4), Stenotrophomonas pavanii (1), Stenotrophomonas sp. (1)
	G CAG UG**N** AUA CUG **N**AC GAC	uncultured bacterium (1)
	G CAG UGG AUA CUG G**NN** GAC	uncultured bacterium (1)
	G CA**N** UGG AUA CU**N** GAC **N**AC	gamma proteobacterium (1)
1 mm	G C**G**G UGG AUA CUG GAC GAC	uncultured bacterium (2)
	G CA**U** UGG AUA CUG GAC GAC	Stenotrophomonas sp. (1)
	G CAG U**A**G AUA CUG GAC GAC	uncultured bacterium (1)
	G CAG UGG A**A**A CUG GAC GAC	Leptolyngbya laminosa (1), Leptolyngbya sp. (1), Stenotrophomonas chelatiphaga (1), Stenotrophomonas maltophilia (23), Stenotrophomonas sp. (20), uncultured bacterium (54), uncultured gamma proteobacterium (1), uncultured Stenotrophomonas sp. (65), uncultured Xanthomonadaceae bacterium (1), Xanthomonadaceae bacterium (1), Xanthomonas group bacterium (1), Xanthomonas sp. (1)
	G CAG UGG A**G**A CUG GAC GAC	uncultured Stenotrophomonas sp. (1)
	G CAG UGG AUA CUG G**C**C GAC	Stenotrophomonas sp. (1)
	G CAG UGG AUA CUG G**G**C GAC	Acetobacter pasteurianus (1), Acetobacter sp. (1), alpha proteobacterium (1), bacterium (7), bacterium enrichment culture clone (2), gamma proteobacterium (6), proteobacterium symbiont (1),

		Pseudomonas aeruginosa (1), Pseudomonas geniculata (15), Pseudomonas hibiscicola (4), Pseudomonas sp. (17), Pseudoxanthomonas dokdonensis (1), Pseudoxanthomonas ginsengisoli (4), Pseudoxanthomonas sacheonensis (1), Pseudoxanthomonas sp. (6), Stenotrophomonas maltophilia (254), Stenotrophomonas pavanii (1), Stenotrophomonas rhizophila (23), Stenotrophomonas sp. (214), Stenotrophomonas-like sp. (1), uncultured Azoarcus sp. (2), uncultured bacterium (539), uncultured Burkholderia sp. (1), uncultured gamma proteobacterium (23), uncultured marine bacterium (1), uncultured microorganism (4), uncultured organism (1), uncultured prokaryote (1), uncultured proteobacterium (2), uncultured Pseudomonas sp. (7), uncultured Pseudoxanthomonas sp. (1), uncultured rumen bacterium (1), uncultured soil bacterium (5), uncultured Stenotrophomonas sp. (98), uncultured Xanthomonadales bacterium (13), uncultured Xanthomonas sp. (7), unidentified (1), Vibrio sp. (2), Xanthomonadaceae bacterium (2), Xanthomonas sp. (10)
	G CAG UGG AUA CUG GA**U** GAC	ant fungus garden metagenome (1), bacterium (2), Pseudomonas sp. (6), Stenotrophomonas maltophilia (35), Stenotrophomonas sp. (4), uncultured alpha proteobacterium (1), uncultured bacterium (288), uncultured gamma proteobacterium (104), uncultured marine bacterium (1), uncultured organism (229), uncultured Pseudomonas sp. (3), uncultured Stenotrophomonas bacterium (6), uncultured Stenotrophomonas sp. (32), uncultured Xanthomonadales bacterium (1)
	G CAG UGG AUA CUG GAC **A**AC	uncultured bacterium (27)
	G CAG UGG AUA CUG GAC G**G**C	uncultured bacterium (3)
	G C**N**G UGG AUA CUG GAC **U**AC	gamma proteobacterium (1)
	G CAG UG**N** A**A**A CUG GAC GAC	uncultured bacterium (1)
	G CAG UGG AUA CUG G**GN** GAC	Stenotrophomonas maltophilia (1)
	G CAG UGG AUA CUG G**G**C **N**AC	Stenotrophomonas maltophilia (1), uncultured rumen bacterium (1)
	G C**N**G UGG AUA CUG G**G**C GA**N**	Stenotrophomonas maltophilia (1)
2 mm	**C** CAG UGG AUA CUG G**G**C GAC	Stenotrophomonas sp. (1)
	U CA**U** UGG AUA CUG GAC GAC	uncultured organism (1)
	G **U**AG UGG A**A**A CUG GAC GAC	uncultured bacterium (1)
	G C**C**G UGG AUA CUG GAC G**U**C	uncultured Anaerophaga sp. (2)
	G C**GA** UGG AUA CUG GAC GAC	uncultured gamma proteobacterium (1)
	G C**G**G UGG A**A**A CUG GAC GAC	uncultured Stenotrophomonas sp. (1)
	G C**G**G UGG AUA CUG GA**A** GAC	uncultured bacterium (1)
	G C**G**G UGG AUA CUG GA**U** GAC	uncultured organism (1)

	G CA**A** UGG AUA CUG G**G**C GAC	Stenotrophomonas sp. (1), uncultured Xanthomonas sp. (1), Xanthomonas sp. (1)
	G CA**A** UGG AUA CUG GAC **C**AC	uncultured bacterium (1)
	G CA**C** UGG AUA CUG G**G**C GAC	Stenotrophomonas sp. (1)
	G CA**C** UGG AUA CUG GA**U** GAC	uncultured organism (1)
	G CA**C** UGG AUA CUG GAC G**G**C	uncultured delta proteobacterium (1)
	G CA**U** U**U**G AUA CUG GAC GAC	uncultured bacterium (1)
	G CA**U** UGG A**A**A CUG GAC GAC	uncultured spirochete (1), uncultured Treponema sp. (1)
	G CA**U** UGG AUA CUG G**C**C GAC	uncultured bacterium (1), uncultured delta proteobacterium (1)
	G CA**U** UGG AUA CUG GA**A** GAC	Geobacter sp. (6), iron-reducing bacterium enrichment culture clone (3), uncultured bacterium (22), uncultured delta proteobacterium (6), uncultured Geobacteraceae bacterium (2), uncultured soil bacterium (1)
	G CA**U** UGG AUA CUG GA**G** GAC	uncultured bacterium (5)
	G CA**U** UGG AUA CUG GA**U** GAC	uncultured bacterium (8)
	G CA**U** UGG AUA CUG GAC **A**AC	uncultured bacterium (2)
	G CAG **A**GG AUA CUG G**G**C GAC	uncultured bacterium (2)
	G CAG **C**GG AUA CUG G**G**C GAC	Stenotrophomonas sp. (1)
	G CAG **C**GG AUA CUG GA**A** GAC	uncultured bacterium (1)
	G CAG **G**GG AUA CUG GAC G**G**C	uncultured bacterium (7)
	G CAG U**U**G AUA CUG **A**AC GAC	uncultured candidate division bacterium (2)
	G CAG U**U**G AUA CUG G**C**C GAC	uncultured alpha proteobacterium (3), uncultured bacterium (35), uncultured deep-sea bacterium (4), uncultured gamma proteobacterium (45), uncultured Haliea sp. (2), uncultured marine bacterium (36), uncultured organism (2), uncultured proteobacterium (1), uncultured soil bacterium (5)
	G CAG U**U**G AUA CUG G**G**C GAC	uncultured bacterium (1)
	G CAG U**U**G AUA CUG G**U**C GAC	uncultured bacterium (1)
	G CAG U**U**G AUA CUG GA**U** GAC	uncultured bacterium (1)
	G CAG U**U**G AUA CUG GAC G**C**C	uncultured bacterium (101)
	G CAG U**U**G AUA CUG GAC G**U**C	uncultured bacterium (3)
	G CAG UG**C** AUA CUG GA**U** GAC	uncultured organism (1)
	G CAG UG**U** AUA CUG G**G**C GAC	uncultured bacterium (1)
	G CAG UGG **G**UA CUG G**G**C GAC	Stenotrophomonas rhizophila (1), Stenotrophomonas sp. (1)
	G CAG UGG **G**UA CUG GA**U** GAC	uncultured bacterium (1)
	G CAG UGG A**A**A **U**UG GAC GAC	uncultured Stenotrophomonas sp. (1)
	G CAG UGG A**A**A CUG **C**AC GAC	uncultured bacterium (4)

	G CAG UGG A**A**A CUG G**G**C GAC	filamentous thermophilic cyanobacterium (2), Geitlerinema sp. (1), Phormidium sp. (1), uncultured bacterium (3), uncultured cyanobacterium (3), uncultured Oscillatoriales cyanobacterium (1), uncultured Stenotrophomonas sp. (2), uncultured Xanthomonas sp. (1)
	G CAG UGG A**A**A CUG GA**A** GAC	Cyanothece sp. (1), Gloeothece sp. (1), microbial mat metagenome (1), Oscillatoria sp. (3), Planktothrix agardhii (100), Planktothrix pseudagardhii (5), Planktothrix rubescens (30), Planktothrix sp. (3), Synechococcus sp. (1), uncultured bacterium (17)
	G CAG UGG A**A**A CUG GA**G** GAC	uncultured bacterium (3), uncultured beta proteobacterium (1), uncultured soil bacterium (1)
	G CAG UGG A**A**A CUG GA**U** GAC	Microcystis elabens (1), Microcystis holsatica (1), Myxosarcina sp. (2), Oscillatoriales cyanobacterium (1), Pleurocapsa sp. (1), Pseudanabaena tremula (1), Stenotrophomonas chelatiphaga (9), Stenotrophomonas sp. (10), uncultured bacterium (18), uncultured cyanobacterium (7), uncultured Stenotrophomonas sp. (1)
	G CAG UGG A**A**A CUG GAC **A**AC	bacterium (1), Pectobacterium carotovorum (4), Pseudomonas geniculata (3), Pseudomonas sp. (1), Stenotrophomonas chelatiphaga (1), Stenotrophomonas maltophilia (67), Stenotrophomonas sp. (39), uncultured bacterium (35), uncultured Burkholderia sp. (1), uncultured gamma proteobacterium (2), uncultured soil bacterium (23), uncultured Stenotrophomonas sp. (34), uncultured Steroidobacter sp. (1), uncultured Xanthomonadaceae bacterium (1), unidentified (2), Xanthomonas citri (1), Xanthomonas retroflexus (3), Xanthomonas sp. (8)
	G CAG UGG A**A**A CUG GAC G**G**C	Chroococcidiopsis sp. (1), Pleurocapsa minor (1), Pleurocapsa sp. (3), uncultured cyanobacterium (3)
	G CAG UGG A**C**A CUG G**G**C GAC	uncultured bacterium (1)
	G CAG UGG A**C**A CUG GAC **A**AC	uncultured soil bacterium (2)
	G CAG UGG A**G**A CUG GA**A** GAC	uncultured bacterium (3)
	G CAG UGG A**G**A CUG GAC **A**AC	uncultured bacterium (1)
	G CAG UGG AU**G** CUG G**G**C GAC	uncultured bacterium (1)
	G CAG UGG AU**G** CUG GA**U** GAC	uncultured bacterium (1)
	G CAG UGG AUA **U**UG G**G**C GAC	uncultured bacterium (1)
	G CAG UGG AUA C**C**G G**G**C GAC	uncultured Stenotrophomonas sp. (1)
	G CAG UGG AUA C**C**G GA**U** GAC	uncultured bacterium (1)
	G CAG UGG AUA C**G**G G**G**C GAC	Stenotrophomonas sp. (1)
	G CAG UGG AUA C**G**G GA**U** GAC	uncultured bacterium (1)
	G CAG UGG AUA CU**A** G**G**C GAC	Pseudomonas sp. (1), Stenotrophomonas sp. (1)
	G CAG UGG AUA CU**C** G**G**C GAC	uncultured bacterium (1)
	G CAG UGG AUA CUG **C**A**U** GAC	uncultured bacterium (1)
	G CAG UGG AUA CUG **U**A**U** GAC	uncultured bacterium (1)

	G CAG UGG AUA CUG GCA GAC	uncultured archaeon (3)
	G CAG UGG AUA CUG GCG GAC	Dokdonella sp. (4), uncultured Aminomonas sp. (1), uncultured bacterium (3), uncultured soil bacterium (1)
	G CAG UGG AUA CUG GCU GAC	Stenotrophomonas sp. (2)
	G CAG UGG AUA CUG GGG GAC	uncultured bacterium (1)
	G CAG UGG AUA CUG GGU GAC	uncultured bacterium (1), uncultured organism (1)
	G CAG UGG AUA CUG GGC AAC	Kurthia sibirica (1), Nanobacterium sp. (1), Pseudoxanthomonas icgebensis (1), Stenotrophomonas maltophilia (12), Stenotrophomonas sp. (15), uncultured bacterium (9), uncultured Burkholderia sp. (1), uncultured compost bacterium (1), Xanthomonas albilineans (13), Xanthomonas campestris (3), Xanthomonas hyacinthi (1), Xanthomonas melonis (1), Xanthomonas oryzae (1), Xanthomonas sacchari (1), Xanthomonas sp. (12), Xanthomonas theicola (1), Xanthomonas translucens (39)
	G CAG UGG AUA CUG GGC CAC	uncultured bacterium (1)
	G CAG UGG AUA CUG GGC GGC	uncultured bacterium (1)
	G CAG UGG AUA CUG GGC GAA	Stenotrophomonas maltophilia (1), uncultured bacterium (2)
	G CAG UGG AUA CUG GGC GAG	Stenotrophomonas maltophilia (1)
	G CAG UGG AUA CUG GUG GAC	uncultured organism (1)
	G CAG UGG AUA CUG GUC GGC	uncultured bacterium (1)
	G CAG UGG AUA CUG GAA GGC	uncultured bacterium (3)
	G CAG UGG AUA CUG GAU AAC	Xylella fastidiosa (1)
	G CAG UGG AUA CUG GAU CAC	Pseudomonas sp. (1), Pseudoxanthomonas byssovorax (1), Pseudoxanthomonas japonensis (2), Pseudoxanthomonas mexicana (12), Pseudoxanthomonas sp. (25), Pseudoxanthomonas spadix (1), Pseudoxanthomonas suwonensis (6), Pseudoxanthomonas taiwanensis (1), simazine-degrading bacterium (1), Stenotrophomonas sp. (1), uncultured Acidovorax sp. (1), uncultured bacterium (63), uncultured beta proteobacterium (2), uncultured compost bacterium (1), uncultured gamma proteobacterium (7), uncultured organism (1), uncultured Pseudoxanthomonas sp. (17), uncultured soil bacterium (1), uncultured Xanthomonadales bacterium (13), uncultured Xanthomonas sp. (4), unidentified (1), Xanthomonas alfalfae (1), Xanthomonas axonopodis (36), Xanthomonas campestris (6), Xanthomonas euvesicatoria (3), Xanthomonas fuscans (6), Xanthomonas melonis (1), Xanthomonas perforans (6), Xanthomonas sp. (5)
	G CAG UGG AUA CUG GAU UAC	Pseudoxanthomonas sp. (1), uncultured bacterium (3)
	G CAG UGG AUA CUG GAU GCC	uncultured bacterium (1)
	G CAG UGG AUA CUG GAU GGC	Thermithiobacillus sp. (1), Thermithiobacillus tepidarius (1), Thiobacillus sp. (1)
	G CAG UGG AUA CUG GAU GUC	uncultured bacterium (1)
	G CAG UGG AUA CUG GAC AGC	uncultured bacterium (2), uncultured Rhodanobacter sp. (1)

	G CA**U** UGG A**A**A CUG GA**N** GAC G CAG **N**GG AUA CUG G**G**C **A**AC G CAG **N**GG AUA CUG GA**U** **C**AC G CAG UGG AUA CUG G**NU** **C**AC	Lactobacillus sp. (1) Xanthomonas albilineans (1) Xanthomonas fragariae (1) Xanthomonas cucurbitae (2)

Name of the probe: Saga

Target organism: *Streptococcus agalactiae*

Sequence of the probe: GTA AAC ACC AAA CMT CAG CG

Date of *in-silico* assessment: September 2017

Variant assessed here: GTA AAC ACC AAA CAT CAG CG

Mismatch count	**Ribosomal RNA sequence corresponding to the probe**	**Matching with known sequences (without italics)**
0 mm	CG CUG AUG UUU GGU GUU UAC CG CUG ANG UUU GGU GUU UAC	Streptococcus agalactiae (31), Streptococcus sp. (1), uncultured bacterium (1) Streptococcus agalactiae (1)
1 mm	CG CUG AGG UUU GGU GUU UAC	Streptococcus agalactiae (134), Streptococcus pyogenes (8), Streptococcus sp. (1), uncultured bacterium (12), uncultured organism (1), uncultured prokaryote (2), uncultured Streptococcus sp. (3), unidentified (45)
2 mm		

Name of the probe: Saga

Target organism: *Streptococcus agalactiae*

Sequence of the probe: GTA AAC ACC AAA CMT CAG CG

Date of *in-silico* assessment: September 2017

Variant assessed here: GTA AAC ACC AAA CCT CAG CG

Mismatch count	**Ribosomal RNA sequence corresponding to the probe**	**Matching with known sequences (without italics)**
0 mm	CG CUG AGG UUU GGU GUU UAC CG CUG ANG UUU GGU GUU UAC	Streptococcus agalactiae (134), Streptococcus pyogenes (8), Streptococcus sp. (1), uncultured bacterium (12), uncultured organism (1), uncultured prokaryote (2), uncultured Streptococcus sp. (3), unidentified (45) Streptococcus agalactiae (1)
1 mm	CG CUG AUG UUU GGU GUU UAC	Streptococcus agalactiae (31), Streptococcus sp. (1), uncultured bacterium (1)
2 mm		

Name of the probe: Spneu

Target organism: *Streptococcus pneumoniae*

Sequence of the probe: GTG ATG CAA GTG CAC CTT

Date of *in-silico* assessment: February 2018

Mismatch count	**Ribosomal RNA sequence corresponding to the probe**	**Matching with known sequences (without italics)**
0 mm	AAG GUG CAC UUG CAU CAC	Streptococcus phage (4), Streptococcus pneumoniae (683), Streptococcus sp. (3), uncultured Streptococcus sp. (1), unidentified (10)
1 mm	AA**A** GUG CAC UUG CAU CAC	Streptococcus pneumoniae (2), uncultured organism (1)
	AAG GUG C**U**C UUG CAU CAC	Streptococcus pneumoniae (1)
	AAG GUG CA**A** UUG CAU CAC	Okadaella gastrococcus (1), Prevotella sp. (1), Streptococcus australis (1), Streptococcus dysgalactiae (125), Streptococcus equinus (1), Streptococcus genomosp. (6), Streptococcus infantis (8), Streptococcus lactarius (1), Streptococcus mitis (68), Streptococcus oralis (38), Streptococcus parasanguinis (8), Streptococcus pneumoniae (14), Streptococcus pseudopneumoniae (3), Streptococcus pyogenes (2), Streptococcus sanguinis (6), Streptococcus sp. (46), uncultured Bacilli bacterium (1), uncultured bacterium (326), uncultured Brevundimonas sp. (1), uncultured Firmicutes bacterium (4), uncultured Gram-positive bacterium (1), uncultured Lactobacillales bacterium (3), uncultured organism (259), uncultured Porphyromonas sp. (1), uncultured soil bacterium (1), uncultured Streptococcaceae bacterium (2), uncultured Streptococcus sp. (265), unidentified (11), unidentified eubacterium (1)
	AAG GUG CA**G** UUG CAU CAC	uncultured Streptococcus sp. (3)
	AAG GUG CA**A** **N**UG CAU CAC	Streptococcus pneumoniae (3), Streptococcus pseudopneumoniae (2), Streptococcus sp. (3)
2 mm	**C**AG GUG CA**A** UUG CAU CAC	uncultured Streptococcus sp. (1)
	GAG GUG CA**A** UUG CAU CAC	uncultured bacterium (1)
	A**C**G GUG CA**A** UUG CAU CAC	uncultured organism (1)
	A**G**G GUG CA**A** UUG CAU CAC	uncultured Streptococcus sp. (2)
	AA**A** GUG CA**A** UUG CAU CAC	uncultured bacterium (1)
	AAG **A**UG C**G**C UUG CAU CAC	uncultured bacterium (1)

	AAG **A**UG CA**A** UUG CAU CAC	Agrobacterium tumefaciens (1), ant fungus garden metagenome (2), bacterium (9), endosymbiont (2), Enterococcus durans (2), Lactobacillus delbrueckii (1), Lactococcus garvieae (1), Lactococcus lactis (579), Lactococcus sp. (23), Leuconostoc pseudomesenteroides (1), rumen bacterium (2), Streptococcus alactolyticus (3), Streptococcus bovis (1), Streptococcus equinus (4), Streptococcus gallolyticus (67), Streptococcus macedonicus (6), Streptococcus pasteuri (2), Streptococcus pasteurianus (5), Streptococcus sanguinis (39), Streptococcus sinensis (4), Streptococcus sp. (18), swine manure bacterium (2), uncultured bacterium (516), uncultured compost bacterium (1), uncultured Firmicutes bacterium (3), uncultured Lactococcus sp. (9), uncultured organism (77), uncultured prokaryote (8), uncultured Streptococcaceae bacterium (1), uncultured streptococcus (1), uncultured Streptococcus sp. (25), unidentified (12), unidentified eubacterium (1)
	AAG **A**UG CA**G** UUG CAU CAC	Lactococcus lactis (1), uncultured bacterium (1)
	AAG G**C**G CA**A** UUG CAU CAC	uncultured bacterium (2)
	AAG GU**A** CA**A** UUG CAU CAC	uncultured Streptococcus sp. (1)
	AAG GUG **U**A**A** UUG CAU CAC	uncultured organism (1), uncultured Streptococcus sp. (1)
	AAG GUG **U**AC UUG CAU CA**A**	Neoptilota densa (1)
	AAG GUG C**GA** UUG CAU CAC	bacterium enrichment culture clone (2), uncultured Streptococcus sp. (1)
	AAG GUG C**GG** UUG CAU CAC	Ruminococcus flavefaciens (1)
	AAG GUG C**GU** UUG CAU CAC	uncultured bacterium (1), uncultured epsilon proteobacterium (1)
	AAG GUG C**G**C UUG CA**C** CAC	uncultured bacterium (1)
	AAG GUG C**UA** UUG CAU CAC	Streptococcus sp. (2)
	AAG GUG CA**A** **A**UG CAU CAC	Streptococcus anginosus (1), Streptococcus constellatus (3), Streptococcus cristatus (1), Streptococcus genomosp. (2), Streptococcus gordonii (2), Streptococcus intermedius (20), Streptococcus mitis (12), Streptococcus oligofermentans (1), Streptococcus oralis (9), Streptococcus parasanguinis (21), Streptococcus pneumoniae (5), Streptococcus pseudopneumoniae (6), Streptococcus sp. (28), Streptococcus tigurinus (1), Synergistetes oral clone (1), uncultured bacterium (52), uncultured Firmicutes bacterium (1), uncultured organism (83), uncultured Streptococcus sp. (16), unidentified (6)
	AAG GUG CA**A** **C**UG CAU CAC	Endosymbiont (1), Lactovum miscens (1), Streptococcus dysgalactiae (79), Streptococcus parasanguinis (2), Streptococcus sp. (4), uncultured bacterium (22), uncultured organism (16), uncultured Streptococcaceae bacterium (1), uncultured Streptococcus sp. (3)
	AAG GUG CA**A** **G**UG CAU CAC	uncultured organism (1)
	AAG GUG CA**A** U**C**G CAU CAC	uncultured Streptococcus sp. (1)

	AAG GUG CA**A** UUG C**G**U CAC	uncultured bacterium (2), uncultured organism (1), uncultured Streptococcus sp. (1)
	AAG GUG CA**A** UUG C**U**U CAC	Streptococcus dysgalactiae (1), uncultured Streptococcus sp. (1)
	AAG GUG CA**A** UUG CA**A** CAC	Streptococcus sp. (1)
	AAG GUG CA**A** UUG CA**C** CAC	Pilibacter termitis (1), Streptococcus australis (1), Streptococcus cristatus (2), Streptococcus gordonii (10), Streptococcus infantis (8), Streptococcus mitis (14), Streptococcus peroris (3), Streptococcus pneumoniae (2), Streptococcus sanguinis (2), Streptococcus sp. (10), uncultured bacterium (91), uncultured Firmicutes bacterium (3), uncultured organism (13), uncultured Streptococcus sp. (14), unidentified (3)
	AAG GUG CA**A** UUG CAU **U**AC	uncultured bacterium (1)
	AAG GUG CA**A** UUG CAU C**C**C	uncultured bacterium (1)
	AAG GUG CA**A** UUG CAU C**G**C	uncultured Streptococcus sp. (1)
	AAG GUG CA**G** **A**UG CAU CAC	Streptococcus sp. (1), uncultured organism (1)
	AAG GUG CA**U** **A**UG CAU CAC	Streptococcus sp. (2), uncultured organism (1)
	AA**U** **C**UG CAC UUG CAU **N**AC	Trachelomonas volvocina (1)
	AAG **AN**G CA**A** UUG CAU CAC	Streptococcus sp. (1)
	AAG **A**UG CA**A** **N**UG CAU CAC	Streptococcus gallolyticus (2)

