

**Supplementary Table 1a** Comparison of 16S rRNA gene sequences of medically important *Clostridium* species

	CA	CAr	CB	CBe	CBi	CBo	CBu	CC	CCr	CCe	CCh	CCl	CCo	CCm	CD	CDi	CF	CG	CGly	CH	CHr
CA	-	78.0	80.4	81.4	79.1	76.5	80.6	80.7	80.3	85.3	81.1	89.8	88.8	77.6	78.1	79.3	80.4	77.5	79.8	78.9	82.1
CAr	82.7	-	91.0	90.7	86.3	91.5	90.7	88.5	88.3	91.2	88.0	79.7	82.0	91.6	84.8	88.7	88.9	86.8	84.7	91.4	84.1
CB	83.7	92.1	-	95.4	85.7	90.6	96.0	91.3	94.2	96.3	93.2	80.9	81.6	91.4	84.6	93.6	92.7	84.8	86.0	93.3	82.0
CBe	83.7	92.3	95.9	-	85.4	91.3	98.8	93.1	93.3	97.1	94.0	82.9	84.4	91.1	85.2	94.0	92.7	84.6	85.5	92.5	83.9
CBi	83.3	85.7	85.7	85.9	-	86.3	85.0	84.7	85.8	83.4	85.7	82.9	84.5	83.9	94.1	86.1	85.2	97.0	94.3	84.6	94.7
CBo	81.0	93.2	91.3	92.1	84.8	-	91.3	88.8	88.7	88.2	88.3	79.5	81.4	93.4	84.6	87.2	88.5	87.3	87.0	91.4	84.3
CBu	82.7	92.1	94.9	98.2	84.8	92.0	-	93.1	93.1	96.6	93.8	82.9	84.4	91.3	84.6	93.8	93.5	84.2	85.1	93.5	83.2
CC	82.3	90.6	91.5	92.3	83.4	90.2	92.1	-	91.9	94.6	92.9	82.2	82.2	88.5	85.1	92.7	92.8	84.5	85.2	91.4	82.2
CCr	83.5	91.0	95.9	95.3	85.5	90.4	94.8	91.9	-	95.8	98.6	81.5	82.0	90.0	85.8	95.0	91.2	85.8	85.5	90.8	84.8
CCe	85.6	92.1	95.6	95.6	84.8	89.9	94.7	92.8	96.4	-	96.1	81.1	81.8	90.2	83.5	100.0	95.3	82.9	85.8	93.1	84.5
CCh	83.1	91.6	95.3	94.8	85.3	90.6	94.4	92.0	98.2	95.8	-	80.9	82.2	89.8	85.6	94.6	90.8	86.0	85.5	91.0	84.3
CCl	90.5	83.2	82.8	83.8	83.2	82.4	83.1	82.5	83.1	83.5	82.8	-	90.6	79.6	82.5	80.7	80.1	82.3	84.2	79.2	81.5
CCo	89.7	83.9	82.1	84.3	84.1	83.0	83.4	82.9	82.7	83.6	82.0	92.6	-	80.8	83.0	82.3	82.7	83.5	84.6	81.2	80.5
CCm	82.1	92.9	90.7	91.2	84.5	92.8	90.9	88.9	90.5	91.2	90.8	81.9	82.9	-	82.7	87.6	86.8	84.0	84.4	91.8	80.6
CD	83.6	85.6	85.5	85.0	94.8	84.6	83.6	83.0	85.6	85.1	85.6	83.2	83.7	83.8	-	85.0	85.2	94.9	93.7	85.2	93.8
CDi	83.6	91.5	94.7	95.2	85.1	89.8	94.8	92.3	96.5	98.9	95.8	83.1	83.4	90.1	85.0	-	93.3	85.2	87.7	90.2	84.8
CF	83.3	92.0	93.3	94.3	85.4	90.7	93.8	92.4	93.7	94.6	94.4	83.4	83.1	90.8	85.3	94.0	-	86.0	85.7	92.3	83.6
CG	83.1	86.7	85.8	85.8	97.7	85.3	84.6	83.2	85.7	85.0	85.9	83.4	84.5	84.3	95.4	85.3	85.4	-	93.9	84.3	95.2
CGly	84.0	84.7	84.9	84.9	95.0	85.2	83.9	82.6	84.6	85.0	84.3	83.5	84.2	83.8	94.4	84.8	85.4	94.3	-	85.3	92.4
CH	81.7	92.1	91.5	92.3	85.8	91.0	92.1	89.5	91.2	91.6	91.4	82.2	82.4	91.3	85.5	90.5	93.2	85.8	85.6	-	82.3
CHr	84.6	85.1	83.4	84.3	92.8	84.5	82.7	81.4	84.4	84.8	84.1	82.9	82.6	83.0	94.2	84.3	84.6	93.6	93.6	84.2	-