Name of the probe: Spn Komp

Target organism: none, prevention of cross-reaction with bacteria other than *Streptococcus pneumoniae*

Sequence of the probe: GTG ATG CAA TTG CAC CTT

Date of *in-silico* assessment: February 2018

Mismatch count	**Ribosomal RNA sequence corresponding to the probe**	**Matching with known sequences (without italics)**
0 mm	AAG GUG CAA UUG CAU CAC	Okadaella gastrococcus (1), Prevotella sp. (1), Streptococcus australis (1), Streptococcus dysgalactiae (125), Streptococcus equinus (1), Streptococcus genomosp. (6), Streptococcus infantis (8), Streptococcus lactarius (1), Streptococcus mitis (68), Streptococcus oralis (38), Streptococcus parasanguinis (8), Streptococcus pneumoniae (14), Streptococcus pseudopneumoniae (3), Streptococcus pyogenes (2), Streptococcus sanguinis (6), Streptococcus sp. (46), uncultured Bacilli bacterium (1), uncultured bacterium (326), uncultured Brevundimonas sp. (1), uncultured Firmicutes bacterium (4), uncultured Gram-positive bacterium (1), uncultured Lactobacillales bacterium (3), uncultured organism (259), uncultured Porphyromonas sp. (1), uncultured soil bacterium (1), uncultured Streptococcaceae bacterium (2), uncultured Streptococcus sp. (265), unidentified (11), unidentified eubacterium (1)
	AAG GUG CAA **N**UG CAU CAC	Streptococcus pneumoniae (3), Streptococcus pseudopneumoniae (2), Streptococcus sp. (3)
	AAG G**N**G CAA UUG C**NN** CAC	Streptococcus oralis (1)
1 mm	**C**AG GUG CAA UUG CAU CAC	uncultured Streptococcus sp. (1)
	GAG GUG CAA UUG CAU CAC	uncultured bacterium (1)
	A**C**G GUG CAA UUG CAU CAC	uncultured organism (1)
	A**G**G GUG CAA UUG CAU CAC	uncultured Streptococcus sp. (2)
	AA**A** GUG CAA UUG CAU CAC	uncultured bacterium (1)
	AAG **A**UG CAA UUG CAU CAC	Agrobacterium tumefaciens (1), ant fungus garden metagenome (2), bacterium (9), endosymbiont (2), Enterococcus durans (2), Lactobacillus delbrueckii (1), Lactococcus garvieae (1), Lactococcus lactis (579), Lactococcus sp. (23), Leuconostoc pseudomesenteroides (1), rumen bacterium (2), Streptococcus alactolyticus (3), Streptococcus bovis (1), Streptococcus equinus (4), Streptococcus gallolyticus (67), Streptococcus macedonicus (6), Streptococcus pasteuri (2), Streptococcus pasteurianus (5), Streptococcus sanguinis (39), Streptococcus sinensis (4),

		Streptococcus sp. (18), swine manure bacterium (2), uncultured bacterium (516), uncultured compost bacterium (1), uncultured Firmicutes bacterium (3), uncultured Lactococcus sp. (9), uncultured organism (77), uncultured prokaryote (8), uncultured Streptococcaceae bacterium (1), uncultured streptococcus (1), uncultured Streptococcus sp. (25), unidentified (12), unidentified eubacterium (1)
	AAG G**C**G CAA UUG CAU CAC	uncultured bacterium (2)
	AAG GU**A** CAA UUG CAU CAC	uncultured Streptococcus sp. (1)
	AAG GUG **U**AA UUG CAU CAC	uncultured organism (1), uncultured Streptococcus sp. (1)
	AAG GUG C**G**A UUG CAU CAC	bacterium enrichment culture clone (2), uncultured Streptococcus sp. (1)
	AAG GUG C**U**A UUG CAU CAC	Streptococcus sp. (2), uncultured organism (1)
	AAG GUG CA**C** UUG CAU CAC	Streptococcus phage (4), Streptococcus pneumoniae (683), Streptococcus sp. (3), uncultured Streptococcus sp. (1), unidentified (10)
	AAG GUG CA**G** UUG CAU CAC	uncultured Streptococcus sp. (3)
	AAG GUG CAA **A**UG CAU CAC	Streptococcus anginosus (1), Streptococcus constellatus (3), Streptococcus cristatus (1), Streptococcus genomosp. (2), Streptococcus gordonii (2), Streptococcus intermedius (20), Streptococcus mitis (12), Streptococcus oligofermentans (1), Streptococcus oralis (9), Streptococcus parasanguinis (21), Streptococcus pneumoniae (5), Streptococcus pseudopneumoniae (6), Streptococcus sp. (28), Streptococcus tigurinus (1), Synergistetes oral clone (1), uncultured bacterium (52), uncultured Firmicutes bacterium (1), uncultured organism (83), uncultured Streptococcus sp. (16), unidentified (6)
	AAG GUG CAA **C**UG CAU CAC	Endosymbiont (1), Lactovum miscens (1), Streptococcus dysgalactiae (79), Streptococcus parasanguinis (2), Streptococcus sp. (4), uncultured bacterium (22), uncultured organism (16), uncultured Streptococcus sp. (4)
	AAG GUG CAA **G**UG CAU CAC	uncultured organism (1)
	AAG GUG CAA U**C**G CAU CAC	uncultured Streptococcus sp. (1)
	AAG GUG CAA UUG C**G**U CAC	uncultured bacterium (2), uncultured organism (1), uncultured Streptococcus sp. (1)
	AAG GUG CAA UUG C**U**U CAC	Streptococcus dysgalactiae (1), uncultured Streptococcus sp. (1)
	AAG GUG CAA UUG CA**A** CAC	Streptococcus sp. (1)
	AAG GUG CAA UUG CA**C** CAC	Pilibacter termitis (1), Streptococcus australis (1), Streptococcus cristatus (2), Streptococcus gordonii (10), Streptococcus infantis (8), Streptococcus mitis (14), Streptococcus peroris (3), Streptococcus pneumoniae (2), Streptococcus sanguinis (2), Streptococcus sp. (10), uncultured bacterium (83), uncultured Firmicutes bacterium (3), uncultured organism (21), uncultured Streptococcus sp. (14), unidentified (3)
	AAG GUG CAA UUG CAU **U**AC	uncultured bacterium (1)

	AAG GUG CAA UUG CAU CCC	uncultured bacterium (1)
	AAG GUG CAA UUG CAU CGC	uncultured Streptococcus sp. (1)
	AAG ANG CAA UUG CAU CAC	Streptococcus sp. (1)
	AAG AUG CAA NUG CAU CAC	Streptococcus gallolyticus (2)
2 mm	GAG AUG CAA UUG CAU CAC	uncultured bacterium (1)
	AAA AUG CAA UUG CAU CAC	uncultured bacterium (1)
	AAA GUG CAC UUG CAU CAC	Streptococcus pneumoniae (2), uncultured organism (1)
	AAG AAG CAA UUG CAU CAC	Streptococcus sp. (1)
	AAG AUG CGA UUG CAU CAC	uncultured bacterium (1)
	AAG AUG CUA UUG CAU CAC	Streptococcus gordonii (1), Streptococcus sp. (1), uncultured bacterium (2), uncultured Streptococcus sp. (1)
	AAG AUG CAG UUG CAU CAC	Lactococcus lactis (1), uncultured bacterium (1)
	AAG AUG CAA AUG CAU CAC	Lactococcus lactis (2), Lactococcus sp. (1), rumen bacterium (7), Streptococcus equinus (2), Streptococcus gallolyticus (65), Streptococcus oligofermentans (2), uncultured bacterium (204), uncultured Streptococcus sp. (3), unidentified (1)
	AAG AUG CAA CUG CAU CAC	Streptococcus dysgalactiae (2), Streptococcus gordonii (5), Streptococcus sanguinis (4), Streptococcus sp. (9), uncultured bacterium (37), unidentified rumen bacterium (1), uncultured Streptococcus sp. (6)
	AAG AUG CAA UCG CAU CAC	uncultured bacterium (1)
	AAG AUG CAA UUA CAU CAC	uncultured bacterium (1)
	AAG AUG CAA UUG UAU CAC	uncultured bacterium (1)
	AAG AUG CAA UUG CGU CAC	uncultured bacterium (1)
	AAG AUG CAA UUG CUU CAC	Streptococcus equinus (3), uncultured bacterium (1), unidentified (1)
	AAG AUG CAA UUG CAC CAC	Streptococcus sp. (1), uncultured bacterium (3), uncultured Firmicutes bacterium (1)
	AAG AUG CAA UUG CAU UAC	uncultured Gram-positive bacterium (1)
	AAG AUG CAA UUG CAU CGC	Streptococcus anginosus (96), Streptococcus milleri (1), Streptococcus sanguinis (1), Streptococcus sp. (9), uncultured bacterium (37), uncultured organism (5), uncultured Streptococcaceae bacterium (1), uncultured Streptococcus sp. (21), unidentified (1)
	AAG AUG CAA UUG CAU CUC	Lactococcus lactis (1)
	AAG AUG CAA UUG CAU CAG	Streptococcus sp. (1)
	AAG CUG CAA AUG CAU CAC	uncultured bacterium (1)
	AAG CUG CAA CUG CAU CAC	uncultured bacterium (1)
	AAG GAG CAA UUG CUU CAC	Mycoplasma gallopavonis (4), rumen bacterium (10), Streptococcus agalactiae (171),

		Streptococcus entericus (1), Streptococcus equinus (63), Streptococcus gallinaceus (1), Streptococcus infantarius (23), Streptococcus iniae (10), Streptococcus luteciae (3), Streptococcus lutetiensis (23), Streptococcus parauberis (18), Streptococcus pluranimalium (6), Streptococcus pyogenes (8), Streptococcus sp. (26), Streptococcus suis (93), swine manure bacterium (2), uncultured bacterium (829), uncultured Firmicutes bacterium (1), uncultured Lactobacillales bacterium (1), uncultured organism (2), uncultured prokaryote (4), uncultured rumen bacterium (8), uncultured sheep mite bacterium (1), uncultured Streptococcus sp. (6), unidentified (56)
	AAG G**C**G CAA UUG C**G**U CAC	Alicyclobacillus aeris (2), Alicyclobacillus sp. (1), uncultured bacterium (23), uncultured Enterococcus sp. (2), uncultured Firmicutes bacterium (1)
	AAG G**C**G CAA UUG CA**C** CAC	uncultured bacterium (1)
	AAG G**G**G CAA UUG C**U**U CAC	Streptococcus ictaluri (6), Streptococcus sp. (7), uncultured bacterium (3), uncultured organism (1)
	AAG G**G**G CAA UUG CA**C** CAC	Streptococcus sp. (1)
	AAG GU**A** CAA UUG C**G**U CAC	uncultured bacterium (1)
	AAG GU**A** CAA UUG CA**C** CAC	uncultured organism (1)
	AAG GUG **U**AA UUG CA**C** CAC	uncultured organism (1)
	AAG GUG C**GG** UUG CAU CAC	Ruminococcus flavefaciens (1)
	AAG GUG C**GU** UUG CAU CAC	uncultured bacterium (1), uncultured epsilon proteobacterium (1)
	AAG GUG C**G**A **C**UG CAU CAC	uncultured organism (1)
	AAG GUG C**G**A UUG **G**AU CAC	uncultured bacterium (1)
	AAG GUG C**UC** UUG CAU CAC	Streptococcus pneumoniae (1)
	AAG GUG CA**G** **A**UG CAU CAC	Streptococcus sp. (1), uncultured organism (1)
	AAG GUG CA**U** **A**UG CAU CAC	Streptococcus sp. (2)
	AAG GUG CAA **AA**G CAU CAC	Streptococcus anginosus (2), Streptococcus constellatus (17), uncultured bacterium (4)
	AAG GUG CAA **A**UG CA**C** CAC	Streptococcus australis (1), Streptococcus infantis (3), Streptococcus cristatus (13), Streptococcus sp. (2), uncultured bacterium (10), uncultured organism (9), uncultured Streptococcus sp. (4)
	AAG GUG CAA **A**UG CAU C**G**C	uncultured bacterium (2)
	AAG GUG CAA **A**UG CAU CA**G**	unidentified eubacterium (1)
	AAG GUG CAA **CA**G CAU CAC	Streptococcus sp. (1), Streptococcus thoraltensis (1)
	AAG GUG CAA **C**UG C**G**U CAC	uncultured organism (1)
	AAG GUG CAA **C**UG CA**C** CAC	Alicyclobacillus sp. (1), Alicyclobacillus tolerans (1), bacterium (1), Streptococcus infantis (1), Streptococcus oralis (2), uncultured bacterium (5), uncultured organism (2)
	AAG GUG CAA **C**UG CAU C**G**C	Alicyclobacillus fastidiosus (2), uncultured bacterium (1)
	AAG GUG CAA **GA**G CAU CAC	Streptococcus constellatus (33), Streptococcus intermedius (2), Streptococcus sp. (1),

		uncultured bacterium (1), uncultured Streptococcus sp. (1)
	AAG GUG CAA **GC**G CAU CAC	Streptococcus mutans (1)
	AAG GUG CAA U**G**G CA**C** CAC	Streptococcus criceti (7), uncultured bacterium (1)
	AAG GUG CAA UUG C**UC** CAC	uncultured bacterium (1)
	AAG GUG CAA UUG CA**C** **U**AC	Streptococcus sp. (1), uncultured bacterium (1)
	AAG GUG CAA UUG CA**C** C**G**C	endosymbiont (1)
	AAG GUG CAA UUG CAU C**CA**	uncultured bacterium (1)
	AAG GUG CAA UUG CAU C**GG**	uncultured bacterium (3)
	AAG GUG CAA UUG CAU C**GU**	Spirochaeta sp. (1), uncultured bacterium (3)
	AAG **A**UG CAA UUG CAU **NG**C	Streptococcus anginosus (1)
	AAG G**AN** CAA UUG C**U**U CAC	Streptococcus sp. (1)
	AAG G**A**G CAA **N**UG C**U**U CAC	Streptococcus iniae (7)
	AAG G**A**G CAA U**N**G C**U**U CAC	Streptococcus iniae (1)
	AAG G**A**G CAA UUG C**UN** CAC	Streptococcus agalactiae (1)

Name of the probe: Strep Franks (= Str 16S 492 Jansen)

Target organism: *Streptococcus* spp.

Sequence of the probe: GTT AGC CGT CCC TTT CTG G

Date of *in-silico* assessment: April 2018

Mismatch count	**Ribosomal RNA sequence corresponding to the probe**	**Matching with known sequences (without italics)**
0 mm	C CAG AAA GGG ACG GCU AAC	Agrobacterium tumefaciens (1), ant fungus garden metagenome (2), bacterium (18), Candidatus Lumbricincola sp. (5), Edwardsiella tarda (1), endosymbiont (various) (3), Enterococcus durans (2), Enterococcus faecium (1), Enterococcus sp. (3), gut bacterium (1), human oral bacterium (2), Lactobacillales bacterium (1), Lactococcus chungangensis (1), Lactococcus fujiensis (1), Lactococcus garvieae (83), Lactococcus lactis (570), Lactococcus piscium (3), Lactococcus plantarum (2), Lactococcus raffinolactis (27), Lactococcus sp. (72), Lactovum miscens (1), Leuconostoc pseudomesenteroides (1), Okadaella gastrococcus (1), Pilibacter termitis (1), primary endosymbiont (1), proteobacterium symbiont (1), rumen bacterium (18), Streptococcus agalactiae (176), Streptococcus alactolyticus (3), Streptococcus anginosus (100), Streptococcus australis (10), Streptococcus bovis (1), Streptococcus caballi (1), Streptococcus canis (43), Streptococcus constellatus (53), Streptococcus criceti (14), Streptococcus cristatus (16), Streptococcus dentapri (1), Streptococcus dentirousetti (1), Streptococcus devriesei (3), Streptococcus didelphis (10), Streptococcus downei (13), Streptococcus dysgalactiae (207), Streptococcus equi (85), Streptococcus equinus (94), Streptococcus ferus (6), Streptococcus fryi (4), Streptococcus gallinaceus (1), Streptococcus gallolyticus (135), Streptococcus genomosp. (8), Streptococcus gordonii (18), Streptococcus halichoeri (1), Streptococcus henryi (1), Streptococcus hyointestinalis (4), Streptococcus ictaluri (6), Streptococcus infantarius (23), Streptococcus infantis (25), Streptococcus iniae (23), Streptococcus intermedius (22), Streptococcus lactarius (1), Streptococcus luteciae (3), Streptococcus lutetiensis (23), Streptococcus macacae (7), Streptococcus macedonicus (6), Streptococcus marimammalium (1), Streptococcus massiliensis (1), Streptococcus merionis (1), Streptococcus milleri (1), Streptococcus minor (20), Streptococcus mitis (94), Streptococcus mutans (118), Streptococcus oligofermentans (3), Streptococcus oralis (51), Streptococcus orisratti (2), Streptococcus orisuis (2), Streptococcus ovis (1), Streptococcus parasanguinis (32),

		Streptococcus parauberis (19), Streptococcus pasteuri (2), Streptococcus pasteurianus (5), Streptococcus peroris (3), Streptococcus phage (40), Streptococcus phocae (5), Streptococcus plurextorum (2), Streptococcus pneumoniae (706), Streptococcus porci (2), Streptococcus porcinus (17), Streptococcus pseudopneumoniae (11), Streptococcus pseudoporcinus (15), Streptococcus pyogenes (154), Streptococcus ratti (2), Streptococcus salivarius (432), Streptococcus sanguinis (52), Streptococcus seminale (3), Streptococcus sinensis (4), Streptococcus sobrinus (22), Streptococcus sp. (204), Streptococcus suis (136), Streptococcus thermophilus (18), Streptococcus tigurinus (1), Streptococcus uberis (13), Streptococcus urinalis (7), Streptococcus ursoris (1), Streptococcus vestibularis (8), swine fecal bacterium (1), swine manure bacterium (4), Synergistetes oral clone (1), uncultured actinobacterium (2), uncultured anaerobic bacterium (1), uncultured Bacilli bacterium (2), uncultured bacterium (2848), uncultured compost bacterium (1), uncultured epsilon proteobacterium (1), uncultured Firmicutes bacterium (20), uncultured Gram-positive bacterium (2), uncultured Lactobacillales bacterium (6), uncultured Lactococcus sp. (19), uncultured organism (861), uncultured prokaryote (15), uncultured rumen bacterium (8), uncultured Selenomonas sp. (1), uncultured sheep mite bacterium (1), uncultured soil bacterium (1), uncultured Streptococcaceae bacterium (34), uncultured streptococcus (1), uncultured Streptococcus sp. (403), unidentified (130), unidentified eubacterium (1)
	N CA**N** AAA GGG ACG GCU AAC	Streptococcus sp. (1)
	N CAG AAA G**N**G ACG GCU AAC	Lactococcus lactis (1)
	C CA**N** A**N**A GGG ACG GCU AAC	Streptococcus alactolyticus (1)
	C CAG AAA G**N**G ACG GCU AAC	Lactococcus lactis (1), uncultured bacterium (1)
	C CAG AAA GGG ACG GCU **N**AC	Streptococcus anginosus (1), unidentified (1)
1 mm	**A** CAG AAA GGG ACG GCU AAC	Candidatus Bacilloplasma mollicute (1), uncultured bacterium (1)
	G CAG AAA GGG ACG GCU AAC	uncultured bacterium (1), uncultured Coprothermobacter sp. (1)
	U CAG AAA GGG ACG GCU AAC	bacterium (2), Streptococcus pluranimalium (7), Streptococcus pneumoniae (1), Streptococcus sp. (4), Streptococcus thoraltensis (1), uncultured bacterium (10)
	C **A**AG AAA GGG ACG GCU AAC	uncultured Mollicutes bacterium (1)
	C **G**AG AAA GGG ACG GCU AAC	Candidatus Bacilloplasma mollicute (1), Streptococcus castoreus (1), Streptococcus sp. (1), Streptococcus vestibularis (1), uncultured bacterium (7), uncultured soil bacterium (1)
	C **U**AG AAA GGG ACG GCU AAC	Streptococcus pyogenes (2), uncultured bacterium (2), uncultured organism (1)

	C C**G**G AAA GGG ACG GCU AAC	uncultured bacterium (3), uncultured Lactococcus sp. (1), uncultured organism (1)
	C C**U**G AAA GGG ACG GCU AAC	Lactococcus lactis (1), Streptococcus pneumoniae (1)
	C CA**A** AAA GGG ACG GCU AAC	Lactococcus lactis (1), Lactococcus sp. (1), Streptococcus dysgalactiae (1), Streptococcus salivarius (2), uncultured bacterium (3), uncultured organism (1)
	C CA**C** AAA GGG ACG GCU AAC	Lactococcus lactis (1), uncultured bacterium (1), uncultured organism (7)
	C CA**U** AAA GGG ACG GCU AAC	uncultured bacterium (1), uncultured organism (4)
	C CAG **G**AA GGG ACG GCU AAC	uncultured bacterium (8), uncultured organism (2)
	C CAG **U**AA GGG ACG GCU AAC	Lactococcus lactis (1),uncultured bacterium (3), uncultured organism (1)
	C CAG A**C**A GGG ACG GCU AAC	uncultured bacterium (1)
	C CAG A**G**A GGG ACG GCU AAC	Lactococcus lactis (2), uncultured bacterium (5), uncultured organism (1), uncultured Streptococcaceae bacterium (1), uncultured Streptococcus sp. (2)
	C CAG A**U**A GGG ACG GCU AAC	uncultured bacterium (1), uncultured organism (1)
	C CAG AA**G** GGG ACG GCU AAC	Streptococcus sp. (1), uncultured bacterium (6), uncultured organism (2), uncultured Streptococcus sp. (1)
	C CAG AAA **A**GG ACG GCU AAC	Lactococcus lactis (1), uncultured bacterium (3)
	C CAG AAA G**A**G ACG GCU AAC	uncultured bacterium (1), uncultured sediment bacterium (1)
	C CAG AAA G**C**G ACG GCU AAC	uncultured bacterium (2), uncultured bacterium (1)
	C CAG AAA G**U**G ACG GCU AAC	Eubacterium cylindroides (1), Facklamia sp. (1), Facklamia tabacinasalis (1), uncultured bacterium (79), uncultured Erysipelotrichaceae bacterium (1), uncultured Facklamia sp. (3), unidentified rumen bacterium (1)
	C CAG AAA GG**C** ACG GCU AAC	Bacillus sp. (1), bacterium (1), uncultured bacterium (1)
	C CAG AAA GG**U** ACG GCU AAC	Lactococcus lactis (4)
	C CAG AAA GGG **C**CG GCU AAC	uncultured bacterium (1)
	C CAG AAA GGG **G**CG GCU AAC	Streptococcus sobrinus (1), uncultured bacterium (1)
	C CAG AAA GGG **U**CG GCU AAC	Streptococcus pneumoniae (1), uncultured bacterium (1)
	C CAG AAA GGG A**U**G GCU AAC	uncultured bacterium (1), uncultured organism (1)
	C CAG AAA GGG AC**A** GCU AAC	Streptococcus pneumoniae (1), uncultured bacterium (3), uncultured Streptococcus sp. (1)
	C CAG AAA GGG AC**C** GCU AAC	Streptococcus entericus (1), uncultured Streptococcus sp. (1)
	C CAG AAA GGG AC**U** GCU AAC	Streptococcus pneumoniae (1), uncultured bacterium (1)
	C CAG AAA GGG ACG **A**CU AAC	uncultured bacterium (1), uncultured organism (1), uncultured Streptococcus sp. (1)
	C CAG AAA GGG ACG **U**CU AAC	uncultured bacterium (1), uncultured Streptococcus sp. (1)
	C CAG AAA GGG ACG G**U**U AAC	uncultured bacterium (2), uncultured Streptococcus sp. (1)
	C CAG AAA GGG ACG GC**A** AAC	uncultured bacterium (1)
	C CAG AAA GGG ACG GC**C** AAC	uncultured bacterium (2)

	C CAG AAA GGG ACG GCU **G**AC	uncultured bacterium (1), uncultured Lactococcus sp. (1)
	C CAG AAA GGG ACG GCU **U**AC	uncultured bacterium (1)
	C CAG AAA GGG ACG GCU A**G**C	Streptococcus gallolyticus (1), Streptococcus pneumoniae (2), uncultured bacterium (5)
	C CAG AAA GGG ACG GCU A**U**C	uncultured bacterium (1)
	C CAG AAA GGG ACG GCU AA**A**	Bacterium (9), endosymbiont (1), Firmicutes bacterium (1), Fructobacillus durionis (1), Fructobacillus ficulneus (1), Fructobacillus fructosus (3), Fructobacillus pseudoficulneus (1), Fructobacillus tropaeoli (3), Lactobacillus casei (1), Lactobacillus delbrueckii (1), Lactobacillus parabuchneri (1), Lactobacillus plantarum (1), Lactococcus lactis (3), Leuconostoc argentinum (1), Leuconostoc carnosum (2), Leuconostoc citreum (60), Leuconostoc fallax (15), Leuconostoc garlicum (11), Leuconostoc gasicomitatum (17), Leuconostoc gelidum (10), Leuconostoc holzapfelii (1), Leuconostoc inhae (6), Leuconostoc kimchii (6), Leuconostoc lactis (100), Leuconostoc mesenteroides (338), Leuconostoc palmae (1), Leuconostoc pseudomesenteroides (51), Leuconostoc sp. (29), uncultured Bacilli bacterium (40), uncultured bacterium (226), uncultured compost bacterium (4), uncultured Firmicutes bacterium (2), uncultured Fructobacillus sp. (1), uncultured Lactobacillales bacterium (2), uncultured Leuconostoc sp. (10), unidentified (4), Weissella soli (4)
	C CAG AAA GGG ACG GCU AA**U**	rumen bacterium (1), uncultured bacterium (2)
	C CAG AAA G**CN** ACG GCU AAC	uncultured bacterium (1)
	C CAG AAA G**NC** ACG GCU AAC	Bacillus safensis (1), Bacillus sp. (2), Enterococcus faecalis (1), Lactobacillus sp. (1)
	C CAG AAA G**U**G ACG GCU **N**AC	uncultured bacterium (1)
	C CAG AAA GGG ACG GCU **N**A**A**	Leuconostoc mesenteroides (1), Leuconostoc pseudomesenteroides (1)
	C **ANN** AAA GGG ACG GCU AAC	uncultured bacterium (1)
2 mm	**A** **A**AG AAA GGG ACG GCU AAC	uncultured planctomycete (5)
	A **G**AG AAA GGG ACG GCU AAC	uncultured bacterium (3), uncultured planctomycete (1), uncultured Thermocrinis sp. (1)
	G **A**AG AAA GGG ACG GCU AAC	uncultured bacterium (7)
	G **G**AG AAA GGG ACG GCU AAC	uncultured bacterium (4)
	G **U**AG AAA GGG ACG GCU AAC	Coprothermobacter platensis (1), Coprothermobacter proteolyticus (4), Coprothermobacter sp. (3), uncultured bacterium (109), uncultured Chloroflexi bacterium (1), uncultured Coprothermobacter sp. (222), unidentified (9)
	U CA**A** AAA GGG ACG GCU AAC	uncultured alpha proteobacterium (1), uncultured bacterium (3), uncultured prokaryote (1)
	U CAG **C**AA GGG ACG GCU AAC	uncultured bacterium (1), uncultured Gram-positive bacterium (1), uncultured organism (1)
	U CAG AAA G**C**G ACG GCU AAC	Mycoplasma iguanae (2), Mycoplasma mobile (1), Staphylococcus aureus (1), uncultured bacterium (1)

	U CAG AAA G**U**G ACG GCU AAC	Mycoplasma equigenitalium (1), Mycoplasma sp. (1), Oncorhynchus mykiss (1), uncultured bacterium (2), uncultured Mycoplasma sp. (1)
	U CAG AAA GGG ACG GCU AA**A**	uncultured compost bacterium (1), Weissella beninensis (1), Weissella fabaria (2), Weissella ghanensis (2), Weissella sp. (1)
	C **A**AG AAA G**U**G ACG GCU AAC	uncultured bacterium (191)
	C **A**AG AAA GG**C** ACG GCU AAC	Bacillus sp. (1), uncultured bacterium (1)
	C **A**AG AAA GGG **U**CG GCU AAC	uncultured bacterium (1)
	C **G**AG AAA G**U**G ACG GCU AAC	uncultured bacterium (1)
	C **G**AG AAA GGG **U**CG GCU AAC	uncultured bacterium (1), uncultured delta proteobacterium (2)
	C **G**AG AAA GGG ACG GC**C** AAC	uncultured bacterium (1)
	C **U**AG AAA G**U**G ACG GCU AAC	uncultured bacterium (1)
	C C**C**G AAA GGG ACG G**G**U AAC	Archiblatta hoeveni (1), Cymbasoma sp. (1), Monstrilla sp. (1), Monstrillopsis sp. (1), Streptococcus sp. (1)
	C C**UA** AAA GGG ACG GCU AAC	uncultured Streptococcus sp. (1)
	C C**U**G AAA G**C**G ACG GCU AAC	Bacillus pumilus (1)
	C C**U**G AAA GGG ACG G**G**U AAC	Lamproglena chinensis (1)
	C CA**A** **G**AA GGG ACG GCU AAC	uncultured bacterium (2)
	C CA**A** A**U**A GGG ACG GCU AAC	Carnobacteriaceae bacterium (1)
	C CA**A** AAA GGG AC**A** GCU AAC	uncultured bacterium (1)
	C CA**A** AAA GGG ACG GCU AA**A**	Leuconostoc citreum (1)
	C CA**C** AAA GG**U** ACG GCU AAC	uncultured Streptococcus sp. (1)
	C CA**U** **U**AA GGG ACG GCU AAC	uncultured organism (1)
	C CA**U** AAA GGG AC**U** GCU AAC	uncultured bacterium (1)
	C CAG AA**G** G**U**G ACG GCU AAC	uncultured bacterium (1)
	C CAG AAA **A**G**C** ACG GCU AAC	uncultured bacterium (1)
	C CAG AAA **C**GG ACG GCU AA**A**	Leuconostoc gasicomitatum (1)
	C CAG AAA G**AC** ACG GCU AAC	Bacillus subtilis (1), Lactobacillus plantarum (1), Streptococcus sp. (1), uncultured bacterium (1)
	C CAG AAA G**CA** ACG GCU AAC	Bacillus thuringiensis (1), bacterium (1), uncultured bacterium (2)
	C CAG AAA G**CC** ACG GCU AAC	Abiotrophia defectiva (4), Abiotrophia para-adiacens (1), Abiotrophia sp. (1), Acetobacter pasteurianus (6), Acholeplasma multilocale (2), Aerococcaceae bacterium (1), Aerococcus christensenii (2), Aerococcus sanguinicola (3), Aerococcus sp. (1), Aerococcus urinae (18), Aerococcus urinaehominis (1), Aerosphaera taetra (2), Alishewanella sp. (1), Alkalibacillus filiformis (1), Alkalibacillus haloalkaliphilus (2), Alkalibacillus silvisoli (2), Alkalibacillus sp. (3), Anaerorhabdus furcosa (2), ant fungus garden metagenome (1), Antarctic bacterium (2), Aquisalibacillus elongatus (1),

		Aquisalibacillus sp. (1), Arthrobacter nitroguajacolicus (1), Arthrobacter sp. (2), Atopobacter phocae (1), Atopococcus tabaci (1), Bacillaceae bacterium (108), Bacillaceae sp. (1), Bacillus acidiceler (6), Bacillus acidicola (4), Bacillus acidiproducens (1), Bacillus aeolius (2), Bacillus aerius (3), Bacillus aerophilus (9), Bacillus aestuarii (4), Bacillus agaradhaerens (1), Bacillus akibai (2), Bacillus alcaliinulinus (1), Bacillus alcalophilus (9), Bacillus algicola (5), Bacillus alkalinitrilicus (1), Bacillus alkalitelluris (10), Bacillus alkalitolerans (1), Bacillus alkalogaya (1), Bacillus altitudinis (33), Bacillus alveayuensis (1), Bacillus aminovorans (1), Bacillus amyloliquefaciens (538), Bacillus anthracis (318), Bacillus aquimaris (48), Bacillus arbutinivorans (6), Bacillus arsenicus (11), Bacillus aryabhattai (49), Bacillus asahii (5), Bacillus atrophaeus (80), Bacillus axarquiensis (13), Bacillus badius (19), Bacillus baekryungensis (21), Bacillus barbaricus (16), Bacillus bataviensis (13), Bacillus beijingensis (8), Bacillus benzoevorans (5), Bacillus beringensis (4), Bacillus bogoriensis (1), Bacillus boroniphilus (13), Bacillus butanolivorans (1), Bacillus carboniphilus (3), Bacillus catenulatus (3), Bacillus cereus (1250), Bacillus chandigarhensis (1), Bacillus cibi (12), Bacillus circulans (31), Bacillus clausii (99), Bacillus coagulans (68), Bacillus coahuilensis (6), Bacillus cohnii (11), Bacillus cytotoxicus (16), Bacillus decolorationis (2), Bacillus deserti (1), Bacillus djibelorensis (2), Bacillus drentensis (18), Bacillus endophyticus (61), Bacillus farraginis (5), Bacillus fastidiosus (2), Bacillus ferrariarum (1), Bacillus firmus (125), Bacillus flexus (113), Bacillus foraminis (10), Bacillus fordii (4), Bacillus fortis (1), Bacillus fucosivorans (1), Bacillus fumarioli (9), Bacillus gaemokensis (1), Bacillus galactosidilyticus (1), Bacillus gelatini (5), Bacillus ginsengi (4), Bacillus ginsengihumi (11), Bacillus granadensis (2), Bacillus hackensackii (1), Bacillus halmapalus (4), Bacillus halodurans (2), Bacillus hemicellulosilyticus (1), Bacillus herbersteinensis (6), Bacillus horikoshii (27), Bacillus horneckiae (11), Bacillus humi (11), Bacillus hunanensis (1), Bacillus hwajinpoensis (14), Bacillus idriensis (8), Bacillus indicus (5), Bacillus infantis (4), Bacillus infernus (2), Bacillus isabeliae (1), Bacillus jeotgali (8), Bacillus koreensis (4), Bacillus korlensis (5), Bacillus kribbensis (1), Bacillus krulwichiae (3), Bacillus lehensis (1), Bacillus lentus (8), Bacillus licheniformis (782), Bacillus litoralis (8), Bacillus longiquaesitum (3), Bacillus luciferensis (6), Bacillus macauensis (1), Bacillus malacitensis (5), Bacillus mangrovensis (1), Bacillus marcorestinctum (1), Bacillus marisflavi (19), Bacillus megaterium (542), Bacillus methanolicus (4), Bacillus methylotrophicus (106), Bacillus mojavensis (44), Bacillus muralis (15), Bacillus mycoides (70), Bacillus nealsonii (17), Bacillus nematocida (1), Bacillus niabensis (24), Bacillus niacini (34), Bacillus novalis (5), Bacillus oceanisediminis (13), Bacillus okhensis (1), Bacillus oleronius (17), Bacillus olivae (1), Bacillus oryzae (1), Bacillus oshimensis (7), Bacillus pallidus (1), Bacillus panaciterrae (3), Bacillus patagoniensis (1), Bacillus phage (24), Bacillus pichinotyi (7), Bacillus pocheonensis (7), Bacillus polyfermenticus (6), Bacillus pseudalcaliphilus (2), Bacillus pseudofirmus (16),

		Bacillus pseudomegaterium (1), Bacillus pseudomycoides (19), Bacillus psychrosaccharolyticus (5), Bacillus pumilus (726), Bacillus racemilacticus (4), Bacillus rigui (1), Bacillus ruris (1), Bacillus safensis (70), Bacillus samanii (5), Bacillus selenatarsenatis (9), Bacillus senegalensis (5), Bacillus seohaeanensis (1), Bacillus shackletonii (2), Bacillus shandongensis (3), Bacillus simplex (148), Bacillus siralis (2), Bacillus smithii (8), Bacillus soli (7), Bacillus solisalsi (1), Bacillus sonorensis (28), Bacillus sp. (5713), Bacillus sporothermodurans (8), Bacillus stratosphericus (7), Bacillus subterraneus (1), Bacillus subtilis (1971), Bacillus taeanensis (1), Bacillus tequilensis (72), Bacillus thioparans (4), Bacillus thuringiensis (539), Bacillus tianmuensis (1), Bacillus trypoxylicola (4), Bacillus vallismortis (61), Bacillus vietnamensis (10), Bacillus vireti (10), Bacillus wakoensis (1), Bacillus weihenstephanensis (50), Bacillus zhanjiangensis (1), bacterium (275), Bavariicoccus seileri (1), Bemisia tabaci (1), Bhargavaea cecembensis (3), Bhargavaea sp. (4), blackwater bioreactor bacterium (1), Brevibacillus brevis (8), Brevibacillus laterosporus (1), Brevibacillus sp. (5), Brevibacterium frigoritolerans (14), Brevibacterium halotolerans (4), Brevibacterium sp. (19), Brochothrix campestris (3), Brochothrix sp. (12), Brochothrix thermosphacta (12), bromate-reducing bacterium (1), Bulleidia extructa (3), Burkholderia cepacia (1), Candidatus Bacilloplasma mollicute (2), Carnobacteriaceae bacterium (1), Carnobacterium alterfunditum (3), Carnobacterium divergens (9), Carnobacterium gallinarum (1), Carnobacterium jeotgali (1), Carnobacterium maltaromaticum (35), Carnobacterium pleistocenium (1), Carnobacterium sp. (39), Carnobacterium viridans (1), Carnococcus allantoicus (1), Catellicoccus marimammalium (1), Catenibacterium mitsuokai (10), Catonella morbi (1), Cloacibacterium normanense (1), Clostridiaceae bacterium (3), Clostridium acetobutylicum (1), Clostridium aff. Innocuum (1), Clostridium innocuum (6), Clostridium sp. (6), Corynebacterineae bacterium (2), Cucumis sativus (1), Delivery vector (1), Dolosicoccus paucivorans (1), Empedobacter brevis (1), endophytic bacterium (7), Enterobacter cloacae (1), Enterococcaceae bacterium (3), Enterococcus aquimarinus (2), Enterococcus asini (3), Enterococcus avium (18), Enterococcus azikeevi (1), Enterococcus caccae (2), Enterococcus camelliae (3), Enterococcus canintestini (3), Enterococcus canis (4), Enterococcus casseliflavus (43), Enterococcus cecorum (10), Enterococcus columbae (4), Enterococcus devriesei (6), Enterococcus dispar (5), Enterococcus durans (199), Enterococcus faecalis (362), Enterococcus faecium (277), Enterococcus gallinarum (52), Enterococcus gilvus (9), Enterococcus haemoperoxidus (3), Enterococcus hawaiiensis (1), Enterococcus hermanniensis (4), Enterococcus hirae (40), Enterococcus inusitatus (3), Enterococcus italicus (21), Enterococcus lactis (8), Enterococcus malodoratus (7), Enterococcus moraviensis (3), Enterococcus mundtii (37), Enterococcus pallens (3), Enterococcus pernyi (1), Enterococcus phoeniculicola (3),

		Enterococcus plantarum (3), Enterococcus pseudoavium (6), Enterococcus quebecensis (1), Enterococcus raffinosus (8), Enterococcus ratti (3), Enterococcus rivorum (5), Enterococcus rottae (1), Enterococcus saccharolyticus (9), Enterococcus silesiacus (6), Enterococcus sp. (183), Enterococcus sulfureus (6), Enterococcus termitis (2), Enterococcus thailandicus (12), Enterococcus ureasiticus (2), Enterococcus viikkiensis (5), Enterococcus villorum (4), Entomoplasma ellychniae (1), Entomoplasma freundtii (1), Entomoplasma lucivorax (1), Entomoplasma luminosum (1), Entomoplasma melaleucae (3), Entomoplasma somnilux (1), Erysipelothrix inopinata (1), Erysipelothrix muris (1), Erysipelothrix rhusiopathiae (28), Erysipelothrix sp. (4), Erysipelothrix tonsillarum (4), Erysipelotrichaceae bacterium (13), Eubacterium cylindroides (1), Eubacterium dolichum (2), Eubacterium sp. (5), Eubacterium tortuosum (1), Exiguobacterium acetylicum (1), Facklamia hominis (1), Facklamia languida (4), Facklamia miroungae (1), Filobacillus milosensis (1), Filobacillus sp. (6), Firmicutes bacterium (5), Flavobacterium sp. (1), Gemella bergeri (1), Gemella haemolysans (14), Gemella morbillorum (3), Gemella palaticanis (2), Gemella sanguinis (4), Gemella sp. (7), Geobacillus sp. (1), Geobacillus stearothermophilus (5), Geobacillus thermoglucosidasius (1), glacial ice bacterium (21), Globicatella sanguinis (1), Globicatella sp. (2), Globicatella sulfidifaciens (2), Gram-positive bacterium (2), Granulicatella (1), Granulicatella adiacens (10), Granulicatella balaenopterae (1), Granulicatella elegans (7), Granulicatella para-adiacens (3), Granulicatella sp. (8), groundwater biofilm bacterium (9), Halalkalibacillus halophilus (2), Halalkalibacillus sp. (1), haloalkaliphilic bacterium (3), Halobacillus sp. (2), Halomonas sp. (1), halophilic bacterium (5), Holdemania filiformis (2), human gut metagenome (3), Ignavigranum ruoffiae (1), Insertion vector (2), intestinal bacterium (3), Isobaculum melis (1), Jeotgalibacillus alimentarius (1), Jeotgalibacillus campisalis (2), Jeotgalibacillus marinus (5), Jeotgalibacillus salarius (2), Jeotgalibacillus soli (3), Jeotgalibacillus sp. (4), Jeotgalicoccus (1), Jeotgalicoccus aerolatus (2), Jeotgalicoccus coquinae (2), Jeotgalicoccus halophilus (2), Jeotgalicoccus halotolerans (3), Jeotgalicoccus huakuii (1), Jeotgalicoccus marinus (1), Jeotgalicoccus nanhaiensis (1), Jeotgalicoccus pinnipedialis (1), Jeotgalicoccus psychrophilus (5), Jeotgalicoccus sp. (5), Kurthia zopfii (1), Lactobacillus (1), Lactobacillus acidifarinae (3), Lactobacillales bacterium (1), Lactobacillus agilis (6), Lactobacillus algidus (1), Lactobacillus alimentarius (23), Lactobacillus animalis (7), Lactobacillus apodemi (2), Lactobacillus backi (3), Lactobacillus bifermentans (1), Lactobacillus bobalius (2), Lactobacillus brantae (1), Lactobacillus brevis (181), Lactobacillus buchneri (29), Lactobacillus cacaonum (1), Lactobacillus camelliae (1), Lactobacillus capillatus (3), Lactobacillus casei (469), Lactobacillus ceti (1), Lactobacillus collinoides (2), Lactobacillus composti (2), Lactobacillus coryniformis (10),

		Lactobacillus crustorum (12), Lactobacillus curvatus (20), Lactobacillus delbrueckii (1), Lactobacillus diolivorans (85), Lactobacillus equi (5), Lactobacillus equigenerosi (1), Lactobacillus fabifermentans (3), Lactobacillus faeni (2), Lactobacillus farciminis (7), Lactobacillus farraginis (50), Lactobacillus fermentum (2), Lactobacillus floricola (5), Lactobacillus fuchuensis (4), Lactobacillus genomosp. (2), Lactobacillus ghanensis (5), Lactobacillus graminis (2), Lactobacillus guizhouensis (3), Lactobacillus halophilus (1), Lactobacillus hammesii (2), Lactobacillus helveticus (7), Lactobacillus hilgardii (19), Lactobacillus hordei (1), Lactobacillus japonicus (1), Lactobacillus kefiri (53), Lactobacillus kimchiensis (1), Lactobacillus kimchii (3), Lactobacillus kisonensis (4), Lactobacillus kunkeei (20), Lactobacillus larvae (1), Lactobacillus letivazi (1), Lactobacillus malefermentans (4), Lactobacillus mali (8), Lactobacillus manihotivorans (2), Lactobacillus mindensis (6), Lactobacillus murinus (12), Lactobacillus nagelii (2), Lactobacillus namurensis (4), Lactobacillus nantensis (2), Lactobacillus nasuensis (2), Lactobacillus nodensis (2), Lactobacillus odoratitofui (2), Lactobacillus oeni (10), Lactobacillus oligofermentans (6), Lactobacillus otakiensis (4), Lactobacillus ozensis (5), Lactobacillus pantheris (4), Lactobacillus parabrevis (5), Lactobacillus parabuchneri (40), Lactobacillus paracasei (118), Lactobacillus paracollinoides (10), Lactobacillus parafarraginis (4), Lactobacillus parakefiri (5), Lactobacillus paralimentarius (17), Lactobacillus paraplantarum (15), Lactobacillus pentosus (81), Lactobacillus plantarum (782), Lactobacillus pontis (1), Lactobacillus rapi (3), Lactobacillus rennini (2), Lactobacillus rhamnosus (97), Lactobacillus rossiae (17), Lactobacillus ruminis (13), Lactobacillus sakei (98), Lactobacillus salivarius (1), Lactobacillus saniviri (2), Lactobacillus satsumensis (3), Lactobacillus selangorensis (2), Lactobacillus senioris (1), Lactobacillus senmaizukei (2), Lactobacillus sharpeae (1), Lactobacillus siliginis (5), Lactobacillus similis (4), Lactobacillus sp. (338), Lactobacillus spicheri (3), Lactobacillus sucicola (3), Lactobacillus suebicus (5), Lactobacillus sunkii (6), Lactobacillus thailandensis (1), Lactobacillus tucceti (1), Lactobacillus uvarum (8), Lactobacillus vaccinostercus (16), Lactobacillus vermiforme (1), Lactobacillus versmoldensis (3), Lactobacillus zeae (5), Lactobacillus zymae (4), Lactococcus lactis (6), Leuconostoc mesenteroides (2), Listeria grayi (7), Listeria innocua (69), Listeria ivanovii (11), Listeria marthii (4), Listeria monocytogenes (164), Listeria rocourtiae (1), Listeria seeligeri (18), Listeria sp. (9), Listeria welshimeri (13), low G+C Gram-positive bacterium (21), Lysinibacillus fusiformis (1), Lysinibacillus macroides (4), Lysinibacillus sp. (1), Lysinibacillus sphaericus (1), Lysobacter sp. (1), Macrococcus bovicus (1), Macrococcus brunensis (4), Macrococcus carouselicus (1), Macrococcus caseolyticus (12), Macrococcus equipercicus (3), Macrococcus hajekii (1), Macrococcus lamae (1), Macrococcus sp. (5), marine bacterium (8), marine firmicute (1),

		Marinibacillus sp. (3), Melissococcus plutonius (46), Mesoplasma chauliocola (1), Mesoplasma coleopterae (2), Mesoplasma corruscae (1), Mesoplasma entomophilum (1), Mesoplasma florum (2), Mesoplasma grammopterae (1), Mesoplasma photuris (1), Mesoplasma seiffertii (1), Mesoplasma syrphidae (1), Mesoplasma tabanidae (1), Mesorhizobium sp. (1), metagenome sequence (1), Micrococcineae bacterium (3), Micrococcus luteus (2), Micrococcus sp. (1), Mollicutes bacterium (1), mouse gut metagenome (2), Mycoplasma capricolum (50), Mycoplasma cottewii (2), Mycoplasma leachii (12), Mycoplasma monodon (1), Mycoplasma mycoides (27), Mycoplasma putrefaciens (3), Mycoplasma sp. (3), Mycoplasma yeatsii (2), Natribacillus halophilus (1), Nosocomiicoccus ampullae (2), Nostocoida sp. (1), Nostocoida limicola (3), Oceanobacillus caeni (3), Oceanobacillus chironomi (1), Oceanobacillus cibarius (1), Oceanobacillus iheyensis (16), Oceanobacillus kimchii (1), Oceanobacillus oncorhynchi (15), Oceanobacillus picturae (28), Oceanobacillus profundus (8), Oceanobacillus sojae (2), Oceanobacillus sp. (79), Ornithinibacillus sp. (9), Paenibacillaceae bacterium (10), Paenibacillus favisporus (2), Paenibacillus fukuinensis (1), Paenibacillus larvae (1), Paenibacillus lentimorbus (1), Paenibacillus mucilaginosus (4), Paenibacillus polymyxa (1), Paenibacillus popilliae (1), Paenibacillus sp. (4), Pasteurella pneumotropica (2), Paucisalibacillus globulus (1), Pediococcus acidilactici (68), Pediococcus argentinicus (1), Pediococcus cellicola (2), Pediococcus claussenii (6), Pediococcus damnosus (15), Pediococcus ethanolidurans (8), Pediococcus inopinatus (2), Pediococcus lolii (1), Pediococcus parvulus (14), Pediococcus pentosaceus (89), Pediococcus siamensis (1), Pediococcus sp. (44), Pediococcus stilesii (1), Piscibacillus salipiscarius (1), Piscibacillus sp. (6), Planococcaceae bacterium (4), Planococcus antarcticus (4), Planococcus citreus (8), Planococcus columbae (1), Planococcus crocinus (1), Planococcus donghaensis (4), Planococcus kazaiensis (1), Planococcus kocurii (2), Planococcus maitriensis (2), Planococcus maritimus (12), Planococcus pelagicus (1), Planococcus psychrotoleratus (3), Planococcus rifietoensis (11), Planococcus salinarum (2), Planococcus sp. (82), Planomicrobium alkanoclasticum (3), Planomicrobium chinense (2), Planomicrobium glaciei (8), Planomicrobium koreense (6), Planomicrobium mcmeekinii (2), Planomicrobium okeanokoites (14), Planomicrobium psychrophilum (1), Planomicrobium sp. (28), Pontibacillus chungwhensis (6), Pontibacillus marinus (3), Pontibacillus sp. (12), Pseudoalteromonas sp. (12), Pseudomonas aeruginosa (1), Pseudomonas monteilii (1), Pseudomonas sp. (2), Pseudomonas xanthomarina (1), Psychrobacter celer (1), rainbow trout intestinal bacterium (1), Rhizobiaceae bacterium (1), Rhizobium sp. (5), rumen bacterium (16), Salinibacillus aidingensis (1), Salinibacillus kushneri (2), Salinicoccus albus (1), Salinicoccus alkaliphilus (3), Salinicoccus carnicancri (1), Salinicoccus halodurans (3), Salinicoccus hispanicus (1), Salinicoccus iranensis (1), Salinicoccus jeotgali (1), Salinicoccus kekensis (1),