CHi	82.6	91.5	90.9	91.7	85.1	92.6	91.0	90.6	89.6	91.1	90.0	82.3	83.0	90.7	85.4	89.6	91.8	84.9	85.1	91.0	84.5
CHy	89.1	80.4	80.3	80.3	81.9	79.6	80.7	79.2	80.5	82.5	80.8	91.7	90.6	78.9	81.8	80.3	82.6	81.5	83.1	80.5	83.4
CI	90.5	82.8	82.6	83.4	85.1	81.9	82.7	82.6	82.9	83.8	82.9	91.1	90.6	82.1	84.1	82.9	83.5	84.6	85.1	83.0	84.4
CIn	80.3	80.7	79.9	79.7	80.7	80.2	79.7	79.3	79.8	80.0	79.6	80.6	80.9	79.2	81.0	79.4	80.0	80.8	79.9	79.2	80.9
CL	82.2	91.9	91.1	92.2	84.9	93.2	91.8	91.2	90.4	91.3	90.5	82.7	83.3	91.3	85.6	89.9	91.9	85.1	84.8	91.1	84.1
CM	82.0	92.7	90.9	90.8	84.6	91.9	90.5	89.3	91.0	91.7	91.1	82.1	82.1	93.9	84.9	91.4	90.7	85.0	83.3	90.6	82.3
CMg	82.7	85.0	85.3	85.7	93.3	84.1	84.3	82.6	85.6	85.0	85.5	82.8	83.8	83.9	94.7	85.0	84.4	93.3	92.9	85.6	92.7
CN	82.0	92.4	90.8	91.9	85.5	90.9	92.0	89.5	90.9	91.5	91.0	82.4	83.0	91.1	85.3	90.3	92.7	85.6	85.2	98.7	84.1
CP	82.8	92.5	96.1	96.3	85.0	91.5	95.9	92.3	96.3	96.1	95.4	83.1	83.0	90.5	85.2	95.9	93.9	85.8	84.4	91.5	84.1
CPf	82.7	91.9	95.3	94.3	86.3	91.4	93.7	89.8	93.7	93.0	93.6	83.4	83.7	90.7	86.2	92.3	93.4	87.1	85.3	91.9	84.8
CR	80.2	81.8	80.8	81.8	81.7	81.3	82.0	80.2	81.2	81.8	81.7	81.5	82.5	80.7	81.0	81.2	81.3	81.0	80.0	81.6	80.7
CS	83.4	91.6	95.4	94.7	85.5	90.5	94.2	91.7	98.3	95.9	99.2	82.9	82.3	90.3	85.8	95.9	94.8	85.9	84.4	91.5	84.5
CSo	83.7	86.1	85.5	85.7	97.7	85.7	84.4	82.9	85.6	85.1	85.6	83.5	84.3	84.1	95.2	84.9	85.1	98.9	94.7	85.0	94.3
CSh	91.7	84.2	84.4	84.6	84.7	83.3	84.5	83.3	83.8	84.8	83.9	93.1	92.5	83.5	84.8	84.0	84.4	84.9	85.6	83.6	83.8
CSi	79.2	82.4	81.4	81.6	81.0	81.7	81.8	80.0	81.5	81.8	81.9	80.9	81.6	80.9	81.1	81.5	81.6	81.2	80.1	81.4	80.0
CSp	81.3	93.7	91.7	92.4	84.8	99.7	92.3	90.2	90.3	90.2	90.8	82.5	83.1	93.1	84.4	90.0	90.9	85.6	84.7	91.6	84.0
CSs	82.3	82.8	81.9	82.5	81.6	82.9	82.5	81.6	82.2	82.2	82.2	81.7	81.9	81.5	81.8	81.9	82.2	81.7	81.1	82.7	82.4
CSu	82.8	99.3	91.9	92.1	85.7	93.1	91.9	90.5	90.7	91.8	91.2	82.9	83.6	92.5	85.5	91.3	92.3	86.6	84.7	92.2	84.9
CSy	90.2	82.8	82.9	83.3	83.4	82.8	83.1	82.2	83.4	83.0	83.4	93.7	91.2	82.3	83.7	82.9	83.3	84.3	84.2	82.4	82.8
CT	83.6	91.0	95.6	95.8	85.7	90.3	94.9	92.3	98.7	96.3	98.0	83.1	82.8	90.7	85.6	96.2	94.2	86.1	84.9	91.7	84.2
CTe	81.7	92.9	91.2	91.6	84.3	92.7	91.3	89.1	90.6	91.2	90.8	81.8	83.1	98.5	84.1	90.3	90.9	85.0	84.1	91.7	83.2

	CHi	CHy	CI	CIn	CL	CM	CMg	CN	CP	CPf	CR	CS	CSo	CSh	CSi	CSp	CSs	CSu	CSy	CT	CTe