		Salinicoccus kunmingensis (1), Salinicoccus luteus (1), Salinicoccus marinus (1), Salinicoccus roseus (14), Salinicoccus salitudinis (1), Salinicoccus salsiraiae (1), Salinicoccus siamensis (2), Salinicoccus sp. (20), Scopulibacillus darangshiensis (2), secondary endosymbiont (2), Serratia marcescens (2), Solobacterium moorei (17), Solobacterium sp. (1), Spiroplasma alleghenense (1), Spiroplasma apis (1), Spiroplasma atrichopogonis (1), Spiroplasma cantharicola (3), Spiroplasma chrysopicola (1), Spiroplasma citri (8), Spiroplasma clarkii (1), Spiroplasma corruscae (1), Spiroplasma diabroticae (1), Spiroplasma diminutum (1), Spiroplasma endosymbiont (71), Spiroplasma eriocheiris (1), Spiroplasma floricola (1), Spiroplasma gladiatoris (1), Spiroplasma helicoides (1), Spiroplasma insolitum (1), Spiroplasma ixodetis (1), Spiroplasma kunkelii (2), Spiroplasma leucomae (1), Spiroplasma lineolae (1), Spiroplasma litorale (1), Spiroplasma melliferum (2), Spiroplasma mirum (1), Spiroplasma monobiae (1), Spiroplasma montanense (1), Spiroplasma penaei (1), Spiroplasma poulsonii (1), Spiroplasma sabaudiense (1), Spiroplasma secondary endosymbiont (1), Spiroplasma sp. (70), Spiroplasma symbiont (2), Spiroplasma syrphidicola (1), Spiroplasma tabanidicola (3), Spiroplasma taiwanense (1), Spiroplasma turonicum (1), Sporolactobacillus inulinus (7), Sporolactobacillus kofuensis (3), Sporolactobacillus laevolacticus (17), Sporolactobacillus laevus (6), Sporolactobacillus nakayamae (20), Sporolactobacillus putidus (1), Sporolactobacillus sp. (16), Sporolactobacillus terrae (4), Sporolactobacillus vineae (3), Sporosarcina newyorkensis (10), Sporosarcina sp. (8), Sporosarcina ureae (4), Staphylococcaceae bacterium (3), Staphylococcus agnetis (15), Staphylococcus carnosus (1), Staphylococcus chromogenes (2), Staphylococcus delphini (18), Staphylococcus epidermidis (1), Staphylococcus felis (3), Staphylococcus fleurettii (1), Staphylococcus hyicus (1), Staphylococcus intermedius (3), Staphylococcus lentus (7), Staphylococcus lutrae (1), Staphylococcus pseudintermedius (22), Staphylococcus saprophyticus (1), Staphylococcus schleiferi (5), Staphylococcus sciuri (39), Staphylococcus sp. (49), Staphylococcus vitulinus (3), Stenotrophomonas maltophilia (2), Stenotrophomonas rhizophila (1), Stenotrophomonas sp. (2), Streptococcus agalactiae (1), Streptococcus sp. (1), Streptomyces clavuligerus (1), Streptomyces indiaensis (1), Streptomyces sp. (5), swine effluent bacterium (1), swine fecal bacterium (13), swine manure bacterium (4), swine manure pit bacterium (3), synthetic Mycoplasma mycoides (2), Tenuibacillus multivorans (2), Tetragenococcus doogicus (1), Tetragenococcus halophilus (45), Tetragenococcus koreensis (2), Tetragenococcus muriaticus (5), Tetragenococcus solitarius (3), Tetragenococcus sp. (18), Thalassobacillus sp. (1), Trichococcus collinsii (10), Trichococcus flocculiformis (12), Trichococcus palustris (1), Trichococcus pasteurii (4), Trichococcus patagoniensis (1), Trichococcus sp. (14), uncultured Abiotrophia sp. (5), uncultured Aerococcaceae bacterium (8), uncultured Aerococcus sp. (2),

		uncultured anaerobic bacterium (7), uncultured Anaerorhabdus sp. (1), uncultured Aneurinibacillus sp. (3), uncultured Bacillaceae bacterium (16), uncultured Bacilli bacterium (401), uncultured Bacillus sp. (686), uncultured bacterium (6363), uncultured Bacteroidetes bacterium (2), uncultured Brevibacterium sp. (1), uncultured Brochothrix sp. (4), uncultured Bulleidia sp. (3), uncultured Carnobacterium sp. (13), uncultured Catenibacterium sp. (4), uncultured compost bacterium (232), uncultured Deinococci bacterium (1), uncultured Enterococcaceae bacterium (7), uncultured Enterococcus sp. (64), uncultured Entomoplasmataceae bacterium (12), uncultured epsilon proteobacterium (1), uncultured Erysipelothrix sp. (1), uncultured Erysipelotrichaceae bacterium (9), uncultured Facklamia sp. (1), uncultured feedlot manure bacterium (1), uncultured Filobacillus sp. (1), uncultured Firmicutes bacterium (80), uncultured Gemella sp. (16), uncultured Gram-positive bacterium (1), uncultured Granulicatella sp. (12), uncultured Halobacillus sp. (4), uncultured hydrocarbon seep bacterium (3), uncultured isopod gut bacterium (2), uncultured Jeotgalibacillus sp. (1), uncultured Jeotgalicoccus sp. (2), uncultured Lachnospiraceae bacterium (1), uncultured Lactobacillales bacterium (23), uncultured Lactobacillus sp. (36), uncultured low G+C Gram-positive bacterium (14), uncultured Macrococcus sp. (1), uncultured marine bacterium (2), uncultured Mesoplasma sp. (1), uncultured microorganism (4), uncultured Mollicutes bacterium (20), uncultured Nitrospira sp. (1), uncultured Oceanobacillus sp. (1), uncultured organism (495), uncultured planctomycete (1), uncultured Planococcaceae bacterium (3), uncultured Planococcus sp. (5), uncultured Planomicrobium sp. (15), uncultured Pontibacillus sp. (2), uncultured prokaryote (7), uncultured rumen bacterium (43), uncultured Salinicoccus sp. (1), uncultured Salirhabdus sp. (2), uncultured soil bacterium (37), uncultured Solobacterium sp. (1), uncultured Sphingomonas sp. (1), uncultured Spiroplasma sp. (16), uncultured Staphylococcaceae bacterium (3), uncultured Staphylococcus sp. (11), uncultured Streptococcaceae bacterium (3), uncultured Streptococcus sp. (2), uncultured Tetragenococcus sp. (1), uncultured Trichococcus sp. (53), uncultured Vagococcus sp. (3), uncultured Vibrio sp. (1), unidentified (125), unidentified plasmid (2), Vagococcus carniphilus (4), Vagococcus elongatus (1), Vagococcus fessus (1), Vagococcus fluvialis (9), Vagococcus lutrae (8), Vagococcus penaei (1), Vagococcus salmoninarum (3), Vagococcus sp. (13), Vagococcus teuberi (5), Variovorax sp. (1), Vibrio cholerae (1), Vibrio fluvialis (1), Vibrio parahaemolyticus (1), Virgibacillus sp. (11)
	C CAG AAA G**CU** ACG GCU AAC	Bacillus sp. (2), Lactobacillus farciminis (1), Lactobacillus plantarum (1), metagenome sequence (1), Staphylococcus saprophyticus (1), uncultured bacterium (182), uncultured Bulleidia sp. (2),

		uncultured Erysipelotrichaceae bacterium (5), uncultured prokaryote (1)
	C CAG AAA G**C**G **G**CG GCU AAC	Bacillaceae bacterium (1)
	C CAG AAA G**C**G A**G**G GCU AAC	Bacillus sp. (1)
	C CAG AAA G**C**G A**U**G GCU AAC	Mycoplasma sp. (1)
	C CAG AAA G**UC** ACG GCU AAC	Alkalibacterium iburiense (4), Alkalibacterium indicireducens (3), Alkalibacterium kapii (7), Alkalibacterium olivapovliticus (4), Alkalibacterium pelagium (2), Alkalibacterium psychrotolerans (2), Alkalibacterium putridalgicola (10), Alkalibacterium sp. (10), Alkalibacterium subtropicum (2), Alkalibacterium thalassium (2), Allobaculum sp. (1), Allobaculum stercoricanis (1), Alloiococcus otitis (3), Apis florea (1), Apis mellifera (12), Atopostipes sp. (1), Atopostipes suicloacalis (1), Bacillus idriensis (1), Bacillus sp. (1), bacterium (12), Bifidobacterium sp. (1), butyrate-producing bacterium (2), Clostridiales bacterium (4), Clostridium sp. (1), Dolosigranulum pigrum (6), Drosophila bipectinata (1), Drosophila kikkawai (4), Eubacterium biforme (2), Eubacterium cylindroides (3), Firmicutes oral clone (1), Gemella sp. (1), human gut metagenome (2), Lactobacillus acetotolerans (4), Lactobacillus acidophilus (40), Lactobacillus alvei (1), Lactobacillus alvi (1), Lactobacillus amylolyticus (3), Lactobacillus amylophilus (3), Lactobacillus amylotrophicus (3), Lactobacillus amylovorus (19), Lactobacillus antri (2), Lactobacillus apis (1), Lactobacillus casei (1), Lactobacillus coleohominis (4), Lactobacillus crispatus (43), Lactobacillus delbrueckii (295), Lactobacillus equicursoris (2), Lactobacillus equigenerosi (4), Lactobacillus fermentum (483), Lactobacillus florum (3), Lactobacillus fornicalis (1), Lactobacillus fructivorans (6), Lactobacillus frumenti (2), Lactobacillus gallinarum (7), Lactobacillus gastricus (2), Lactobacillus hamsteri (3), Lactobacillus helveticus (793), Lactobacillus homohiochii (5), Lactobacillus iners (1), Lactobacillus ingluviei (8), Lactobacillus intestinalis (5), Lactobacillus jensenii (17), Lactobacillus kalixensis (2), Lactobacillus kefiranofaciens (62), Lactobacillus kitasatonis (5), Lactobacillus lindneri (5), Lactobacillus mobilis (1), Lactobacillus mucosae (19), Lactobacillus oris (9), Lactobacillus panis (2), Lactobacillus perolens (3), Lactobacillus plantarum (2), Lactobacillus pontis (8), Lactobacillus psittaci (1), Lactobacillus reuteri (120), Lactobacillus rhamnosus (1), Lactobacillus sanfranciscensis (15), Lactobacillus secaliphilus (2), Lactobacillus sp. (133), Lactobacillus ultunensis (3), Lactobacillus vaginalis (17), Lactobacillus vini (3), Lactococcus lactis (1), Lactococcus raffinolactis (1), Leuconostoc mesenteroides (1), Marinilactibacillus piezotolerans (3), Marinilactibacillus psychrotolerans (18), Marinilactibacillus sp. (6), Mesoplasma lactucae (1), Streptococcus pleomorphus (1), swine fecal bacterium (6), synthetic construct (16), uncultured Alkalibacterium sp. (2), uncultured Atopostipes sp. (1), uncultured Bacilli bacterium (1), uncultured bacterium (4733), uncultured Carnobacteriaceae bacterium (48), uncultured compost bacterium (22), uncultured Dolosigranulum sp. (1),

		uncultured Erysipelotrichaceae bacterium (4), uncultured feedlot manure bacterium (2), uncultured Firmicutes bacterium (9), uncultured gamma proteobacterium (1), uncultured Lactobacillaceae bacterium (65), uncultured Lactobacillus sp. (434), uncultured Marinilactibacillus sp. (3), uncultured Mollicutes bacterium (2), uncultured Mycoplasmataceae bacterium (3), uncultured organism (64), uncultured prokaryote (6), uncultured rumen bacterium (3), uncultured sediment bacterium (1), unidentified (20), unidentified Hailaer soda lake bacterium (3), wallaby gut metagenome (1)
	C CAG AAA G**UU** ACG GCU AAC	uncultured bacterium (3)
	C CAG AAA G**U**G A**U**G GCU AAC	Candidatus Mycoplasma ravipulmonis (1)
	C CAG AAA G**U**G ACG GCU **G**AC	uncultured bacterium (1)
	C CAG AAA GG**A** ACG GCU AA**A**	Lactobacillus fermentum (1), Lactobacillus sp. (1), Leuconostocaceae bacterium (1), Sporolactobacillus laevolacticus (1), uncultured Bacilli bacterium (37), uncultured bacterium (30), uncultured compost bacterium (1), uncultured Lactobacillales bacterium (1), uncultured Weissella sp. (14), Weissella cibaria (60), Weissella confusa (36), Weissella halotolerans (2), Weissella hanii (1), Weissella hellenica (18), Weissella kandleri (2), Weissella koreensis (39), Weissella minor (2), Weissella paramesenteroides (26), Weissella salipiscis (1), Weissella sp. (54), Weissella viridescens (9)
	C CAG AAA GG**C** **C**CG GCU AAC	Bacillus clausii (1), Bacillus mojavensis (1)
	C CAG AAA GG**C** ACG **U**CU AAC	Bacillus cereus (1)
	C CAG AAA GG**C** ACG G**G**U AAC	Bacillus sp. (1)
	C CAG AAA GG**C** ACG GCU **U**AC	Bacillus sp. (1)
	C CAG AAA GG**U** **C**CG GCU AAC	uncultured bacterium (1)
	C CAG AAA GGG **GG**G GCU AAC	Bacillus sp. (1)
	C CAG AAA GGG A**U**G GCU AA**A**	Oenococcus kitaharae (5), Oenococcus oeni (34), Oenococcus sp. (2), uncultured bacterium (1)
	C CAG AAA GGG ACG GCU **G**A**A**	uncultured bacterium (1)
	C CAG AAA GGG ACG GCU **U**A**A**	Lactobacillus delbrueckii (1), Lactococcus lactis (1), Mycoplasma iguanae (1), uncultured bacterium (1)
	C CAG AAA GGG ACG GCU A**CU**	Streptococcus salivarius (1), uncultured bacterium (1)
	C CAG AAA GGG ACG GCU A**UA**	Leuconostoc mesenteroides (1)
	N **G**AG **G**AA GGG ACG GCU AAC	uncultured verrucomicrobium (1)
	N CAG AAA G**CC** ACG GCU AAC	Bacillus badius (1), uncultured bacterium (1)
	U CAG AAA G**C**G ACG GC**N** AAC	Mycoplasma mobile (1)
	U CAG AAA G**NC** ACG GCU AAC	uncultured bacterium (1)
	C **AGN** AAA GGG ACG GCU AAC	uncultured bacterium (1)

	C **N**AG AAA G**CC** ACG GCU AAC	Exiguobacterium sp. (1), uncultured Planomicrobium sp. (1)
	C C**N**G AAA G**CC** ACG GCU AAC	Bacterium (1)
	C C**N**G AAA G**UC** ACG GCU AAC	Lactobacillus fermentum (1)
	C CA**N** AAA G**CC** ACG GCU AAC	Bacillales bacterium (1), Bacillus horneckiae (1), Bacillus sp. (9), bacterium (5), Lactobacillus sp. (1), Planococcus sp. (1), Tetragenococcus sp. (1), uncultured bacterium (1)
	C CAG **N**AA G**CC** ACG GCU AAC	Bacillus novalis (1), Bacillus sp. (1)
	C CAG A**N**A G**CC** ACG GCU AAC	Bacillus amyloliquefaciens (1), bacterium (1), Enterococcus sp. (1), Pediococcus damnosus (1), uncultured bacterium (1)
	C CAG AAA **NCC** ACG GCU AAC	Bacterium (1)
	C CAG AAA G**CC** **N**CG GCU AAC	Bacillus caldolyticus (1), Bacillus caldovelox (1), Bacillus licheniformis (1)
	C CAG AAA G**CC** A**N**G GCU AAC	Bacillus cereus (1), Bacillus drentensis (1)
	C CAG AAA G**CC** AC**N** GCU AAC	Lactobacillus fermentum (1)
	C CAG AAA G**CC** ACG **N**CU AAC	Bacillus sp. (1)
	C CAG AAA G**CC** ACG G**N**U AAC	Bacillus licheniformis (1), Bacillus mojavensis (1), Bacillus sonorensis (1)
	C CAG AAA G**CC** ACG GCU **N**AC	Bacillus benzoevorans (1), Bacillus niacini (1), Bacillus simplex (1), Enterococcus faecium (1), Enterococcus sulfureus (1)
	C CAG AAA G**CC** ACG GCU A**N**C	Bacillus subtilis (1), Lysinibacillus macroides (1), uncultured bacterium (1)
	C CAG AAA G**CC** ACG GCU AA**N**	Bacillus cereus (1), Bacillus licheniformis (2), Bacillus sp. (4), bacterium (1), uncultured bacterium (5), unidentified eubacterium clone (1)
	C CAG AAA G**UC** **N**CG GCU AAC	uncultured bacterium (1), uncultured Firmicutes bacterium (1)
	C CAG AAA G**UC** ACG G**N**U AAC	Marinilactibacillus piezotolerans (1)
	C CAG AAA GG**A** ACG G**N**U AA**A**	Weissella hellenica (1)
	C CAG AAA GG**A** ACG GCU **N**A**A**	Weissella sp. (1)

Name of the probe: Bact 16 S 389

Target organism: *Bacteroides* spp.

Sequence of the probe: CAT CCT TCA CGC TAC TTG GCT GG

Date of *in-silico* assessment: May 2018

Mismatch count	**Ribosomal RNA sequence corresponding to the probe**	**Matching with known sequences (without italics)**
0 mm	CC AGC CAA GUA GCG UGA AGG AUG	Bacterium (13), Bacteroidaceae bacterium (5), Bacteroides acidifaciens (19), Bacteroides barnesiae (5), Bacteroides caccae (3), Bacteroides cellulosilyticus (3), Bacteroides chinchillae (4), Bacteroides clarus (3), Bacteroides coprocola (8), Bacteroides coprophilus (4), Bacteroides denticanum (6), Bacteroides dorei (5), Bacteroides eggerthii (6), Bacteroides faecis (5), Bacteroides finegoldii (4), Bacteroides fluxus (3), Bacteroides fragilis (62), Bacteroides gallinarum (2), Bacteroides graminisolvens (2), Bacteroides helcogenes (11), Bacteroides intestinalis (10), Bacteroides massiliensis (4), Bacteroides nordii (3), Bacteroides oleiciplenus (2), Bacteroides ovatus (15), Bacteroides paurosaccharolyticus (1), Bacteroides plebeius (7), Bacteroides propionicifaciens (4), Bacteroides pyogenes (14), Bacteroides rodentium (2), Bacteroides salyersiae (3), Bacteroides sartorii (2), Bacteroides sp. (76), Bacteroides stercoris (6), Bacteroides thetaiotaomicron (35), Bacteroides uniformis (19), Bacteroides vulgatus (25), Bacteroides xylanisolvens (3), human gut metagenome (31), iron-reducing bacterium enrichment culture clone (5), iron-reducing enrichment clone (1), Prevotella heparinolytica (6), Prevotella sp. (2), Prevotella zoogleoformans (1), rumen bacterium enrichment culture clone (1), swine fecal bacterium (2), uncultured bacterium (15252), uncultured Bacteroidaceae bacterium (14), uncultured Bacteroidales bacterium (20), uncultured Bacteroides sp. (76), uncultured Bacteroidetes bacterium (25), uncultured Firmicutes bacterium (1), uncultured isopod gut bacterium (1), uncultured marine bacterium (2), uncultured microorganism (1), uncultured organism (5502), uncultured Prevotella sp. (2), uncultured Prevotellaceae bacterium (5), uncultured rumen bacterium (34), unidentified (1), unidentified rumen bacterium (2), wallaby gut metagenome (1), Xenopus Silurana tropicalis (1)
	CC A**N**C CAA GUA GCG UGA AGG AUG	Bacteroides thetaiotaomicron (1)

	CC AGC CAA GU**N** GCG UGA AGG AUG	Prevotella zoogleoformans (1)
1 mm	**A**C AGC CAA GUA GCG UGA AGG AUG	uncultured bacterium (2), uncultured organism (1)
	UC AGC CAA GUA GCG UGA AGG AUG	uncultured bacterium (9), uncultured organism (1)
	C**G** AGC CAA GUA GCG UGA AGG AUG	Bacteroides sp. (1)
	C**U** AGC CAA GUA GCG UGA AGG AUG	uncultured bacterium (9)
	CC **C**GC CAA GUA GCG UGA AGG AUG	uncultured bacterium (1), uncultured organism (1)
	CC **G**GC CAA GUA GCG UGA AGG AUG	uncultured bacterium (12), uncultured organism (2)
	CC **U**GC CAA GUA GCG UGA AGG AUG	uncultured organism (2)
	CC A**A**C CAA GUA GCG UGA AGG AUG	uncultured bacterium (13), uncultured organism (12)
	CC A**C**C CAA GUA GCG UGA AGG AUG	uncultured bacterium (12), uncultured organism (16)
	CC A**U**C CAA GUA GCG UGA AGG AUG	uncultured bacterium (6), uncultured organism (2)
	CC AG**A** CAA GUA GCG UGA AGG AUG	uncultured organism (1)
	CC AG**G** CAA GUA GCG UGA AGG AUG	uncultured bacterium (1)
	CC AG**U** CAA GUA GCG UGA AGG AUG	uncultured bacterium (5), uncultured organism (7)
	CC AGC **U**AA GUA GCG UGA AGG AUG	uncultured bacterium (3), uncultured organism (28)
	CC AGC C**C**A GUA GCG UGA AGG AUG	uncultured bacterium (3), uncultured organism (3)
	CC AGC C**G**A GUA GCG UGA AGG AUG	uncultured bacterium (12), uncultured organism (3)
	CC AGC C**U**A GUA GCG UGA AGG AUG	uncultured bacterium (3)
	CC AGC CA**C** GUA GCG UGA AGG AUG	uncultured Bacteroidales bacterium (1)
	CC AGC CA**G** GUA GCG UGA AGG AUG	uncultured bacterium (24), uncultured Bacteroidales bacterium (1), uncultured organism (5)
	CC AGC CA**U** GUA GCG UGA AGG AUG	Bacteroidales oral clone (1), Bacteroides-like sp. (1), Bacteroidetes bacterium oral taxon (2), Phocaeicola abscessus (2), uncultured bacterium (1), uncultured Bacteroidales bacterium (1), uncultured Prevotella sp. (1), uncultured Prevotellaceae bacterium (1)
	CC AGC CAA **A**UA GCG UGA AGG AUG	uncultured bacterium (3), uncultured organism (2)
	CC AGC CAA **C**UA GCG UGA AGG AUG	uncultured bacterium (1), uncultured organism (1)
	CC AGC CAA **U**UA GCG UGA AGG AUG	uncultured bacterium (2)
	CC AGC CAA G**A**A GCG UGA AGG AUG	uncultured organism (1)
	CC AGC CAA G**C**A GCG UGA AGG AUG	uncultured bacterium (15), uncultured organism (4)
	CC AGC CAA G**G**A GCG UGA AGG AUG	uncultured organism (1)
	CC AGC CAA GU**C** GCG UGA AGG AUG	Bacterium (3), Bacteroides (1), Bacteroides sp. (9), Capnocytophaga sp. (1), Dysgonomonas capnocytophagoides (2), human gut metagenome (1), Parabacteroides goldsteinii (3), Parabacteroides gordonii (3), Parabacteroides johnsonii (2), Parabacteroides sp. (1),

		Petrimonas sulfuriphila (1), Porphyromonas catoniae (2), Porphyromonas gulae (10), Porphyromonas levii (402), Porphyromonas somerae (2), Porphyromonas sp. (43), rumen bacterium (1), Tannerella forsythia (24), uncultured anaerobic bacterium (5), uncultured bacterium (783), uncultured Bacteroidaceae bacterium (5), uncultured Bacteroidales bacterium (10), uncultured Bacteroides sp. (2), uncultured Bacteroidetes bacterium (15), uncultured compost bacterium (1), uncultured organism (112), uncultured Paludibacter sp. (3), uncultured Porphyromonadaceae bacterium (24), uncultured Porphyromonas sp. (17), uncultured prokaryote (7), uncultured rumen bacterium (30), uncultured Tannerella sp. (3), unidentified rumen bacterium (10)
	CC AGC CAA GU**G** GCG UGA AGG AUG	uncultured bacterium (10), uncultured organism (4)
	CC AGC CAA GU**U** GCG UGA AGG AUG	uncultured organism (1)
	CC AGC CAA GUA **A**CG UGA AGG AUG	uncultured bacterium (4), uncultured organism (4)
	CC AGC CAA GUA **C**CG UGA AGG AUG	uncultured bacterium (6), uncultured organism (11)
	CC AGC CAA GUA **U**CG UGA AGG AUG	uncultured bacterium (6), uncultured organism (3)
	CC AGC CAA GUA G**G**G UGA AGG AUG	uncultured bacterium (1)
	CC AGC CAA GUA G**U**G UGA AGG AUG	uncultured bacterium (8), uncultured organism (5)
	CC AGC CAA GUA GC**A** UGA AGG AUG	uncultured bacterium (5), uncultured organism (1)
	CC AGC CAA GUA GC**C** UGA AGG AUG	uncultured bacterium (1)
	CC AGC CAA GUA GCG **A**GA AGG AUG	uncultured bacterium (2)
	CC AGC CAA GUA GCG **C**GA AGG AUG	uncultured bacterium (12), uncultured organism (7)
	CC AGC CAA GUA GCG **G**GA AGG AUG	uncultured organism (1)
	CC AGC CAA GUA GCG U**A**A AGG AUG	uncultured bacterium (4), uncultured organism (1)
	CC AGC CAA GUA GCG UG**C** AGG AUG	Bacterium (1), Bacteroidales str. (3), Candidatus Prevotella conceptionensis (2), Hallella seregens (1), human gut metagenome (1), Prevotella aff. Ruminicola (1), Prevotella amnii (2), Prevotella aurantiaca (2), Prevotella baroniae (7), Prevotella bergensis (1), Prevotella bivia (27), Prevotella brevis (5), Prevotella bryantii (13), Prevotella buccae (10), Prevotella buccalis (4), Prevotella copri (5), Prevotella corporis (4), Prevotella dentalis (5), Prevotella denticola (13), Prevotella disiens (14), Prevotella enoeca (2), Prevotella falsenii (6), Prevotella genomosp. (3), Prevotella histicola (7), Prevotella loescheii (3), Prevotella maculosa (8), Prevotella marshii (3), Prevotella melaninogenica (23), Prevotella micans (5), Prevotella multisaccharivorax (5), Prevotella nanceiensis (15), Prevotella nigrescens (24), Prevotella oralis (7), Prevotella oris (4), Prevotella paludivivens (4), Prevotella pleuritidis (1), Prevotella ruminicola (29), Prevotella saccharolytica (3), Prevotella salivae (6), Prevotella scopos (2), Prevotella shahii (1),

		Prevotella sp. (88), Prevotella stercorea (1), Prevotella timonensis (4), Prevotella veroralis (2), Prevotellaceae bacterium (5), rumen bacterium (7), uncultured bacterium (5537), uncultured Bacteroidales bacterium (4), uncultured Bacteroidetes bacterium (4), uncultured eubacterium (4), uncultured Lachnospiraceae bacterium (1), uncultured marine bacterium (1), uncultured organism (109), uncultured Prevotella (1), uncultured Prevotella sp. (69), uncultured Prevotellaceae bacterium (49), uncultured prokaryote (36), uncultured rumen bacterium (499), unidentified (1), unidentified eubacterium clone (1), unidentified rumen bacterium (35), wallaby gut metagenome (2)
	CC AGC CAA GUA GCG UG**G** AGG AUG	Bacteroides salanitronis (7), Prevotella genomosp. (1), uncultured bacterium (123), uncultured Bacteroidales bacterium (3), uncultured organism (6), uncultured rumen bacterium (20)
	CC AGC CAA GUA GCG UG**U** AGG AUG	uncultured bacterium (7), uncultured rumen bacterium (1)
	CC AGC CAA GUA GCG UGA **G**GG AUG	Bacterium (1), Bacteroidaceae bacterium (1), human gut metagenome (1), Prevotellaceae bacterium (1), uncultured bacterium (111), uncultured Bacteroidales bacterium (1), uncultured organism (14), uncultured Prevotellaceae bacterium (12), uncultured rumen bacterium (28), unidentified rumen bacterium (1)
	CC AGC CAA GUA GCG UGA A**A**G AUG	uncultured bacterium (14), uncultured organism (6)
	CC AGC CAA GUA GCG UGA A**C**G AUG	uncultured bacterium (1), uncultured organism (1)
	CC AGC CAA GUA GCG UGA A**U**G AUG	uncultured bacterium (2)
	CC AGC CAA GUA GCG UGA AG**A** AUG	uncultured bacterium (6), uncultured organism (2)
	CC AGC CAA GUA GCG UGA AG**C** AUG	uncultured bacterium (1)
	CC AGC CAA GUA GCG UGA AGG **G**UG	uncultured bacterium (11), uncultured organism (2)
	CC AGC CAA GUA GCG UGA AGG A**A**G	Bacteroides coprosuis (6), Bacteroides sp. (2), rumen bacterium (1), swine fecal bacterium (1), uncultured bacterium (88), uncultured Bacteroidales bacterium (2), uncultured rumen bacterium (21)
	CC AGC CAA GUA GCG UGA AGG A**C**G	Paraprevotella clara (2), uncultured bacterium (158), uncultured organism (3), uncultured prokaryote (1)
	CC AGC CAA GUA GCG UGA AGG A**G**G	uncultured bacterium (2)
	CC AGC CAA GUA GCG UGA AGG AU**A**	uncultured bacterium (8), uncultured organism (4)
	CC AGC CAA GUA GCG UGA AGG AU**U**	uncultured bacterium (40)
	CC A**N**C CAA GUA GCG UGA AGG A**A**G	uncultured bacterium (1)
	CC AG**N** CAA GUA GCG UG**C** AGG AUG	uncultured bacterium oral clone (1)
	CC AGC C**N**A GUA GCG UG**C** AGG AUG	uncultured bacterium (1), uncultured rumen bacterium (1)
	CC AGC CAA **N**UA GCG UG**C** AGG AUG	Prevotella disiens (1)

	CC AGC CAA GUA **N**CG UG**C** AGG AUG	Prevotella sp. (1)
	CC AGC CAA GUA **N**CG UGA AGG A**A**G	uncultured bacterium (1)
	CC AGC CAA GUA GCG UG**C** AGG A**N**G	Prevotella bergensis (1), Prevotella buccae (4), Prevotella buccalis (1), Prevotellaceae bacterium (1), Prevotella corporis (1), Prevotella copri (3), Prevotella denticola (2), Prevotella histicola (2), Prevotella oris (3), Prevotella ruminicola (3), Prevotella timonensis (1), Prevotella veroralis (1), unidentified (1)
	CC AGC CAA GUA **NN**G UG**C** AGG AUG	uncultured Prevotellaceae bacterium (1)
	C**N** AGC C**N**A GUA GCG UG**C** AGG AUG	uncultured bacterium (1)
2 mm	**A**C AGC C**C**A GUA GCG UGA AGG AUG	uncultured bacterium (1)
	GG AGC CAA GUA GCG UGA AGG AUG	uncultured bacterium (1)
	UC AGC CAA GUA GCG UG**C** AGG AUG	uncultured bacterium (1), uncultured rumen bacterium (1)
	UC AGC CAA GUA GCG UGA AGG AU**U**	uncultured bacterium (1)
	C**U** A**C**C CAA GUA GCG UGA AGG AUG	uncultured bacterium (1)
	C**U** AGC CAA GUA GCG UG**C** AGG AUG	uncultured bacterium (3)
	CC **CU**C CAA GUA GCG UGA AGG AUG	uncultured organism (1)
	CC **C**GC CAA GU**C** GCG UGA AGG AUG	uncultured rumen bacterium (1)
	CC **G**GC CAA GUA GCG UG**C** AGG AUG	Prevotella sp. (1), uncultured bacterium (3)
	CC **G**GC CAA GUA GCG UG**G** AGG AUG	uncultured bacterium (1)
	CC **U**GC CAA GU**C** GCG UGA AGG AUG	Porphyromonas sp. (1), uncultured bacterium (1)
	CC **U**GC CAA GUA GCG UG**C** AGG AUG	uncultured bacterium (3), uncultured rumen bacterium (1)
	CC A**A**C CAA **C**UA GCG UGA AGG AUG	uncultured organism (1)
	CC A**A**C CAA GU**C** GCG UGA AGG AUG	uncultured bacterium (1), uncultured organism (1)
	CC A**A**C CAA GUA **A**CG UGA AGG AUG	uncultured bacterium (1)
	CC A**A**C CAA GUA **C**CG UGA AGG AUG	uncultured bacterium (1), uncultured organism (2)
	CC A**A**C CAA GUA **U**CG UGA AGG AUG	uncultured organism (2)
	CC A**A**C CAA GUA GCG UG**C** AGG AUG	uncultured bacterium (5), uncultured prokaryote (1)
	CC A**A**C CAA GUA GCG UGA A**C**G AUG	uncultured organism (1)
	CC A**CG** CAA GUA GCG UGA AGG AUG	uncultured bacterium (1)
	CC A**C**C C**G**A GUA GCG UGA AGG AUG	uncultured organism (1)
	CC A**C**C CA**C** GUA GCG UGA AGG AUG	uncultured bacterium (1)
	CC A**C**C CAA **A**UA GCG UGA AGG AUG	uncultured organism (1)
	CC A**C**C CAA GUA **A**CG UGA AGG AUG	uncultured bacterium (1)

	CC A**C**C CAA GUA **C**CG UGA AGG AUG	uncultured bacterium (1), uncultured organism (5)
	CC A**C**C CAA GUA **U**CG UGA AGG AUG	uncultured bacterium (5), uncultured organism (3)
	CC A**C**C CAA GUA GCG UG**C** AGG AUG	uncultured bacterium (15), uncultured organism (1)
	CC A**C**C CAA GUA GCG UG**G** AGG AUG	uncultured bacterium (2)
	CC A**C**C CAA GUA GCG UGA A**A**G AUG	uncultured bacterium (1), uncultured organism (3)
	CC A**C**C CAA GUA GCG UGA A**C**G AUG	uncultured bacterium (2), uncultured organism (3)
	CC A**C**C CAA GUA GCG UGA AGG A**C**G	uncultured organism (1)
	CC A**U**C CAA GUA **C**CG UGA AGG AUG	uncultured organism (1)
	CC A**U**C CAA GUA GCG UG**C** AGG AUG	uncultured bacterium (5)
	CC A**U**C CAA GUA GCG UG**G** AGG AUG	uncultured bacterium (1)
	CC AG**A** CAA GUA GCG UG**C** AGG AUG	uncultured rumen bacterium (1)
	CC AG**U** C**C**A GUA GCG UGA AGG AUG	uncultured bacterium (1)
	CC AG**U** CAA GU**C** GCG UGA AGG AUG	uncultured bacterium (1), uncultured rumen bacterium (1)
	CC AG**U** CAA GUA GCG UG**C** AGG AUG	uncultured bacterium (3), uncultured rumen bacterium (2)
	CC AGC **A**AA GU**C** GCG UGA AGG AUG	uncultured bacterium (1)
	CC AGC **U**A**U** GUA GCG UGA AGG AUG	uncultured bacterium (29), uncultured Bacteroidales bacterium (26), uncultured prokaryote (6)
	CC AGC **U**AA GUA GCG **C**GA AGG AUG	uncultured organism (1)
	CC AGC **U**AA GUA GCG UG**C** AGG AUG	uncultured bacterium (1)
	CC AGC C**C**A **A**UA GCG UGA AGG AUG	uncultured bacterium (1)
	CC AGC C**C**A GUA GCG UG**C** AGG AUG	uncultured bacterium (1)
	CC AGC C**G**A GUA GCG UG**C** AGG AUG	uncultured bacterium (3), uncultured rumen bacterium (1)
	CC AGC C**G**A GUA GCG UG**G** AGG AUG	uncultured organism (1)
	CC AGC C**G**A GUA GCG UGA A**C**G AUG	uncultured organism (2)
	CC AGC C**G**A GUA GCG UGA AGG A**A**G	uncultured rumen bacterium (1)
	CC AGC C**U**A GUA GCG UG**C** AGG AUG	uncultured bacterium (3)
	CC AGC CA**C** GU**C** GCG UGA AGG AUG	uncultured bacterium (267), uncultured compost bacterium (2), uncultured prokaryote (8)
	CC AGC CA**G** GUA GCG UG**C** AGG AUG	uncultured bacterium (5), uncultured rumen bacterium (1)
	CC AGC CA**U** G**C**A GCG UGA AGG AUG	uncultured marine bacterium (1)
	CC AGC CA**U** GU**C** GCG UGA AGG AUG	uncultured bacterium (12), uncultured Bacteroidetes bacterium (6), uncultured organism (1)
	CC AGC CA**U** GUA GCG UG**C** AGG AUG	uncultured bacterium (2)
	CC AGC CAA **A**U**C** GCG UGA AGG AUG	Bacteroides nordii (1), uncultured bacterium (78), uncultured Bacteroides sp. (1), uncultured Bacteroidetes bacterium (8), uncultured Porphyromonadaceae bacterium (6), uncultured soil bacterium (2)

	CC AGC CAA **A**UA **A**CG UGA AGG AUG	uncultured organism (1)
	CC AGC CAA **A**UA G**U**G UGA AGG AUG	uncultured bacterium (1)
	CC AGC CAA **A**UA GCG UG**C** AGG AUG	uncultured bacterium (4)
	CC AGC CAA **A**UA GCG UGA A**A**G AUG	uncultured bacterium (1)
	CC AGC CAA **C**UA GCG UG**C** AGG AUG	uncultured bacterium (1)
	CC AGC CAA **U**U**C** GCG UGA AGG AUG	Porphyromonas canoris (7), Porphyromonas sp. (1)
	CC AGC CAA G**A**A GCG UG**C** AGG AUG	uncultured bacterium (1), uncultured rumen bacterium (1)
	CC AGC CAA G**CC** GCG UGA AGG AUG	uncultured bacterium (5)
	CC AGC CAA G**C**A GCG UG**C** AGG AUG	uncultured bacterium (12)
	CC AGC CAA GU**C** G**G**G UGA AGG AUG	uncultured bacterium (1)
	CC AGC CAA GU**C** GCG **C**GA AGG AUG	uncultured bacterium (2)
	CC AGC CAA GU**C** GCG **G**GA AGG AUG	uncultured Bacteroidetes bacterium (1)
	CC AGC CAA GU**C** GCG UG**C** AGG AUG	Candidatus Prevotella conceptionensis (1), uncultured bacterium (7), uncultured Porphyromonadaceae bacterium (2), uncultured Rikenellaceae bacterium (1)
	CC AGC CAA GU**C** GCG UG**G** AGG AUG	uncultured bacterium (8)
	CC AGC CAA GU**C** GCG UGA **G**GG AUG	Bacterium (1), Bacteroides sp. (3), Bacteroidetes bacterium (1), human gut metagenome (3), Odoribacter laneus (5), Parabacteroides distasonis (27), Parabacteroides sp. (3), Porphyromonadaceae bacterium (1), uncultured bacterium (2042), uncultured Bacteroidales bacterium (4), uncultured Bacteroidetes bacterium (1), uncultured organism (360), uncultured Parabacteroides sp. (2), uncultured Porphyromonadaceae bacterium (5), uncultured Porphyromonas sp. (1), uncultured rumen bacterium (8), wallaby gut metagenome (1)
	CC AGC CAA GU**C** GCG UGA **U**GG AUG	uncultured bacterium (9)
	CC AGC CAA GU**C** GCG UGA A**C**G AUG	uncultured bacterium (1)
	CC AGC CAA GU**C** GCG UGA AGG A**A**G	Bacterium (12), Bacteroidales bacterium (1), Bacteroides sp. (6), Bacteroides-like sp. oral clone (1), Bacteroidetes bacterium (2), Bacteroidetes oral taxon (1), Barnesiella viscericola (1), Candidatus Armantifilum devescovinae (8), Candidatus Vestibaculum illigatum (1), human gut metagenome (1), iron-reducing bacterium enrichment culture clone (6), iron-reducing enrichment clone (2), Paludibacter propionicigenes (4), Parabacteroides merdae (5), Parabacteroides sp. (3), Porphyromonadaceae bacterium (7), Porphyromonas asaccharolytica (9), Porphyromonas bennonis (2), Porphyromonas cangingivalis (4), Porphyromonas circumdentaria (2), Porphyromonas gingivalis (39), Porphyromonas gulae (3), Porphyromonas sp. (19), Porphyromonas uenonis (4), Proteiniphilum acetatigenes (1), Proteiniphilum sp. (1),

		swine fecal bacterium (1), uncultured anaerobic bacterium (9), uncultured bacterium (982), uncultured Bacteroidaceae bacterium (12), uncultured Bacteroidales bacterium (35), uncultured Bacteroides sp. (5), uncultured Bacteroidetes bacterium (32), uncultured compost bacterium (1), uncultured Dysgonomonas sp. (4), uncultured microorganism (1), uncultured organism (211), uncultured Paludibacter sp. (1), uncultured Parabacteroides sp. (2), uncultured Porphyromonadaceae bacterium (24), uncultured Porphyromonas sp. (4), uncultured rumen bacterium (2), uncultured soil bacterium (2), unidentified (2)
	CC AGC CAA GU**C** GCG UGA AGG A**C**G	Paludibacter sp. (1), Porphyromonas canis (1), Porphyromonas endodontalis (4), Porphyromonas gingivicanis (4), Porphyromonas sp. (3), uncultured bacterium (56), uncultured Bacteroidales bacterium (1), uncultured Porphyromonadaceae bacterium (3), uncultured Porphyromonas sp. (3), uncultured Tannerella sp. (1), unidentified eubacterium clone (1)
	CC AGC CAA GU**C** GCG UGA AGG A**G**G	Porphyromonas sp. (1), uncultured bacterium (29), uncultured Bacteroidetes bacterium (1), uncultured rumen bacterium (2)
	CC AGC CAA GU**C** GCG UGA AGG AU**A**	uncultured bacterium (3)
	CC AGC CAA GU**C** GCG UGA AGG AU**C**	uncultured bacterium (1)
	CC AGC CAA GU**G** GCG UG**C** AGG AUG	uncultured bacterium (5), uncultured Prevotellaceae bacterium (1)
	CC AGC CAA GU**G** GCG UGA AGG A**C**G	uncultured bacterium (1)
	CC AGC CAA GU**U** GCG UGA **G**GG AUG	uncultured organism (4)
	CC AGC CAA GU**U** GCG UGA AGG A**A**G	uncultured bacterium (1)
	CC AGC CAA GUA **A**C**C** UGA AGG AUG	uncultured bacterium (1)
	CC AGC CAA GUA **A**CG UG**C** AGG AUG	uncultured bacterium (3), uncultured organism (2)
	CC AGC CAA GUA **A**CG UG**G** AGG AUG	uncultured rumen bacterium (1)
	CC AGC CAA GUA **A**CG UGA A**C**G AUG	uncultured bacterium (1)
	CC AGC CAA GUA **A**CG UGA AGG A**C**G	uncultured bacterium (1)
	CC AGC CAA GUA **C**CG UG**C** AGG AUG	uncultured bacterium (4)
	CC AGC CAA GUA **C**CG UGA A**A**G AUG	uncultured organism (2)
	CC AGC CAA GUA **C**CG UGA A**C**G AUG	uncultured bacterium (1)
	CC AGC CAA GUA **U**CG UGA A**U**G AUG	uncultured bacterium (1)
	CC AGC CAA GUA G**G**G UG**C** AGG AUG	uncultured bacterium (2)
	CC AGC CAA GUA G**U**G UG**C** AGG AUG	uncultured bacterium (4)
	CC AGC CAA GUA G**U**G UGA AGG **G**UG	uncultured organism (1)
	CC AGC CAA GUA G**U**G UGA AGG A**C**G	uncultured bacterium (1)
	CC AGC CAA GUA GC**A** UG**C** AGG AUG	uncultured bacterium (4)

	CC AGC CAA GUA GC**A** UGA AGG A**C**G	uncultured bacterium (1)
	CC AGC CAA GUA GCG **A**G**C** AGG AUG	Prevotella ruminicola (1), uncultured bacterium (1)
	CC AGC CAA GUA GCG **C**G**C** AGG AUG	uncultured bacterium (10), uncultured prokaryote (1), uncultured rumen bacterium (3)
	CC AGC CAA GUA GCG **C**GA AGG A**C**G	uncultured bacterium (1)
	CC AGC CAA GUA GCG U**AC** AGG AUG	uncultured bacterium (1)
	CC AGC CAA GUA GCG U**UU** AGG AUG	Bacteroidaceae bacterium (1)
	CC AGC CAA GUA GCG UG**C** **C**GG AUG	uncultured bacterium (1)
	CC AGC CAA GUA GCG UG**C** **G**GG AUG	Prevotella genomosp. (1), Prevotella tannerae (10), uncultured bacterium (48), uncultured eubacterium (1), uncultured organism (16), uncultured Prevotella sp. (2), uncultured rumen bacterium (20), unidentified eubacterium clone (1)
	CC AGC CAA GUA GCG UG**C** **U**GG AUG	uncultured bacterium (1)
	CC AGC CAA GUA GCG UG**C** A**A**G AUG	uncultured bacterium (1)
	CC AGC CAA GUA GCG UG**C** A**C**G AUG	uncultured bacterium (1), uncultured organism (1)
	CC AGC CAA GUA GCG UG**C** A**U**G AUG	uncultured bacterium (1)
	CC AGC CAA GUA GCG UG**C** AGG **G**UG	uncultured bacterium (7), uncultured organism (1), uncultured rumen bacterium (1)
	CC AGC CAA GUA GCG UG**C** AGG **U**UG	uncultured bacterium (2)
	CC AGC CAA GUA GCG UG**C** AGG A**A**G	human gut metagenome (2), Prevotella copri (1), Prevotella oris (3), Prevotella oulorum (3), Prevotella pallens (6), Prevotella sp. (10), Prevotella veroralis (3), Prevotellaceae bacterium (1), uncultured bacterium (2205), uncultured Bacteroides sp. (1), uncultured Bacteroidetes bacterium (3), uncultured eubacterium (1), uncultured organism (27), uncultured Prevotella sp. (11), uncultured Prevotellaceae bacterium (3), uncultured rumen bacterium (161), unidentified rumen bacterium (7)
	CC AGC CAA GUA GCG UG**C** AGG A**C**G	bacterium (2), Prevotella albensis (2), Prevotella baroniae (4), Prevotella bergensis (3), Prevotella buccae (2), Prevotella dentasini (2), Prevotella fusca (2), Prevotella genomosp. (1), Prevotella loescheii (3), Prevotella multiformis (1), Prevotella oulorum (2), Prevotella ruminicola (1), Prevotella sp. (10), Prevotellaceae bacterium (1), rumen bacterium (1), uncultured bacterium (1297), uncultured Bacteroidales bacterium (2), uncultured organism (5), uncultured Prevotella sp. (4), uncultured Prevotellaceae bacterium (15), uncultured rumen bacterium (146), unidentified (3), unidentified rumen bacterium (18), wallaby gut metagenome (1)
	CC AGC CAA GUA GCG UG**C** AGG A**G**G	Prevotella denticola (6), Prevotella multiformis (4), Prevotella sp. (4), uncultured bacterium (35), uncultured Prevotella sp. (1), uncultured prokaryote (1), uncultured rumen bacterium (2), unidentified rumen bacterium (1)
	CC AGC CAA GUA GCG UG**C** AGG AU**A**	uncultured bacterium (1)

	CC AGC CAA GUA GCG UG**C** AGG AU**U**	Prevotella falsenii (2), Prevotella intermedia (29), uncultured bacterium (17), uncultured Prevotella sp. (10)
	CC AGC CAA GUA GCG UG**G** **G**GG AUG	uncultured bacterium (1), uncultured rumen bacterium (14)
	CC AGC CAA GUA GCG UG**G** AGG A**A**G	uncultured bacterium (10), uncultured rumen bacterium (1)
	CC AGC CAA GUA GCG UG**G** AGG A**C**G	Paraprevotella xylaniphila (3), Prevotella genomosp. (1), Prevotella sp. (1), uncultured bacterium (10), uncultured Bacteroidetes bacterium (1), uncultured Prevotella sp. (1), unidentified rumen bacterium (1)
	CC AGC CAA GUA GCG UG**U** **G**GG AUG	uncultured bacterium (2), uncultured rumen bacterium (8)
	CC AGC CAA GUA GCG UG**U** AGG A**A**G	uncultured bacterium (5)
	CC AGC CAA GUA GCG UG**U** AGG A**C**G	uncultured bacterium (1)
	CC AGC CAA GUA GCG UG**U** AGG AU**U**	uncultured bacterium (1)
	CC AGC CAA GUA GCG UGA **G**GG A**A**G	Bacteroidales str. (3), human gut metagenome (2), uncultured bacterium (309), uncultured Bacteroidales bacterium (1), uncultured organism (1), uncultured Prevotellaceae bacterium (5), uncultured rumen bacterium (4), Xylanibacter oryzae (3)
	CC AGC CAA GUA GCG UGA **G**GG A**C**G	uncultured bacterium (39), uncultured Prevotellaceae bacterium (2), uncultured rumen bacterium (14)
	CC AGC CAA GUA GCG UGA **G**GG A**G**G	uncultured bacterium (1), uncultured rumen bacterium (1), unidentified rumen bacterium (1)
	CC AGC CAA GUA GCG UGA **G**GG AU**U**	uncultured bacterium (1), uncultured rumen bacterium (8)
	CC AGC CAA GUA GCG UGA AGG **GC**G	uncultured organism (1)
	CC AGC CAA GUA GCG UGA AGG A**AA**	uncultured bacterium (1)
	CC AGC CAA GUA GCG UGA AGG A**AU**	uncultured bacterium (4)
	CC AGC CAA GUA GCG UGA AGG A**CU**	uncultured bacterium (2)
	CC A**N**C CAA GUA GCG UG**C** AGG A**C**G	uncultured bacterium (1)

Name of the probe: Bact Komp

Target organism: none, prevention of cross-reaction with *Porphyromonas* spp.