CA	80.1	87.5	89.8	78.0	78.9	77.1	77.5	78.7	78.9	78.1	75.2	81.4	79.1	92.5	73.6	77.3	81.8	78.8	90.4	80.6	77.2
CAR	90.1	72.3	79.4	80.8	90.8	90.8	83.9	91.6	91.3	90.8	79.5	88.0	86.3	82.5	80.6	92.4	80.8	98.8	80.0	87.6	91.2
CB	93.2	74.6	80.6	80.3	92.8	90.2	84.4	92.4	96.6	94.2	77.7	93.2	85.1	84.3	79.2	91.6	83.7	90.6	82.5	92.7	91.2
CBe	93.6	75.4	81.3	80.6	95.2	89.8	85.2	92.6	95.2	92.9	79.7	93.4	85.9	85.7	79.4	92.1	82.5	90.5	82.8	93.5	91.1
CBi	84.4	77.2	84.1	80.7	83.7	84.4	92.0	84.9	85.2	85.0	80.3	86.1	97.2	85.4	79.4	86.5	80.9	86.5	86.4	85.6	83.3
CBo	90.7	72.0	78.6	80.0	93.4	90.4	84.1	91.2	89.9	89.7	79.0	87.1	86.5	82.5	78.7	99.0	79.0	91.1	81.0	87.7	92.9
CBu	93.4	75.6	81.5	80.8	95.4	89.8	84.8	93.6	95.4	93.5	80.3	93.2	85.3	86.1	80.0	92.1	83.5	90.5	83.6	93.1	90.9
CC	92.2	75.1	81.2	78.2	94.2	87.8	84.4	91.1	92.7	89.0	81.0	91.5	84.6	83.7	80.5	89.5	84.3	88.7	82.8	93.3	88.6
CCr	90.6	75.7	81.9	80.2	91.2	89.2	85.4	89.7	96.0	91.5	79.6	98.2	85.3	83.6	79.9	89.3	83.1	87.7	83.9	97.7	89.9
CCe	94.4	81.9	81.4	79.2	93.9	90.1	83.1	91.9	97.5	92.4	79.0	96.8	83.7	83.5	79.4	89.2	83.0	90.9	81.5	95.6	90.2
CCh	90.8	76.3	81.2	79.3	91.6	89.2	86.0	90.2	95.4	90.6	79.5	98.4	86.1	84.1	79.2	88.9	83.3	87.6	83.6	98.1	89.6
CCl	80.7	90.4	91.2	79.2	81.8	79.5	81.9	80.3	80.4	80.8	79.5	80.9	83.1	92.8	77.9	80.3	79.6	79.4	93.4	80.6	79.4
CCo	81.7	89.2	91.1	80.2	83.3	79.9	83.1	81.8	82.3	83.4	81.6	82.2	82.6	92.1	80.2	82.2	80.1	81.8	90.6	81.7	81.1
CCm	89.6	72.7	77.9	77.1	91.6	93.5	83.3	91.8	90.3	90.5	76.8	88.8	83.9	82.9	77.5	94.2	79.6	90.8	80.7	89.4	99.0
CD	85.5	74.8	82.0	80.8	85.2	85.3	94.5	85.3	85.2	84.7	76.7	85.4	94.6	82.7	77.8	84.4	80.8	84.8	85.2	84.9	82.9
CDi	91.1	74.9	80.7	78.3	90.7	90.3	84.1	89.1	95.9	89.3	77.6	95.5	85.2	83.2	79.0	87.8	82.3	88.9	81.5	94.2	87.8
CF	92.9	81.0	80.5	79.6	93.9	87.5	81.9	92.1	92.5	90.8	78.0	92.1	84.4	83.4	78.5	89.3	81.3	89.4	81.1	92.5	86.8
CG	83.6	74.4	82.4	81.4	84.4	85.4	92.4	84.7	85.2	86.4	78.6	85.6	98.1	84.0	78.7	87.3	80.1	86.6	85.8	85.7	84.1
CGly	85.1	78.7	83.4	78.9	84.6	84.0	91.3	84.9	85.3	84.4	76.4	84.9	94.3	85.5	76.9	86.8	79.7	84.7	86.3	85.3	84.2
CH	94.6	75.3	78.8	78.4	94.8	90.9	85.0	98.3	92.0	92.1	78.8	90.6	83.5	82.6	78.4	92.2	82.0	91.0	80.6	91.6	92.1
CHr	82.7	79.0	82.4	79.1	82.2	81.8	91.0	81.6	83.2	83.6	76.9	84.8	96.3	81.9	75.4	84.1	81.6	84.3	81.9	84.1	80.9
CHi	-	74.4	80.3	81.1	96.7	90.1	85.1	94.3	92.0	91.2	80.9	90.1	85.0	83.5	80.0	91.4	82.0	90.1	81.1	90.4	89.7
CHy	80.5	-	88.2	71.6	73.7	71.5	74.8	73.1	74.2	71.3	74.2	76.1	76.0	90.4	72.3	72.8	80.0	72.9	90.6	76.5	72.4
CI	83.0	90.3	-	80.4	80.2	79.0	82.7	78.9	80.9	80.6	82.0	81.6	83.3	90.4	80.9	79.4	80.0	79.7	91.6	80.8	78.0
CIn	80.8	79.0	81.8	-	80.5	77.6	75.7	79.3	79.4	80.4	82.6	80.1	80.5	81.6	83.6	80.6	76.5	80.4	79.3	78.5	77.8
CL	97.2	80.2	83.0	80.4	-	90.7	83.4	94.5	93.2	91.5	81.5	90.4	83.9	85.1	80.4	94.0	82.2	90.4	82.3	91.7	91.8
CM	90.1	78.9	81.1	78.5	90.7	-	83.2	89.6	90.2	90.0	78.4	88.2	85.3	82.6	77.7	91.2	81.0	90.4	80.2	89.0	93.9
CMg	85.5	81.5	84.2	79.5	84.2	84.1	-	87.0	83.9	84.9	75.7	86.0	93.2	84.7	78.0	84.4	78.9	84.1	84.8	85.7	83.2
CN	91.1	79.6	82.7	79.7	90.9	90.1	86.1	-	91.4	91.8	80.1	89.8	84.1	83.5	80.2	92.2	81.3	91.2	80.4	90.5	91.6
CP	90.8	80.7	82.6	79.7	91.4	90.9	84.9	91.0	-	93.5	79.9	94.4	85.1	83.0	80.5	90.7	82.7	91.1	82.2	95.4	90.5
CPf	90.9	79.2	82.4	80.0	91.5	90.9	86.2	91.3	94.1	-	78.6	90.2	84.8	84.6	78.3	90.5	82.2	90.4	81.4	90.5	90.8
CR	82.7	80.7	83.0	84.2	82.8	80.2	81.4	81.7	81.9	81.8	-	79.3	77.9	80.9	94.9	79.0	77.8	79.7	80.4	79.6	77.0
CS	90.0	81.0	82.7	80.2	90.3	90.8	85.7	91.0	95.3	93.5	81.5	-	86.1	83.9	79.2	88.1	81.6	88.0	83.4	97.3	88.6
CSo	85.4	81.4	84.9	80.3	84.8	84.8	93.8	85.1	85.3	86.4	80.8	85.9	-	84.4	78.0	86.7	80.5	86.5	85.5	85.6	83.1
CSh	84.0	91.7	91.0	82.1	84.4	83.5	84.5	84.2	84.2	84.8	82.9	84.0	85.0	-	80.2	83.5	80.0	82.3	93.2	83.5	82.4
CSi	82.5	79.9	82.5	85.0	82.5	80.2	80.8	81.8	82.0	82.1	96.1	81.6	80.8	83.4	-	78.7	76.3	80.6	80.3	79.3	76.9
CSp	92.7	80.1	82.2	80.4	93.3	92.2	84.0	91.2	91.7	91.9	81.5	90.9	85.5	83.7	82.0	-	79.8	92.0	81.7	88.8	93.8
CSs	82.5	82.2	82.4	79.7	82.3	81.5	80.9	82.6	82.4	82.0	80.8	81.9	81.5	83.6	80.7	83.1	-	80.0	78.7	82.8	79.8
CSu	91.5	80.2	82.7	80.3	91.7	92.5	84.9	92.3	92.5	91.9	81.7	91.4	86.4	84.1	82.2	93.7	82.7	-	80.5	87.1	90.4
CSy	82.5	90.9	90.6	80.5	83.1	82.1	83.5	82.2	83.4	83.6	81.5	83.3	84.2	93.0	81.3	82.8	81.1	82.6	-	83.3	80.8
CT	89.8	81.0	82.9	79.3	90.6	91.0	85.7	91.1	96.3	93.8	81.8	97.8	85.8	83.9	81.7	90.6	81.9	90.7	83.5	-	89.4
CTe	90.7	79.2	81.6	79.2	91.4	93.9	84.1	91.3	91.1	91.2	81.1	90.6	84.1	83.6	80.8	93.2	81.9	92.7	82.1	90.9	-

The percentage similarities between the full 16S rRNA gene sequences of the species are indicated in the lower left triangle, the percentage differences between the 5' end 527-bp 16S rRNA gene sequences of the species are indicated in the upper right triangle. Percentage similarities of >97% were highlighted in gray.