Sequence of the probe: TCC TTC ACG CGA CTT GGC TGG TT

Date of *in-silico* assessment: May 2018

Mismatch count	**Ribosomal RNA sequence corresponding to the probe**	**Matching with known sequences (without italics)**
0 mm	AA CCA GCC AAG UCG CGU GAA GGA	Bacterium (15), Bacteroidales bacterium (1), Bacteroidales genomosp. (1), Bacteroides cf. forsythus oral clone (1), Bacteroides sp. (15), Bacteroides-like sp. (1), Bacteroidetes bacterium (2), Bacteroidetes oral taxon (1), Bacteroidetes sp. (1), Barnesiella viscericola (1), Candidatus Armantifilum devescovinae (8), Candidatus Vestibaculum illigatum (1), Capnocytophaga sp. (1), Dysgonomonas capnocytophagoides (2), human gut metagenome (2), iron-reducing bacterium enrichment culture clone (6), iron-reducing enrichment clone (2), Odoribacter denticanis (4), Paludibacter propionicigenes (4), Paludibacter sp. (1), Parabacteroides goldsteinii (3), Parabacteroides gordonii (3), Parabacteroides johnsonii (2), Parabacteroides merdae (5), Parabacteroides sp. (4), Petrimonas sulfuriphila (1), Porphyromonadaceae bacterium (7), Porphyromonas asaccharolytica (9), Porphyromonas bennonis (2), Porphyromonas cangingivalis (4), Porphyromonas canis (1), Porphyromonas catoniae (2), Porphyromonas circumdentaria (2), Porphyromonas endodontalis (4), Porphyromonas gingivalis (39), Porphyromonas gingivicanis (4), Porphyromonas gulae (13), Porphyromonas levii (402), Porphyromonas somerae (2), Porphyromonas sp. (66), Porphyromonas uenonis (4), Proteiniphilum acetatigenes (1), Proteiniphilum sp. (1), rumen bacterium (1), swine fecal bacterium (1), Tannerella forsythia (24), uncultured anaerobic bacterium (14), uncultured bacterium (1851), uncultured Bacteroidaceae bacterium (17), uncultured Bacteroidales bacterium (47), uncultured Bacteroides sp. (7), uncultured Bacteroidetes bacterium (48), uncultured compost bacterium (2), uncultured Dysgonomonas sp. (4), uncultured microorganism (1), uncultured organism (322), uncultured Paludibacter sp. (4), uncultured Parabacteroides sp. (2), uncultured Porphyromonadaceae bacterium (50), uncultured Porphyromonas sp. (24), uncultured prokaryote (7), uncultured rumen bacterium (35), uncultured soil bacterium (2), uncultured Tannerella sp. (4), unidentified (2), unidentified eubacterium clone (1),

		unidentified rumen bacterium (10)
	AA CCA GCC AAG U**N**G CGU GAA GGA	Prevotella zoogleoformans (1)
1 mm	**G**A CCA GCC AAG UCG CGU GAA GGA	uncultured bacterium (1)
	UA CCA GCC AAG UCG CGU GAA GGA	uncultured bacterium (2)
	A**C** CCA GCC AAG UCG CGU GAA GGA	uncultured Porphyromonadaceae bacterium (1)
	A**G** CCA GCC AAG UCG CGU GAA GGA	uncultured bacterium (1), uncultured organism (1)
	AA CC**C** GCC AAG UCG CGU GAA GGA	uncultured rumen bacterium (1)
	AA CC**G** GCC AAG UCG CGU GAA GGA	Porphyromonas gingivicanis (1), uncultured bacterium (1)
	AA CC**U** GCC AAG UCG CGU GAA GGA	Porphyromonas sp. (7), uncultured bacterium (1)
	AA CCA **A**CC AAG UCG CGU GAA GGA	uncultured bacterium (3), uncultured organism (1)
	AA CCA **C**CC AAG UCG CGU GAA GGA	uncultured bacterium (1), uncultured organism (1)
	AA CCA G**U**C AAG UCG CGU GAA GGA	uncultured bacterium (1), uncultured rumen bacterium (1)
	AA CCA GC**A** AAG UCG CGU GAA GGA	uncultured bacterium (1)
	AA CCA GC**U** AAG UCG CGU GAA GGA	uncultured bacterium (1)
	AA CCA GCC **C**AG UCG CGU GAA GGA	swine fecal bacterium (1)
	AA CCA GCC **G**AG UCG CGU GAA GGA	uncultured organism (2)
	AA CCA GCC A**C**G UCG CGU GAA GGA	Bacterium (1), Bacteroides sp. (1), bioreactor metagenome (1), Porphyromonas (1), Porphyromonas macacae (9), Proteiniphilum acetatigenes (2), Ruminobacillus xylanolyticum (1), uncultured anaerobic bacterium (1), uncultured bacterium (571), uncultured Bacteroides sp. (3), uncultured Bacteroidetes bacterium (15), uncultured compost bacterium (2), uncultured eubacterium (1), uncultured Porphyromonadaceae bacterium (4), uncultured prokaryote (9)
	AA CCA GCC A**G**G UCG CGU GAA GGA	uncultured bacterium (1), uncultured Bacteroidales bacterium (1)
	AA CCA GCC A**U**G UCG CGU GAA GGA	Cytophaga sp. (2), uncultured bacterium (44), uncultured Bacteroidetes bacterium (8), uncultured organism (1)
	AA CCA GCC AA**A** UCG CGU GAA GGA	Bacteroides nordii (1), Bacteroidetes bacterium (1), Candidatus Azobacteroides pseudotrichonymphae genomovar. (2), Candidatus Symbiothrix dinenymphae (1), Cluster III of the termite bacteroides symbiont (1), Dysgonomonas gadei (3), Dysgonomonas hofstadii (2), Dysgonomonas mossii (3), Dysgonomonas sp. (3), Dysgonomonas wimpennyi (1), gut bacterium (1), uncultured alpha proteobacterium (1), uncultured bacterium (125), uncultured Bacteroidaceae bacterium (12), uncultured Bacteroidales bacterium (33),

		uncultured Bacteroides sp. (2), uncultured Bacteroidetes bacterium (34), uncultured Dysgonomonas sp. (3), uncultured organism (1), uncultured Porphyromonadaceae bacterium (15), uncultured soil bacterium (2)
	AA CCA GCC AA**U** UCG CGU GAA GGA	Porphyromonas canoris (11), Porphyromonas sp. (1)
	AA CCA GCC AAG **C**CG CGU GAA GGA	uncultured bacterium (303), uncultured Bacteroidales bacterium (2), uncultured organism (5)
	AA CCA GCC AAG U**A**G CGU GAA GGA	Bacterium (13), Bacteroidaceae bacterium (5), Bacteroides acidifaciens (19), Bacteroides barnesiae (5), Bacteroides caccae (3), Bacteroides cellulosilyticus (3), Bacteroides chinchillae (4), Bacteroides clarus (3), Bacteroides coprocola (8), Bacteroides coprophilus (4), Bacteroides coprosuis (6), Bacteroides denticanum (6), Bacteroides dorei (5), Bacteroides eggerthii (6), Bacteroides faecis (5), Bacteroides finegoldii (4), Bacteroides fluxus (3), Bacteroides fragilis (62), Bacteroides gallinarum (2), Bacteroides graminisolvens (2), Bacteroides helcogenes (10), Bacteroides intestinalis (10), Bacteroides massiliensis (4), Bacteroides nordii (3), Bacteroides oleiciplenus (2), Bacteroides ovatus (15), Bacteroides paurosaccharolyticus (1), Bacteroides plebeius (7), Bacteroides propionicifaciens (4), Bacteroides pyogenes (14), Bacteroides rodentium (2), Bacteroides salyersiae (3), Bacteroides sartorii (2), Bacteroides sp. (77), Bacteroides stercoris (6), Bacteroides thetaiotaomicron (35), Bacteroides uniformis (19), Bacteroides vulgatus (25), Bacteroides xylanisolvens (3), human gut metagenome (31), iron-reducing bacterium enrichment culture clone (5), iron-reducing enrichment clone (1), Paraprevotella clara (2), Prevotella heparinolytica (6), Prevotella sp. (2), Prevotella zoogleoformans (1), rumen bacterium (2), swine fecal bacterium (3), uncultured bacterium (15508), uncultured Bacteroidaceae bacterium (13), uncultured Bacteroidales bacterium (20), uncultured Bacteroides sp. (75), uncultured Bacteroidetes bacterium (26), uncultured Firmicutes bacterium (1), uncultured isopod gut bacterium (1), uncultured marine bacterium (2), uncultured microorganism (1), uncultured organism (5491), uncultured Prevotella sp. (2), uncultured Prevotellaceae bacterium (5), uncultured prokaryote (1), uncultured rumen bacterium (55), unidentified (1), unidentified rumen bacterium (2), wallaby gut metagenome (1), Xenopus Silurana tropicalis (1)
	AA CCA GCC AAG U**G**G CGU GAA GGA	uncultured bacterium (11), uncultured organism (4)
	AA CCA GCC AAG U**U**G CGU GAA GGA	uncultured bacterium (1), uncultured organism (1)
	AA CCA GCC AAG UC**C** CGU GAA GGA	uncultured bacterium (1)
	AA CCA GCC AAG UCG **G**GU GAA GGA	uncultured bacterium (1)
	AA CCA GCC AAG UCG **U**GU GAA GGA	uncultured bacterium (2)
	AA CCA GCC AAG UCG C**A**U GAA GGA	uncultured bacterium (1)

	AA CCA GCC AAG UCG CG**A** GAA GGA	uncultured Bacteroidetes bacterium (1)
	AA CCA GCC AAG UCG CG**C** GAA GGA	uncultured bacterium (4)
	AA CCA GCC AAG UCG CG**G** GAA GGA	uncultured Bacteroidetes bacterium (1)
	AA CCA GCC AAG UCG CGU G**C**A GGA	Candidatus Prevotella conceptionensis (1), Porphyromonas sp. (1), rod-shaped symbiont (1), uncultured bacterium (37), uncultured Bacteroidaceae bacterium (2), uncultured Bacteroidales bacterium (5), uncultured Bacteroides sp. (2), uncultured Bacteroidetes bacterium (4), uncultured Porphyromonadaceae bacterium (2), uncultured rumen bacterium (2)
	AA CCA GCC AAG UCG CGU G**G**A GGA	Barnesiella sp. (1), Tannerella sp. (1), uncultured bacterium (41), uncultured Bacteroidaceae bacterium (1), uncultured organism (7)
	AA CCA GCC AAG UCG CGU GA**C** GGA	uncultured bacterium (1)
	AA CCA GCC AAG UCG CGU GA**G** GGA	Bacterium (1), Bacteroidales bacterium (1), Bacteroides sp. (3), Bacteroidetes bacterium (1), Barnesiella intestinihominis (2), Barnesiella sp. (1), Butyricimonas synergistica (1), Butyricimonas virosa (1), Gram-negative bacterium (1), human gut metagenome (7), Odoribacter laneus (5), Odoribacter splanchnicus (7), Parabacteroides distasonis (27), Parabacteroides sp. (3), Porphyromonadaceae bacterium (2), uncultured bacterium (6236), uncultured Bacteroidaceae bacterium (1), uncultured Bacteroidales bacterium (4), uncultured Bacteroidetes bacterium (4), uncultured Firmicutes bacterium (2), uncultured organism (496), uncultured Parabacteroides sp. (2), uncultured Porphyromonadaceae bacterium (9), uncultured Porphyromonas sp. (1), uncultured rumen bacterium (15), wallaby gut metagenome (2)
	AA CCA GCC AAG UCG CGU GA**U** GGA	uncultured bacterium (10)
	AA CCA GCC AAG UCG CGU GAA **A**GA	uncultured Dysgonomonas sp. (1)
	AA CCA GCC AAG UCG CGU GAA **C**GA	uncultured bacterium (1), uncultured organism (1)
	AA CCA GCC AAG UCG CGU GAA **U**GA	uncultured Bacteroidetes bacterium (1)
	AA CCA GCC AAG UCG CGU GAA GG**C**	uncultured Bacteroidetes bacterium (2)
	AA CCA GCC AAG UCG CGU GAA GG**G**	uncultured bacterium (1)
	A**N** CCA GCC AAG U**A**G CGU GAA GGA	uncultured Bacteroidales bacterium (1)
	AA CCA **N**CC AAG U**A**G CGU GAA GGA	Bacteroides thetaiotaomicron (1), uncultured bacterium (1)
	AA CCA GCC A**C**G UCG CGU GAA **N**GA	uncultured bacterium (1)
	AA CCA GCC AAG U**AN** CGU GAA GGA	uncultured bacterium (1)

2 mm	CA CCA GCC AAG UAG CGU GAA GGA	uncultured bacterium (2)
	GA CCA GCC AAA UCG CGU GAA GGA	uncultured Bacteroidetes bacterium (1)
	GA CCA GCC AAG CCG CGU GAA GGA	uncultured bacterium (2)
	GA CCA GCC AAG UAG CGU GAA GGA	Bacteroides helcogenes (1), uncultured bacterium (15), uncultured Bacteroidaceae bacterium (1), uncultured organism (8)
	GA CCA GCC AAG UCG CGU GAG GGA	uncultured bacterium (5)
	UA CCA GCC AAG UAG CGU GAA GGA	uncultured Bacteroidetes bacterium (1), uncultured organism (2)
	AC CCA GCC AAG UAG CGU GAA GGA	Bacteroides sp. (1), uncultured bacterium (8), uncultured organism (1)
	AC CCA GCC AAG UCG CGU GAG GGA	uncultured bacterium (4)
	AG CCA GCC ACG UCG CGU GAA GGA	uncultured bacterium (5)
	AG CCA GCC AAG UAG CGU GAA GGA	uncultured bacterium (12), uncultured Bacteroides sp. (1), uncultured organism (6)
	AG CCA GCC AAG UCG CGU GCA GGA	uncultured Rikenellaceae bacterium (1)
	AG CCA GCC AAG UCG CGU GAG GGA	uncultured bacterium (8), uncultured organism (2)
	AU CCA GCC AUG UCG CGU GAA GGA	uncultured bacterium (2), uncultured Bacteroidetes bacterium (1)
	AU CCA GCC AAG UAG CGU GAA GGA	uncultured bacterium (9), uncultured organism (1)
	AU CCA GCC AAG UCG CGU GAG GGA	uncultured bacterium (1)
	AA ACA GCC AAG UCG CGU GAG GGA	uncultured bacterium (1)
	AA UCA GCC AAG UAG CGU GAA GGA	uncultured bacterium (11)
	AA UCA GCC AAG UCG CGU GCA GGA	uncultured bacterium (1)
	AA UCA GCC AAG UCG CGU GAG GGA	uncultured bacterium (8)
	AA CAA GCC AAG CCG CGU GAA GGA	uncultured bacterium (1)
	AA CAA GCC AAG UCG CGU CAA GGA	uncultured bacterium (1)
	AA CGA GCC AAG UAG CGU GAA GGA	Bacteroides sp. (1)
	AA CUA GCC AAG UAG CGU GAA GGA	uncultured bacterium (9)
	AA CUA GCC AAG UCG CGU GCA GGA	uncultured bacterium (1)
	AA CUA GCC AAG UCG CGU GAG GGA	uncultured organism (1)
	AA CCC GCC AAG UAG CGU GAA GGA	uncultured bacterium (1), uncultured organism (1)
	AA CCC GCC AAG UCG CGU GAG GGA	uncultured bacterium (1)
	AA CCG GCC AAG UAG CGU GAA GGA	uncultured bacterium (12), uncultured organism (2)
	AA CCG GCC AAG UCG CGU GAG GGA	uncultured bacterium (7)
	AA CCU GCC AAG UAG CGU GAA GGA	uncultured organism (2)
	AA CCU GCC AAG UCG CGU GAG GGA	uncultured bacterium (2)
	AA CCA ACC AAG CCG CGU GAA GGA	uncultured bacterium (1)

	AA CCA **A**CC AAG U**A**G CGU GAA GGA	uncultured bacterium (14), uncultured organism (10)
	AA CCA **A**CC AAG UC**A** CGU GAA GGA	uncultured organism (3)
	AA CCA **A**CC AAG UCG CGU GA**G** GGA	uncultured bacterium (4), uncultured organism (2)
	AA CCA **C**CC A**C**G UCG CGU GAA GGA	uncultured bacterium (4)
	AA CCA **C**CC AA**U** UCG CGU GAA GGA	uncultured bacterium (1)
	AA CCA **C**CC AAG **C**CG CGU GAA GGA	uncultured bacterium (3)
	AA CCA **C**CC AAG U**A**G CGU GAA GGA	uncultured bacterium (13), uncultured organism (15)
	AA CCA **C**CC AAG UCG CGU GA**G** GGA	uncultured bacterium (6)
	AA CCA **U**CC AAG **C**CG CGU GAA GGA	uncultured bacterium (1)
	AA CCA **U**CC AAG U**A**G CGU GAA GGA	uncultured bacterium (6), uncultured organism (2)
	AA CCA **U**CC AAG UCG CGU GA**G** GGA	uncultured bacterium (9)
	AA CCA G**A**C AAG U**A**G CGU GAA GGA	uncultured organism (1)
	AA CCA G**A**C AAG UCG CGU GA**G** GGA	uncultured bacterium (3)
	AA CCA G**G**C AAG U**A**G CGU GAA GGA	uncultured bacterium (1)
	AA CCA G**G**C AAG UCG CGU GA**G** GGA	uncultured bacterium (1)
	AA CCA G**U**C AAG U**A**G CGU GAA GGA	uncultured bacterium (5), uncultured organism (7)
	AA CCA G**U**C AAG UCG CGU GA**G** GGA	uncultured bacterium (6)
	AA CCA GC**A** AAG UCG CGU GA**G** GGA	uncultured bacterium (2)
	AA CCA GC**U** A**U**G UCG CGU GAA GGA	uncultured marine bacterium (1)
	AA CCA GC**U** AAG **A**CG CGU GAA GGA	uncultured bacterium (1)
	AA CCA GC**U** AAG **C**CG CGU GAA GGA	uncultured bacterium (1)
	AA CCA GC**U** AAG U**A**G CGU GAA GGA	uncultured bacterium (30), uncultured organism (1)
	AA CCA GC**U** AAG UCG CGU GA**G** GGA	uncultured bacterium (5)
	AA CCA GCC **C**AG U**A**G CGU GAA GGA	uncultured bacterium (3), uncultured organism (3)
	AA CCA GCC **G**AG **C**CG CGU GAA GGA	uncultured bacterium (1)
	AA CCA GCC **G**AG U**A**G CGU GAA GGA	uncultured bacterium (18), uncultured organism (3), uncultured rumen bacterium (1)
	AA CCA GCC **G**AG UCG CGU GA**G** GGA	uncultured bacterium (4), uncultured organism (2)
	AA CCA GCC **U**AG U**A**G CGU GAA GGA	uncultured bacterium (2)
	AA CCA GCC A**C**G **C**CG CGU GAA GGA	Flexibacteraceae bacterium (1), Marivirga sp. (1), uncultured bacterium (16), uncultured Bacteroidetes bacterium (2), uncultured Sphingobacteria bacterium (1)
	AA CCA GCC A**C**G U**A**G CGU GAA GGA	uncultured Bacteroidales bacterium (1)
	AA CCA GCC A**C**G UC**A** CGU GAA GGA	uncultured bacterium (2)
	AA CCA GCC A**C**G UC**C** CGU GAA GGA	uncultured bacterium (1)

	AA CCA GCC A**C**G UCG **U**GU GAA GGA	uncultured Bacteroidetes bacterium (1)
	AA CCA GCC A**C**G UCG CGU G**C**A GGA	Blattabacterium sp. (2), uncultured bacterium (13), uncultured Bacteroidetes bacterium (2), uncultured prokaryote (1)
	AA CCA GCC A**C**G UCG CGU G**G**A GGA	uncultured bacterium (1)
	AA CCA GCC A**C**G UCG CGU GA**G** GGA	Porphyromonas sp. (2), uncultured bacterium (3)
	AA CCA GCC A**C**G UCG CGU GAA **A**GA	uncultured bacterium (1)
	AA CCA GCC A**C**G UCG CGU GAA **U**GA	uncultured bacterium (1)
	AA CCA GCC A**C**G UCG CGU GAA GG**C**	uncultured Bacteroidetes bacterium (2)
	AA CCA GCC A**C**G UCG CGU GAA GG**U**	uncultured bacterium (1)
	AA CCA GCC A**GA** UCG CGU GAA GGA	uncultured bacterium (1)
	AA CCA GCC A**G**G U**A**G CGU GAA GGA	uncultured bacterium (18), uncultured Bacteroidales bacterium (1), uncultured organism (5)
	AA CCA GCC A**G**G UCG CGU G**G**A GGA	uncultured Porphyromonadaceae bacterium (1)
	AA CCA GCC A**G**G UCG CGU GA**G** GGA	uncultured bacterium (6), uncultured organism (1)
	AA CCA GCC A**UA** UCG CGU GAA GGA	uncultured bacterium (3)
	AA CCA GCC A**UC** UCG CGU GAA GGA	uncultured bacterium (25), uncultured Bacteroidales bacterium (1), uncultured rumen bacterium (3)
	AA CCA GCC A**U**G **C**CG CGU GAA GGA	Aureibacter tunicatorum (2), bacterium (10), Bacteroidales genomosp. (1), Bacteroidales oral clone (1), Bacteroidetes bacterium (6), Bacteroidia bacterium canine oral taxon (1), Chitinophaga arvensicola (1), Chitinophaga filiformis (2), Chitinophaga ginsengisoli (1), Chitinophaga pinensis (8), Chitinophaga sancti (7), Chitinophaga skermanii (1), Chitinophaga sp. (7), Chitinophagaceae bacterium (4), eubacterium sp. (1), Ferruginibacter alkalilentus (1), Ferruginibacter lapsinanis (1), Filimonas sp. (1), Flavisolibacter ginsengisoli (2), Flavisolibacter sp. (10), Flavobacteria bacterium (1), Flavobacteriaceae bacterium (4), Flavobacterium-like sp. (1), Flavosolibacter sp. (1), Haliscomenobacter sp. (2), iron-reducing bacterium enrichment culture clone (2), marine metagenome (3), metagenome sequence (1), Porphyromonas-like sp. (1), Sediminibacterium sp. (4), Segetibacter aerophilus (2), Segetibacter koreensis (1), soil bacterium (1), Solibius ginsengiterrae (1), Sphingobacteriaceae bacterium (2), Sphingobacteriales bacterium (1), Sphingobacterium sp. (1), symbiont (1), uncultured anaerobic bacterium (1), uncultured Anaerophaga sp. (2), uncultured bacterium (1408), uncultured Bacteroidaceae bacterium (2), uncultured Bacteroidales bacterium (25), uncultured Bacteroides sp. (1), uncultured Bacteroidetes bacterium (210), uncultured beta proteobacterium (1), uncultured Chitinophaga sp. (3), uncultured Chitinophagaceae bacterium (1), uncultured Cryomorphaceae bacterium (1), uncultured Cytophaga sp. (5),

		uncultured Cytophagales bacterium (5), uncultured Flavisolibacter sp. (3), uncultured Flavobacteriaceae bacterium (1), uncultured Flavobacteriales bacterium (2), uncultured Flavobacteriia bacterium (20), uncultured Flavobacterium sp. (20), uncultured Flexibacter sp. (5), uncultured Flexibacteraceae bacterium (2), uncultured Fluviicola sp. (1), uncultured Haliscomenobacter sp. (1), uncultured marine bacterium (58), uncultured marine microorganism (1), uncultured Niastella sp. (1), uncultured organism (45), uncultured prokaryote (2), uncultured rumen bacterium (58), uncultured Saprospiraceae bacterium (2), uncultured Sediminibacterium sp. (6), uncultured Segetibacter sp. (3), uncultured sludge bacterium (1), uncultured soil bacterium (23), uncultured Sphingobacteria bacterium (26), uncultured Sphingobacteriales bacterium (10), uncultured Sphingobacteriales cum Crenotrichaceae bacterium (6), uncultured Sphingobacterium sp. (4), uncultured Sphingobacterium sp. (2)
	AA CCA GCC A**U**G U**A**G CGU GAA GGA	Bacteroidales oral clone (1), Bacteroides-like sp. (1), Bacteroidetes bacterium oral taxon (2), Phocaeicola abscessus (2), uncultured bacterium (1), uncultured Bacteroidales bacterium (1), uncultured Prevotella sp. (1), uncultured Prevotellaceae bacterium (1)
	AA CCA GCC A**U**G UCG CGU G**C**A GGA	Alkaliflexus imshenetskii (2), Anaerophaga sp. (2), Anaerophaga thermohalophila (1), bacterium endosymbiont (5), bacterium enrichment culture clone (1), Bacteroidales bacterium (3), Bacteroidetes bacterium (3), Cytophaga fermentans (3), Cytophaga sp. (2), Cytophaga xylanolytica (1), Lactobacillales bacterium (1), marine bacterium (1), Marinifilum fragile (1), Marinifilum sp. (1), Marinilabiaceae bacterium (1), Marinilabilia salmonicolor (4), Marinilabilia sp. (1), Rikenellaceae bacterium (1), Ruminofilibacter xylanolyticum (1), uncultured alpha proteobacterium (1), uncultured Anaerophaga sp. (3), uncultured bacterium (269), uncultured Bacteroidales bacterium (5), uncultured Bacteroidetes bacterium (28), uncultured Cytophaga sp. (1), uncultured marine bacterium (3), uncultured microorganism (2), uncultured organism (11), uncultured prokaryote (63), uncultured Rikenellaceae bacterium (10)
	AA CCA GCC A**U**G UCG CGU G**G**A GGA	uncultured bacterium (41)
	AA CCA GCC A**U**G UCG CGU G**U**A GGA	uncultured bacterium (139), uncultured Bacteroidetes bacterium (3)
	AA CCA GCC A**U**G UCG CGU GA**G** GGA	uncultured bacterium (2), uncultured organism (1)
	AA CCA GCC AA**A** U**A**G CGU GAA GGA	uncultured bacterium (3), uncultured organism (2)
	AA CCA GCC AA**A** UCG CG**C** GAA GGA	uncultured Bacteroidetes bacterium (1)
	AA CCA GCC AA**A** ACG CGU G**C**A GGA	uncultured bacterium (2)
	AA CCA GCC AA**A** UCG CGU GA**G** GGA	uncultured bacterium (1)
	AA CCA GCC AA**A** UCG CGU GAA GG**G**	uncultured Bacteroides sp. (1)

	AA CCA GCC AA**C** U**A**G CGU GAA GGA	uncultured bacterium (1), uncultured organism (1)
	AA CCA GCC AA**U** **C**CG CGU GAA GGA	uncultured bacterium (2)
	AA CCA GCC AA**U** U**A**G CGU GAA GGA	uncultured bacterium (2)
	AA CCA GCC AAG **A**CG CGU GA**G** GGA	uncultured bacterium (2)
	AA CCA GCC AAG **AA**G CGU GAA GGA	uncultured organism (1)
	AA CCA GCC AAG **CA**G CGU GAA GGA	uncultured bacterium (14), uncultured organism (4)
	AA CCA GCC AAG **C**CG C**A**U GAA GGA	uncultured bacterium (1)
	AA CCA GCC AAG **C**CG CGU G**C**A GGA	uncultured bacterium (1), uncultured Cytophagales bacterium (2)
	AA CCA GCC AAG **C**CG CGU G**G**A GGA	uncultured bacterium (14)
	AA CCA GCC AAG **C**CG CGU GA**G** GGA	Gram-negative bacterium (1), mouse gut metagenome (2), uncultured bacterium (1388), uncultured Barnesiella sp. (1), uncultured organism (8)
	AA CCA GCC AAG **GA**G CGU GAA GGA	uncultured organism (1)
	AA CCA GCC AAG **G**CG CG**G** GAA GGA	uncultured bacterium (1)
	AA CCA GCC AAG U**AA** CGU GAA GGA	uncultured bacterium (5), uncultured organism (4)
	AA CCA GCC AAG U**AC** CGU GAA GGA	uncultured bacterium (6), uncultured organism (11)
	AA CCA GCC AAG U**AU** CGU GAA GGA	uncultured bacterium (6), uncultured organism (2)
	AA CCA GCC AAG U**A**G **G**GU GAA GGA	uncultured bacterium (1)
	AA CCA GCC AAG U**A**G **U**GU GAA GGA	uncultured bacterium (9), uncultured organism (5)
	AA CCA GCC AAG U**A**G C**A**U GAA GGA	uncultured bacterium (5), uncultured organism (2)
	AA CCA GCC AAG U**A**G C**C**U GAA GGA	uncultured bacterium (1)
	AA CCA GCC AAG U**A**G CG**A** GAA GGA	uncultured bacterium (2)
	AA CCA GCC AAG U**A**G CG**C** GAA GGA	uncultured bacterium (13), uncultured organism (7)
	AA CCA GCC AAG U**A**G CG**G** GAA GGA	uncultured organism (1)
	AA CCA GCC AAG U**A**G CGU **A**AA GGA	uncultured bacterium (4), uncultured organism (1)
	AA CCA GCC AAG U**A**G CGU G**C**A GGA	Bacterium (3), Bacteroidales str. (3), Candidatus Prevotella conceptionensis (2), Hallella seregens (1), human gut metagenome (3), Prevotella aff. Ruminicola (1), Prevotella albensis (2), Prevotella amnii (2), Prevotella aurantiaca (2), Prevotella baroniae (11), Prevotella bergensis (5), Prevotella bivia (27), Prevotella brevis (5), Prevotella bryantii (13), Prevotella buccae (16), Prevotella buccalis (5), Prevotella copri (9), Prevotella corporis (5), Prevotella dentalis (5), Prevotella dentasini (2), Prevotella denticola (21), Prevotella disiens (14), Prevotella enoeca (2), Prevotella falsenii (8), Prevotella fusca (2), Prevotella genomosp. (4), Prevotella histicola (9), Prevotella intermedia (29), Prevotella loescheii (6), Prevotella maculosa (8), Prevotella marshii (3), Prevotella melaninogenica (23), Prevotella micans (5), Prevotella multiformis (5), Prevotella multisaccharivorax (5),

		Prevotella nanceiensis (15), Prevotella nigrescens (24), Prevotella oralis (7), Prevotella oris (10), Prevotella oulorum (5), Prevotella pallens (6), Prevotella paludivivens (4), Prevotella pleuritidis (1), Prevotella ruminicola (33), Prevotella saccharolytica (3), Prevotella salivae (6), Prevotella scopos (2), Prevotella shahii (1), Prevotella sp. (112), Prevotella stercorea (1), Prevotella timonensis (5), Prevotella veroralis (6), Prevotellaceae bacterium (8), rumen bacterium (8), uncultured bacterium (9074), uncultured Bacteroidales bacterium (5), uncultured Bacteroides sp. (1), uncultured Bacteroidetes bacterium (8), uncultured eubacterium (5), uncultured Lachnospiraceae bacterium (1), uncultured marine bacterium (1), uncultured organism (141), uncultured Prevotella (1), uncultured Prevotella sp. (94), uncultured Prevotellaceae bacterium (67), uncultured prokaryote (36), uncultured rumen bacterium (805), unidentified (5), unidentified eubacterium clone (1), unidentified rumen bacterium (60), wallaby gut metagenome (3)
	AA CCA GCC AAG U**A**G CGU G**G**A GGA	Bacteroides salanitronis (7), Paraprevotella xylaniphila (3), Prevotella genomosp. (2), Prevotella sp. (1), uncultured bacterium (143), uncultured Bacteroidales bacterium (4), uncultured organism (6), uncultured Prevotella sp. (1), uncultured rumen bacterium (21), unidentified rumen bacterium (1)
	AA CCA GCC AAG U**A**G CGU G**U**A GGA	uncultured bacterium (14), uncultured rumen bacterium (1)
	AA CCA GCC AAG U**A**G CGU GA**G** GGA	Bacterium (1), Bacteroidaceae bacterium (1), Bacteroidales str. (3), human gut metagenome (3), Prevotellaceae bacterium (1), uncultured bacterium (460), uncultured Bacteroidales bacterium (2), uncultured organism (15), uncultured Prevotellaceae bacterium (19), uncultured rumen bacterium (55), unidentified rumen bacterium (5)
	AA CCA GCC AAG U**A**G CGU GAA **A**GA	uncultured bacterium (14), uncultured organism (6)
	AA CCA GCC AAG U**A**G CGU GAA **C**GA	uncultured bacterium (1), uncultured organism (1)
	AA CCA GCC AAG U**A**G CGU GAA **U**GA	uncultured bacterium (2)
	AA CCA GCC AAG U**A**G CGU GAA G**A**A	uncultured bacterium (6), uncultured organism (2)
	AA CCA GCC AAG U**A**G CGU GAA G**C**A	uncultured bacterium (1)
	AA CCA GCC AAG U**A**G CGU GAA GG**G**	uncultured bacterium (11), uncultured organism (3)
	AA CCA GCC AAG U**C**G CGU GAA GG**G**	uncultured bacterium (1)
	AA CCA GCC AAG U**G**G CGU G**C**A GGA	uncultured bacterium (9), uncultured Prevotellaceae bacterium (1)
	AA CCA GCC AAG U**G**G CGU G**G**A GGA	uncultured bacterium (1)
	AA CCA GCC AAG U**G**G CGU GA**G** GGA	uncultured bacterium (1)
	AA CCA GCC AAG U**U**G CGU GA**G** GGA	uncultured bacterium (4), uncultured organism (4)
	AA CCA GCC AAG UC**A** CGU GA**G** GGA	uncultured bacterium (7), uncultured organism (1)
	AA CCA GCC AAG UC**C** CGU GA**C** GGA	uncultured bacterium (1)

	AA CCA GCC AAG UCG **G**GU GA**G** GGA	uncultured bacterium (3)
	AA CCA GCC AAG UCG **U**GU GA**G** GGA	uncultured bacterium (6)
	AA CCA GCC AAG UCG C**A**U G**C**A GGA	uncultured rumen bacterium (1)
	AA CCA GCC AAG UCG C**A**U GA**G** GGA	uncultured bacterium (6)
	AA CCA GCC AAG UCG C**C**U GA**G** GGA	uncultured bacterium (2)
	AA CCA GCC AAG UCG C**U**U GA**G** GGA	uncultured bacterium (1)
	AA CCA GCC AAG UCG CG**C** GA**G** GGA	uncultured bacterium (10), uncultured Bacteroidetes bacterium (1)
	AA CCA GCC AAG UCG CGU **A**A**G** GGA	uncultured bacterium (2)
	AA CCA GCC AAG UCG CGU G**CG** GGA	uncultured bacterium (71), uncultured rumen bacterium (118)
	AA CCA GCC AAG UCG CGU G**GG** GGA	uncultured bacterium (8), uncultured rumen bacterium (28)
	AA CCA GCC AAG UCG CGU G**UG** GGA	uncultured bacterium (3)
	AA CCA GCC AAG UCG CGU GA**G** **A**GA	uncultured bacterium (13), uncultured organism (1)
	AA CCA GCC AAG UCG CGU GA**G** **U**GA	uncultured bacterium (1)
	AA CCA GCC AAG UCG CGU GA**G** G**A**A	uncultured bacterium (2)
	AA CCA GCC AAG UCG CGU GA**G** G**C**A	uncultured bacterium (1)
	AA CCA GCC AAG UCG CGU GA**G** GG**C**	Porphyromonas cansulci (2), Porphyromonas crevioricanis (5)
	AA CCA GCC AAG UCG CGU GA**G** GG**G**	uncultured bacterium (3)
	AA CCA GCC AAG UCG CGU GA**G** GG**U**	uncultured bacterium (1)
	AA CCA **N**CC A**U**G **C**CG CGU GAA GGA	uncultured Bacteroidetes bacterium (1)
	AA CCA **N**CC AAG U**A**G CGU G**C**A GGA	uncultured bacterium (1)
	AA CCA G**N**C AAG U**A**G CGU G**C**A GGA	uncultured bacterium oral clone (1)
	AA CCA GCC **N**AG U**A**G CGU G**C**A GGA	uncultured bacterium (1), uncultured rumen bacterium (1)
	AA CCA GCC A**C**G **C**CG CGU G**N**A GGA	Flexibacter polymorphus (1)
	AA CCA GCC AA**N** U**A**G CGU G**C**A GGA	Prevotella disiens (1)
	AA CCA GCC AAG **C**C**N** CGU G**G**A GGA	uncultured bacterium (1)
	AA CCA GCC AAG **N**CG CG**A** GA**G** GGA	uncultured bacterium (1)
	AA CCA GCC AAG U**AN** CGU G**C**A GGA	Prevotella sp. (1)

Name of the probe: Bact Komp 2

Target organism: none, prevention of cross-reaction with *Prevotella* spp.

Sequence of the probe: TCC TGC ACG CTA CTT GGC TGG T

Date of *in-silico* assessment: May 2018

Mismatch count	**Ribosomal RNA sequence corresponding to the probe**	**Matching with known sequences (without italics)**
0 mm	A CCA GCC AAG UAG CGU GCA GGA	Bacterium (3), Bacteroidales str. (3), Candidatus Prevotella conceptionensis (2), Hallella seregens (1), human gut metagenome (3), Prevotella aff. Ruminicola (1), Prevotella albensis (2), Prevotella amnii (2), Prevotella aurantiaca (2), Prevotella baroniae (11), Prevotella bergensis (5), Prevotella bivia (27), Prevotella brevis (5), Prevotella bryantii (13), Prevotella buccae (16), Prevotella buccalis (5), Prevotella copri (9), Prevotella corporis (5), Prevotella dentalis (5), Prevotella dentasini (2), Prevotella denticola (21), Prevotella disiens (14), Prevotella enoeca (2), Prevotella falsenii (8), Prevotella fusca (2), Prevotella genomosp. (4), Prevotella histicola (9), Prevotella intermedia (29), Prevotella loescheii (6), Prevotella maculosa (8), Prevotella marshii (3), Prevotella melaninogenica (23), Prevotella micans (5), Prevotella multiformis (5), Prevotella multisaccharivorax (5), Prevotella nanceiensis (15), Prevotella nigrescens (24), Prevotella oralis (7), Prevotella oris (10), Prevotella oulorum (5), Prevotella pallens (6), Prevotella paludivivens (4), Prevotella pleuritidis (1), Prevotella ruminicola (33), Prevotella saccharolytica (3), Prevotella salivae (6), Prevotella scopos (2), Prevotella shahii (1), Prevotella sp. (112), Prevotella stercorea (1), Prevotella timonensis (5), Prevotella veroralis (6), Prevotellaceae bacterium (8), rumen bacterium (8), uncultured bacterium (9087), uncultured Bacteroidales bacterium (5), uncultured Bacteroides sp. (1), uncultured Bacteroidetes bacterium (8), uncultured eubacterium (5), uncultured Lachnospiraceae bacterium (1), uncultured marine bacterium (1), uncultured organism (141), uncultured Prevotella (1), uncultured Prevotella sp. (95), uncultured Prevotellaceae bacterium (67), uncultured prokaryote (36), uncultured rumen bacterium (809), unidentified (5), unidentified eubacterium clone (1), unidentified rumen bacterium (61), wallaby gut metagenome (3)
	A CCA **N**CC AAG UAG CGU GCA GGA	uncultured bacterium (1)
	A CCA G**N**C AAG UAG CGU GCA GGA	uncultured bacterium oral clone (1)
	A CCA GCC **N**AG UAG CGU GCA GGA	uncultured bacterium (1), uncultured rumen bacterium (1)

	A CCA GCC AA**N** UAG CGU GCA GGA	Prevotella disiens (1)
	A CCA GCC AAG UA**N** CGU GCA GGA	Prevotella sp. (1)
	A CCA GCC AAG UA**N** **N**GU GCA GGA	uncultured Prevotellaceae bacterium (1)
	A CC**N** **NN**C AAG UAG CGU GCA GGA	uncultured rumen bacterium (1)
1 mm	**C** CCA GCC AAG UAG CGU GCA GGA	uncultured bacterium (2)
	G CCA GCC AAG UAG CGU GCA GGA	uncultured bacterium (11), uncultured prokaryote (1)
	U CCA GCC AAG UAG CGU GCA GGA	uncultured bacterium (3)
	A **U**CA GCC AAG UAG CGU GCA GGA	uncultured bacterium (3), uncultured rumen bacterium (1)
	A C**G**A GCC AAG UAG CGU GCA GGA	uncultured rumen bacterium (1)
	A C**U**A GCC AAG UAG CGU GCA GGA	uncultured bacterium (7), uncultured rumen bacterium (1)
	A CC**G** GCC AAG UAG CGU GCA GGA	Prevotella sp. (1), uncultured bacterium (8), uncultured rumen bacterium (1)
	A CC**U** GCC AAG UAG CGU GCA GGA	uncultured bacterium (3), uncultured rumen bacterium (1)
	A CCA **A**CC AAG UAG CGU GCA GGA	uncultured bacterium (7), uncultured prokaryote (1)
	A CCA **C**CC AAG UAG CGU GCA GGA	uncultured bacterium (21), uncultured organism (2)
	A CCA **U**CC AAG UAG CGU GCA GGA	uncultured bacterium (8)
	A CCA G**A**C AAG UAG CGU GCA GGA	uncultured rumen bacterium (1)
	A CCA G**U**C AAG UAG CGU GCA GGA	uncultured bacterium (4), uncultured rumen bacterium (2)
	A CCA GC**U** AAG UAG CGU GCA GGA	uncultured bacterium (3)
	A CCA GCC **C**AG UAG CGU GCA GGA	uncultured bacterium (1)
	A CCA GCC **G**AG UAG CGU GCA GGA	uncultured bacterium (9), uncultured rumen bacterium (1)
	A CCA GCC **U**AG UAG CGU GCA GGA	uncultured bacterium (4)
	A CCA GCC A**C**G UAG CGU GCA GGA	uncultured bacterium (1)
	A CCA GCC A**G**G UAG CGU GCA GGA	uncultured bacterium (7), uncultured Prevotellaceae bacterium (1), uncultured rumen bacterium (1)
	A CCA GCC A**U**G UAG CGU GCA GGA	uncultured bacterium (2)
	A CCA GCC AA**A** UAG CGU GCA GGA	uncultured bacterium (5)
	A CCA GCC AA**C** UAG CGU GCA GGA	uncultured bacterium (1)
	A CCA GCC AAG **A**AG CGU GCA GGA	uncultured bacterium (1), uncultured rumen bacterium (1)
	A CCA GCC AAG **C**AG CGU GCA GGA	uncultured bacterium (16)
	A CCA GCC AAG U**C**G CGU GCA GGA	Candidatus Prevotella conceptionensis (1), Porphyromonas sp. (1), rod-shaped symbiont (1), uncultured bacterium (37), uncultured Bacteroidaceae bacterium (2), uncultured Bacteroidales bacterium (5), uncultured Bacteroides sp. (2), uncultured Bacteroidetes bacterium (4), uncultured Porphyromonadaceae bacterium (2),

		uncultured rumen bacterium (2)
	A CCA GCC AAG U**G**G CGU GCA GGA	uncultured bacterium (9), uncultured Prevotellaceae bacterium (1)
	A CCA GCC AAG UA**A** CGU GCA GGA	uncultured bacterium (3), uncultured organism (2)
	A CCA GCC AAG UA**C** CGU GCA GGA	uncultured bacterium (6)
	A CCA GCC AAG UA**U** CGU GCA GGA	uncultured bacterium (1)
	A CCA GCC AAG UAG **G**GU GCA GGA	uncultured bacterium (2)
	A CCA GCC AAG UAG **U**GU GCA GGA	uncultured bacterium (5), uncultured rumen bacterium (1)
	A CCA GCC AAG UAG C**A**U GCA GGA	uncultured bacterium (5)
	A CCA GCC AAG UAG CG**A** GCA GGA	Prevotella ruminicola (1), uncultured bacterium (2)
	A CCA GCC AAG UAG CG**C** GCA GGA	uncultured bacterium (20), uncultured Bacteroidaceae bacterium (1), uncultured prokaryote (1), uncultured rumen bacterium (3)
	A CCA GCC AAG UAG CGU **A**CA GGA	uncultured bacterium (4)
	A CCA GCC AAG UAG CGU G**A**A GGA	Bacterium (13), Bacteroidaceae bacterium (5), Bacteroides acidifaciens (19), Bacteroides barnesiae (5), Bacteroides caccae (3), Bacteroides cellulosilyticus (3), Bacteroides chinchillae (4), Bacteroides clarus (3), Bacteroides coprocola (8), Bacteroides coprophilus (4), Bacteroides coprosuis (6), Bacteroides denticanum (6), Bacteroides dorei (5), Bacteroides eggerthii (6), Bacteroides faecis (5), Bacteroides finegoldii (4), Bacteroides fluxus (3), Bacteroides fragilis (62), Bacteroides gallinarum (2), Bacteroides graminisolvens (2), Bacteroides helcogenes (11), Bacteroides intestinalis (10), Bacteroides massiliensis (4), Bacteroides nordii (3), Bacteroides oleiciplenus (2), Bacteroides ovatus (15), Bacteroides paurosaccharolyticus (1), Bacteroides plebeius (7), Bacteroides propionicifaciens (4), Bacteroides pyogenes (14), Bacteroides rodentium (2), Bacteroides salyersiae (3), Bacteroides sartorii (2), Bacteroides sp. (77), Bacteroides stercoris (6), Bacteroides thetaiotaomicron (35), Bacteroides uniformis (19), Bacteroides vulgatus (25), Bacteroides xylanisolvens (3), human gut metagenome (31), iron-reducing bacterium enrichment culture clone (5), iron-reducing enrichment clone (1), Paraprevotella clara (2), Prevotella heparinolytica (6), Prevotella sp. (2), Prevotella zoogleoformans (1), rumen bacterium (2), swine fecal bacterium (3), uncultured bacterium (15525), uncultured Bacteroidaceae bacterium (14), uncultured Bacteroidales bacterium (20), uncultured Bacteroides sp. (75), uncultured Bacteroidetes bacterium (26), uncultured Firmicutes bacterium (1), uncultured isopod gut bacterium (1), uncultured marine bacterium (2), uncultured microorganism (1), uncultured organism (5501), uncultured Prevotella sp. (2), uncultured Prevotellaceae bacterium (5), uncultured prokaryote (1), uncultured rumen bacterium (55), unidentified (1), unidentified rumen bacterium (2), wallaby gut metagenome (1), Xenopus Silurana tropicalis (1)

	A CCA GCC AAG UAG CGU G**G**A GGA	Bacteroides salanitronis (7), Paraprevotella xylaniphila (3), Prevotella genomosp. (2), Prevotella sp. (1), uncultured bacterium (143), uncultured Bacteroidales bacterium (4), uncultured organism (6), uncultured Prevotella sp. (1), uncultured rumen bacterium (21), unidentified rumen bacterium (1)
	A CCA GCC AAG UAG CGU G**U**A GGA	uncultured bacterium (14), uncultured rumen bacterium (1)
	A CCA GCC AAG UAG CGU GC**C** GGA	uncultured bacterium (1)
	A CCA GCC AAG UAG CGU GC**G** GGA	Prevotella genomosp. (1), Prevotella tannerae (10), uncultured bacterium (81), uncultured eubacterium (1), uncultured organism (16), uncultured Prevotella sp. (2), uncultured rumen bacterium (29), unidentified eubacterium clone (1), unidentified rumen bacterium (2)
	A CCA GCC AAG UAG CGU GC**U** GGA	uncultured bacterium (1)
	A CCA GCC AAG UAG CGU GCA **A**GA	uncultured bacterium (2)
	A CCA GCC AAG UAG CGU GCA **C**GA	uncultured bacterium (3), uncultured organism (1)
	A CCA GCC AAG UAG CGU GCA **U**GA	uncultured bacterium (1)
	A CCA GCC AAG UAG CGU GCA G**A**A	uncultured bacterium (2)
	A CCA GCC AAG UAG CGU GCA GG**C**	uncultured rumen bacterium (1)
	A CCA GCC AAG UAG CGU GCA GG**G**	uncultured bacterium (12), uncultured organism (1), uncultured rumen bacterium (1)
	A CCA GCC AAG UAG CGU GCA GG**U**	uncultured bacterium (6)
	N CCA GCC AAG UAG CGU G**A**A GGA	uncultured Bacteroidales bacterium (1)
	A CCA **N**CC AAG UAG CGU G**A**A GGA	Bacteroides thetaiotaomicron (1), uncultured bacterium (1)
	A CCA GCC AAG U**N**G CGU G**A**A GGA	Prevotella zoogleoformans (1)
	A CCA GCC AAG UA**N** CGU G**A**A GGA	uncultured bacterium (1)
	C C**N**A GCC **N**AG UAG CGU GCA GGA	uncultured bacterium (1)
2 mm	**C** CCA GCC AAG UAG CGU G**A**A GGA	Bacteroides sp. (1), uncultured bacterium (8), uncultured organism (1)
	G CCA GCC **U**AG UAG CGU GCA GGA	uncultured bacterium (1)
	G CCA GCC AAG U**C**G CGU GCA GGA	uncultured Rikenellaceae bacterium (1)
	G CCA GCC AAG UAG CGU G**A**A GGA	uncultured bacterium (21), uncultured Bacteroides sp. (1), uncultured organism (7)
	U CCA GCC AAG UAG CGU G**A**A GGA	uncultured bacterium (1)
	A **A**CA GCC AAG UAG CGU G**A**A GGA	uncultured bacterium (1)
	A **A**CA GCC AAG UAG CGU GCA GG**G**	uncultured bacterium (1)
	A **U**CA GCC AAG U**C**G CGU GCA GGA	uncultured bacterium (1)
	A **U**CA GCC AAG UAG CGU G**A**A GGA	uncultured bacterium (10), uncultured organism (1)
	A C**G**A GCC AAG UAG CGU G**A**A GGA	Bacteroides sp. (1)

	A C**U**A GCC AAG U**C**G CGU GCA GGA	uncultured bacterium (1)
	A C**U**A GCC AAG U**G**G CGU GCA GGA	uncultured rumen bacterium (1)
	A C**U**A GCC AAG UAG CGU G**A**A GGA	uncultured bacterium (9)
	A CC**C** GCC AAG UAG CGU G**A**A GGA	uncultured bacterium (1), uncultured organism (1)
	A CC**G** G**U**C AAG UAG CGU GCA GGA	uncultured bacterium (1)
	A CC**G** GCC AAG UAG CGU G**A**A GGA	uncultured bacterium (12), uncultured organism (2)
	A CC**G** GCC AAG UAG CGU G**G**A GGA	uncultured bacterium (1)
	A CC**U** GCC **U**AG UAG CGU GCA GGA	uncultured bacterium (1)
	A CC**U** GCC AAG UAG CGU G**A**A GGA	uncultured organism (2)
	A CCA **A**CC AAG UAG CGU G**A**A GGA	uncultured bacterium (13), uncultured organism (12)
	A CCA **A**CC AAG UAG CGU GCA **C**GA	uncultured bacterium (1)
	A CCA **A**CC AAG UAG CGU GCA **U**GA	uncultured bacterium (1)
	A CCA **C**CC AAG UA**A** CGU GCA GGA	uncultured bacterium (1)
	A CCA **C**CC AAG UA**C** CGU GCA GGA	uncultured bacterium (7)
	A CCA **C**CC AAG UA**U** CGU GCA GGA	uncultured bacterium (1)
	A CCA **C**CC AAG UAG CG**C** GCA GGA	uncultured organism (1)
	A CCA **C**CC AAG UAG CGU G**A**A GGA	uncultured bacterium (17), uncultured organism (12)
	A CCA **C**CC AAG UAG CGU G**G**A GGA	uncultured bacterium (2)
	A CCA **C**CC AAG UAG CGU GCA **A**GA	uncultured bacterium (2)
	A CCA **C**CC AAG UAG CGU GCA **C**GA	uncultured bacterium (2)
	A CCA **UG**C AAG UAG CGU GCA GGA	uncultured bacterium (2)
	A CCA **U**CC AA**A** UAG CGU GCA GGA	uncultured bacterium (1)
	A CCA **U**CC AAG UA**C** CGU GCA GGA	uncultured bacterium (2)
	A CCA **U**CC AAG UA**U** CGU GCA GGA	uncultured bacterium (1)
	A CCA **U**CC AAG UAG CGU G**A**A GGA	uncultured bacterium (6), uncultured organism (2)
	A CCA **U**CC AAG UAG CGU G**G**A GGA	uncultured bacterium (1)
	A CCA **U**CC AAG UAG CGU GCA **C**GA	uncultured organism (1)
	A CCA G**A**C AAG UAG CGU G**A**A GGA	uncultured organism (1)
	A CCA G**G**C AAG UA**C** CGU GCA GGA	uncultured bacterium (1)
	A CCA G**G**C AAG UAG CGU G**A**A GGA	uncultured bacterium (1)
	A CCA G**U**C AAG UAG CGU G**A**A GGA	uncultured bacterium (5), uncultured organism (7)
	A CCA GC**U** AAG UAG CGU G**A**A GGA	uncultured bacterium (3), uncultured organism (28)
	A CCA GCC **C**AG UAG CGU G**A**A GGA	uncultured bacterium (3), uncultured organism (3)

	A CCA GCC **G**AG **G**AG CGU GCA GGA	uncultured bacterium (1)
	A CCA GCC **G**AG UAG CGU G**A**A GGA	uncultured bacterium (18), uncultured organism (3), uncultured rumen bacterium (1)
	A CCA GCC **G**AG UAG CGU G**G**A GGA	uncultured organism (1)
	A CCA GCC **U**AG UAG CGU G**A**A GGA	uncultured bacterium (3)
	A CCA GCC A**C**G U**C**G CGU GCA GGA	Blattabacterium sp. (2), uncultured bacterium (13), uncultured Bacteroidetes bacterium (2), uncultured prokaryote (1)
	A CCA GCC A**C**G UAG CGU G**A**A GGA	uncultured Bacteroidales bacterium (1)
	A CCA GCC A**G**G U**C**G CGU GCA GGA	uncultured Porphyromonadaceae bacterium (1)
	A CCA GCC A**G**G UAG CGU G**A**A GGA	uncultured bacterium (18), uncultured Bacteroidales bacterium (1), uncultured organism (5)
	A CCA GCC A**G**G UAG CGU GC**G** GGA	uncultured rumen bacterium (1)
	A CCA GCC A**U**G **C**AG CGU GCA GGA	Sphingobacterium sp. (1)
	A CCA GCC A**U**G U**C**G CGU GCA GGA	Alkaliflexus imshenetskii (2), Anaerophaga sp. (2), Anaerophaga thermohalophila (1), bacterium (1), bacterium endosymbiont (5), Bacteroidales bacterium (3), Bacteroidetes bacterium (3), Cytophaga fermentans (3), Cytophaga sp. (2), Cytophaga xylanolytica (1), Lactobacillales bacterium (1), marine bacterium (1), Marinifilum fragile (1), Marinifilum sp. (1), Marinilabiaceae bacterium (1), Marinilabilia salmonicolor (4), Marinilabilia sp. (1), Rikenellaceae bacterium (1), Ruminofilibacter xylanolyticum (1), uncultured alpha proteobacterium (1), uncultured Anaerophaga sp. (3), uncultured bacterium (271), uncultured Bacteroidales bacterium (5), uncultured Bacteroidetes bacterium (28), uncultured Cytophaga sp. (1), uncultured marine bacterium (3), uncultured microorganism (2), uncultured organism (11), uncultured prokaryote (63), uncultured Rikenellaceae bacterium (10)
	A CCA GCC A**U**G UA**U** CGU GCA GGA	uncultured rumen bacterium (1)
	A CCA GCC A**U**G UAG CGU G**A**A GGA	Bacteroidales oral clone (1), Bacteroides-like sp. (1), Bacteroidetes bacterium oral taxon (2), Phocaeicola abscessus (2), uncultured bacterium (1), uncultured Bacteroidales bacterium (1), uncultured Prevotella sp. (1), uncultured Prevotellaceae bacterium (1)
	A CCA GCC AA**A** U**C**G CGU GCA GGA	uncultured bacterium (2)
	A CCA GCC AA**A** UAG CGU G**A**A GGA	uncultured bacterium (3), uncultured organism (2)
	A CCA GCC AA**C** UAG CGU G**A**A GGA	uncultured bacterium (1), uncultured organism (1)
	A CCA GCC AA**C** UAG CGU GCA **C**GA	uncultured bacterium (1)
	A CCA GCC AA**U** UAG CG**A** GCA GGA	uncultured bacterium (1)
	A CCA GCC AA**U** UAG CGU G**A**A GGA	uncultured bacterium (2)
	A CCA GCC AAG **CC**G CGU GCA GGA	uncultured bacterium (1), uncultured Cytophagales bacterium (2)
	A CCA GCC AAG **A**AG CGU G**A**A GGA	uncultured organism (1)

	A CCA GCC AAG **C**AG CGU G**A**A GGA	uncultured bacterium (15), uncultured organism (4)
	A CCA GCC AAG **G**AG CGU G**A**A GGA	uncultured organism (1)
	A CCA GCC AAG U**C**G C**A**U GCA GGA	uncultured rumen bacterium (1)
	A CCA GCC AAG U**C**G CGU G**A**A GGA	Bacterium (15), Bacteroidales bacterium (1), Bacteroidales genomosp. (1), Bacteroides cf. forsythus oral clone (1), Bacteroides sp. (15), Bacteroides-like sp. (1), Bacteroidetes bacterium (2), Bacteroidetes oral taxon (1), Bacteroidetes sp. (1), Barnesiella viscericola (1), Candidatus Armantifilum devescovinae (8), Candidatus Vestibaculum illigatum (1), Capnocytophaga sp. (1), Dysgonomonas capnocytophagoides (2), human gut metagenome (2), iron-reducing bacterium enrichment culture clone (6), iron-reducing enrichment clone (2), Odoribacter denticanis (4), Paludibacter propionicigenes (4), Paludibacter sp. (1), Parabacteroides goldsteinii (3), Parabacteroides gordonii (3), Parabacteroides johnsonii (2), Parabacteroides merdae (5), Parabacteroides sp. (4), Petrimonas sulfuriphila (1), Porphyromonadaceae bacterium (7), Porphyromonas asaccharolytica (9), Porphyromonas bennonis (2), Porphyromonas cangingivalis (4), Porphyromonas canis (1), Porphyromonas catoniae (2), Porphyromonas circumdentaria (2), Porphyromonas endodontalis (4), Porphyromonas gingivalis (39), Porphyromonas gingivicanis (4), Porphyromonas gulae (13), Porphyromonas levii (402), Porphyromonas somerae (2), Porphyromonas sp. (66), Porphyromonas uenonis (4), Proteiniphilum acetatigenes (1), Proteiniphilum sp. (1), rumen bacterium (1), swine fecal bacterium (1), Tannerella forsythia (24), uncultured anaerobic bacterium (14), uncultured bacterium (1854), uncultured Bacteroidaceae bacterium (17), uncultured Bacteroidales bacterium (47), uncultured Bacteroides sp. (7), uncultured Bacteroidetes bacterium (48), uncultured compost bacterium (2), uncultured Dysgonomonas sp. (4), uncultured microorganism (1), uncultured organism (322), uncultured Paludibacter sp. (4), uncultured Parabacteroides sp. (2), uncultured Porphyromonadaceae bacterium (50), uncultured Porphyromonas sp. (24), uncultured prokaryote (7), uncultured rumen bacterium (35), uncultured soil bacterium (2), uncultured Tannerella sp. (4), unidentified (2), unidentified eubacterium clone (1), unidentified rumen bacterium (10)
	A CCA GCC AAG U**C**G CGU G**G**A GGA	Barnesiella sp. (1), Tannerella sp. (1), uncultured bacterium (41), uncultured Bacteroidaceae bacterium (1), uncultured organism (7)
	A CCA GCC AAG U**C**G CGU GC**G** GGA	uncultured bacterium (71), uncultured rumen bacterium (118)
	A CCA GCC AAG U**G**G CGU G**A**A GGA	uncultured bacterium (11), uncultured organism (3)
	A CCA GCC AAG U**G**G CGU G**G**A GGA	uncultured bacterium (1), uncultured organism (1)

	A CCA GCC AAG U**U**G **U**GU GCA GGA	uncultured rumen bacterium (1)
	A CCA GCC AAG U**U**G CG**C** GCA GGA	uncultured rumen bacterium (1)
	A CCA GCC AAG U**U**G CGU G**A**A GGA	uncultured bacterium (1), uncultured organism (1)
	A CCA GCC AAG UA**A** CGU G**A**A GGA	uncultured bacterium (5), uncultured organism (4)
	A CCA GCC AAG UA**A** CGU G**G**A GGA	uncultured rumen bacterium (1)
	A CCA GCC AAG UA**A** CGU GCA **C**GA	uncultured bacterium (1)
	A CCA GCC AAG UA**C** CGU G**A**A GGA	uncultured bacterium (6), uncultured organism (11)
	A CCA GCC AAG UA**U** CGU G**A**A GGA	uncultured bacterium (6), uncultured organism (2)
	A CCA GCC AAG UAG **G**GU G**A**A GGA	uncultured bacterium (1)
	A CCA GCC AAG UAG **U**GU G**A**A GGA	uncultured bacterium (9), uncultured organism (5)
	A CCA GCC AAG UAG C**A**U G**A**A GGA	uncultured bacterium (5), uncultured organism (2)
	A CCA GCC AAG UAG C**C**U G**A**A GGA	uncultured bacterium (1)
	A CCA GCC AAG UAG CG**A** G**A**A GGA	uncultured bacterium (2)
	A CCA GCC AAG UAG CG**C** G**A**A GGA	uncultured bacterium (13), uncultured organism (7)
	A CCA GCC AAG UAG CG**G** G**A**A GGA	uncultured organism (1)
	A CCA GCC AAG UAG CG**G** GC**G** GGA	uncultured organism (1)
	A CCA GCC AAG UAG CGU **AA**A GGA	uncultured bacterium (4), uncultured organism (1)
	A CCA GCC AAG UAG CGU **UU**A GGA	Bacteroidaceae bacterium (1)
	A CCA GCC AAG UAG CGU G**AG** GGA	Bacterium (1), Bacteroidaceae bacterium (1), Bacteroidales str. (3), human gut metagenome (3), Prevotellaceae bacterium (1), uncultured bacterium (462), uncultured Bacteroidales bacterium (2), uncultured organism (15), uncultured Prevotellaceae bacterium (19), uncultured rumen bacterium (55), unidentified rumen bacterium (2), Xylanibacter oryzae (3)
	A CCA GCC AAG UAG CGU G**A**A **A**GA	uncultured bacterium (14), uncultured organism (6)
	A CCA GCC AAG UAG CGU G**A**A **C**GA	uncultured bacterium (1), uncultured organism (1)
	A CCA GCC AAG UAG CGU G**A**A **U**GA	uncultured bacterium (2)
	A CCA GCC AAG UAG CGU G**A**A G**A**A	uncultured bacterium (6), uncultured organism (2)
	A CCA GCC AAG UAG CGU G**A**A G**C**A	uncultured bacterium (1)
	A CCA GCC AAG UAG CGU G**A**A GG**G**	uncultured bacterium (11), uncultured organism (3)
	A CCA GCC AAG UAG CGU G**GG** GGA	uncultured bacterium (2), uncultured rumen bacterium (17)
	A CCA GCC AAG UAG CGU G**UG** GGA	Bacterium (1), uncultured bacterium (6), uncultured rumen bacterium (10)
	A CCA GCC AAG UAG CGU GC**U** GG**U**	uncultured rumen bacterium (1)
	A CCA GCC AAG UAG CGU GCA G**AU**	Prevotella intermedia (1), uncultured rumen bacterium (1)
	A CCA GCC AAG UAG CGU GCA G**CC**	uncultured rumen bacterium (1)

Name of the probe: Mic

Taget organism: *Micrococcus* spp.

Sequence of the probe: GTA TCT CTA CGG CGA TCG

Date of *in-silico* assessment: October 2017

Mismatch count	**Ribosomal RNA sequence corresponding to the probe**	**Matching with known sequences (without italics)**
0 mm	CGA UCG CCG UAG AGA UAC	actinobacterium (9), Antarctic bacterium (1), Arthrobacter sp. (2), Bacillus decisifrondis (1), bacterium (2), bacterium enrichment culture clone (3), glacial ice bacterium (1), Macrococcus sp. (1), Micrococcaceae bacterium (8), Micrococcus alkanovora (2), Micrococcus antarcticus (3), Micrococcus endophyticus (2), Micrococcus indicus (7), Micrococcus luteus (148), Micrococcus lylae (5), Micrococcus sp. (165), Micrococcus thailandicus (1), Micrococcus yunnanensis (11), Pseudonocardia sp. (1), rape rhizosphere bacterium (1), sponge bacterium (1), uncultured bacterium (58), uncultured Micrococcus sp. (7), uncultured organism (5), uncultured Paenibacillus sp. (1), unidentified (1), Variovorax sp. (1)
	CGA UCG CCG U**N**G AGA UAC	Micrococcus luteus (2)
	CGA UCG CCG UA**N** AGA UAC	Micrococcus sp. (1)
	CGA UCG CCG UAG AGA UA**N**	Micrococcus sp. (1)
	CGA **N**CG CCG UAG AGA **N**AC	blackwater bioreactor bacterium (1)
1 mm	**A**GA UCG CCG UAG AGA UAC	Corynebacterium afermentans (3), Corynebacterium mucifaciens (4), Corynebacterium sp. (10), Rhodococcus sp. (3), uncultured bacterium (30), uncultured Corynebacterium sp. (2), uncultured organism (1), unidentified (2)
	GGA UCG CCG UAG AGA UAC	Corynebacteriaceae (1), Prauserella alba (1), Rhodococcus sp. (1)
	UGA UCG CCG UAG AGA UAC	Micrococcus terreus (1), uncultured bacterium (1)
	CG**U** UCG CCG UAG AGA UAC	Micrococcus lylae (10), Micrococcus sp. (4), uncultured Micrococcus sp. (3)
	CGA **C**CG CCG UAG AGA UAC	uncultured bacterium (1), uncultured Clostridiaceae bacterium (1)
	CGA U**U**G CCG UAG AGA UAC	Micrococcus endophyticus (1), Micrococcus indicus (1), Micrococcus luteus (2), uncultured bacterium (1)
	CGA UC**A** CCG UAG AGA UAC	Micrococcus luteus (1)
	CGA UC**C** CCG UAG AGA UAC	Micrococcus luteus (1)

	CGA UCG UCG UAG AGA UAC	Micrococcus luteus (3)
	CGA UCG CGG UAG AGA UAC	Micrococcus sp. (1)
	CGA UCG CCC UAG AGA UAC	uncultured bacterium (1)
	CGA UCG CCG CAG AGA UAC	uncultured bacterium (1)
	CGA UCG CCG UGG AGA UAC	Actinobacterium (1), Micrococcus luteus (2)
	CGA UCG CCG UAA AGA UAC	Micrococcus luteus (1)
	CGA UCG CCG UAG AGA UGC	Micrococcus luteus (1), uncultured organism (1)
	CGA UCG CCG UNG AGA UGC	Micrococcus luteus (1)
	CGA UCG CCG UAG AGA GAN	Micrococcus luteus (1)
2 mm	AGA ACG CCG UAG AGA UAC	Microbacterium sp. (3)
	AGA CCG CCG UAG AGA UAC	Oscillospira guilliermondii (1), uncultured bacterium (1)
	AGA UUG CCG UAG AGA UAC	Prauserella sp. (2), Pseudonocardiaceae bacterium (1), uncultured Actinobacteridae bacterium (1), uncultured bacterium (1)
	AGA UCG GCG UAG AGA UAC	Corynebacterium diphtheriae (2), Corynebacterium durum (4), Corynebacterium pseudotuberculosis (49), Corynebacterium sp. (1), Corynebacterium ulcerans (13), uncultured bacterium (7), uncultured Corynebacterium sp. (1), uncultured organism (1)
	AGA UCG UCG UAG AGA UAC	Corynebacterium ureicelerivorans (2), uncultured bacterium (4)
	AGA UCG CUG UAG AGA UAC	Corynebacterium mycetoides (2)
	AGA UCG CCG CAG AGA UAC	Corynebacterium mucifaciens (1)
	AGA UCG CCG UAG AAA UAC	Arthrobacter gangotriensis (1), Arthrobacter sp. (3), uncultured actinobacterium (1)
	GGA CCG CCG UAG AGA UAC	Rhodococcus phenolicus (3), Rhodococcus sp. (12), uncultured bacterium (2), uncultured soil bacterium (1)
	GGA UCG GCG UAG AGA UAC	Actinomycetales bacterium (1), Corynebacterium acetoacidophilum (1), Corynebacterium auriscanis (5), Corynebacterium callunae (2), Corynebacterium diphtheriae (8), Corynebacterium glutamicum (66), Corynebacterium resistens (4), Corynebacterium sp. (3), Corynebacterium vitaeruminis (1), Pseudonocardineae bacterium (1), Rhodococcus globerulus (1), Saccharomonospora glauca (6), uncultured bacterium (12), uncultured compost bacterium (1), uncultured Corynebacterium sp. (3), unidentified (7)
	GGA UCG UCG UAG AGA UAC	uncultured bacterium (1)
	GGA UCG CUG UAG AGA UAC	Rhodococcus sp. (1), Tomitella biformata (2), Tsukamurella sp. (1), uncultured Acidobacteriales bacterium (1)
	GGA UCG CCG UAG AGA UAU	Corynebacterium sp. (1)
	UGA ACG CCG UAG AGA UAC	uncultured bacterium (4)

	UGA **C**CG CCG UAG AGA UAC	Citricoccus sp. (6), Methylomicrobium sp. (1), Micrococcus chenggongense (1), Micrococcus indicus (1), Micrococcus luteus (2), Micrococcus sp. (9), Micrococcus terreus (2), uncultured bacterium (15), uncultured proteobacterium (1)
	UGA U**A**G CCG UAG AGA UAC	uncultured bacterium (1)
	UGA UCG **A**CG UAG AGA UAC	uncultured bacterium (1)
	UGA UCG **U**CG UAG AGA UAC	uncultured bacterium (1)
	UGA UCG C**U**G UAG AGA UAC	Clostridiaceae bacterium (1), Jeotgalicoccus psychrophilus (1), Paenibacillaceae bacterium (1), Streptococcus sp. (1), uncultured bacterium (8), uncultured Clostridiaceae bacterium (1), uncultured Jeotgalicoccus sp. (1), uncultured prokaryote (2), uncultured soil bacterium (1), uncultured rumen bacterium (1)
	UGA UCG CCG UAG AGA UA**U**	uncultured bacterium (1)
	C**AU** UCG CCG UAG AGA UAC	uncultured Micrococcus sp. (1)
	C**U**A UCG **A**CG UAG AGA UAC	uncultured bacterium (1)
	CG**U** UCG C**U**G UAG AGA UAC	uncultured Micrococcus sp. (4)
	CGA **AA**G CCG UAG AGA UAC	uncultured bacterium (2)
	CGA **AU**G CCG UAG AGA UAC	uncultured bacterium (1)
	CGA **A**CG C**U**G UAG AGA UAC	uncultured bacterium (8)
	CGA **A**CG CCG UAG **C**GA UAC	uncultured bacterium (1)
	CGA **CA**G CCG UAG AGA UAC	Bifidobacterium adolescentis (4), Bifidobacterium catenulatum (4), Bifidobacterium sp. (5), human gut metagenome (1), metagenome sequence (1), uncultured Acidobacteria bacterium (9), uncultured bacterium (123), uncultured Bifidobacterium sp. (5), uncultured delta proteobacterium (1), uncultured organism (1), uncultured soil bacterium (2)
	CGA **CG**G CCG UAG AGA UAC	Bifidobacterium dentium (10), Bifidobacterium longum (7), Bifidobacterium sp. (1), metagenome sequence (1), uncultured bacterium (2)
	CGA **C**CG **G**CG UAG AGA UAC	uncultured bacterium (2)
	CGA **C**CG C**U**G UAG AGA UAC	uncultured bacterium (6)
	CGA UCG CC**A** UAG AGA UA**U**	uncultured bacterium (1)
	CGA UCG CCG **C**AG AGA U**G**C	Rhizobium sp. (1)
	CGA UCG CCG U**G**G AGA **C**AC	Micrococcus flavus (2), Micrococcus sp. (1), uncultured bacterium (2)
	CGA UCG CCG UAG AG**C** **G**AC	Micrococcus antarcticus (1)
	GGA **C**CG C**N**G UAG AGA UAC	uncultured bacterium (1)
	GGA **NA**G CCG UAG AGA UAC	Rhodococcus sp. (1)

	NGA **C**CG **G**CG UAG AGA UAC	Saccharomonospora viridis (1)
	CGA **CG**G CCG UAG A**N**A UAC	uncultured bacterium (1)

Name of the probe: Spy1

Target organism: *Streptococcus pyogenes*

Sequence of the probe: CTA ACA TGC GTT AGT CTC TC

Date of *in-silico* assessment: September 2017

Mismatch count	**Ribosomal RNA sequence corresponding to the probe**	**Matching with known sequences (without italics)**
0 mm	GA GAG ACU AAC GCA UGU UAG	Streptococcus phage (28), Streptococcus pyogenes (143), Streptococcus sp. (1), uncultured Streptococcus sp. (1), unidentified (25)
1 mm	**U**A GAG ACU AAC GCA UGU UAG	Streptococcus pyogenes (1)
2 mm	GA G**U**G ACU AAC **A**CA UGU UAG GA G**U**G A**N**U AAC **A**CA UGU UAG	Streptococcus devriesei (1) Streptococcus devriesei (1)