Abbreviations: CA, *Clostridium aminovalericum*; CAR, *Clostridium argentinense*; CB, *Clostridium baratii*; CBe, *Clostridium beijerinckii*; CBi, *Clostridium bifermentans*; CBo, *Clostridium botulinum*; CBu, *Clostridium butyricum*; CC, *Clostridium cadaveris*; CCr, *Clostridium carnis*; CCe, *Clostridium celatum*; CCh, *Clostridium chauvoei*; CCl, *Clostridium clostridioforme*; CCo, *Clostridium coccooides*; CCm, *Clostridium cochlearium*; CD, *Clostridium difficile*; CDi, *Clostridium disporicum*; CF, *Clostridium fallax*; CG, *Clostridium ghonii*; CGly, *Clostridium glycolicum*; CH, *Clostridium haemolyticum*; CHr, *Clostridium hiranonis*; CHi, *Clostridium histolyticum*; CHy, *Clostridium hylemonae*; CI, *Clostridium indolis*; CIn, *Clostridium innocuum*; CL, *Clostridium limosum*; CM, *Clostridium malenominatum*; CMg, *Clostridium mangenotii*; CN, *Clostridium novyi*; CP, *Clostridium paraputrificum*; CPf, *Clostridium perfringens*; CR, *Clostridium ramosum*; CS, *Clostridium septicum*; CSo, *Clostridium sordellii*; CSh, *Clostridium sphenoides*; CSi, *Clostridium spiroforme*; CSp, *Clostridium sporogenes*; CSs, *Clostridium sporosphaeroides*; CSu, *Clostridium subterminale*; CSy, *Clostridium symbiosum*; CT, *Clostridium tertium*; CTe, *Clostridium tetani*.

**Supplementary Table 1b** Comparison of 16S rRNA gene sequences of medically important *Propionibacterium*, *Pseudoramibacter*, *Bifidobacterium*, *Mobiluncus*, *Collinsella*, *Mogibacterium*, *Atopobium*, *Olsenella* and *Lactobacillus* species

	PA	PAv	PG	PP	PAI	BAd	BB	BBr	BC	BD	BI	BL	BG	MCC	MCH	MM	CA
PA	-	94.0	92.0	89.4	74.7	79.3	81.3	80.7	78.4	79.0	80.7	80.2	80.5	83.0	83.3	82.9	77.0
PAv	96.3	-	93.4	88.6	76.8	81.2	83.3	82.5	80.9	80.5	82.3	80.7	81.5	82.2	82.6	82.6	78.0
PG	94.5	95.1	-	90.8	74.9	79.6	81.4	81.5	79.9	79.3	80.6	80.0	79.9	81.5	81.8	82.1	78.2
PP	93.1	93.4	93.0	-	76.6	79.7	82.7	81.3	80.9	80.7	81.1	82.3	82.2	82.1	82.4	82.4	78.2
PAI	76.7	78.2	77.3	78.0	-	72.6	75.6	74.8	72.0	74.6	76.0	74.8	73.2	71.0	71.6	72.1	73.9
BAd	83.9	84.9	84.5	84.4	76.5	-	91.8	91.8	92.5	96.1	92.3	92.3	90.0	77.1	77.4	79.1	77.8
BB	83.7	84.8	84.3	84.6	77.0	94.1	-	93.4	91.9	91.8	93.3	92.8	91.6	82.0	82.2	82.7	76.0
BBr	83.6	84.9	84.6	84.4	77.3	94.5	95.4	-	92.1	91.8	94.4	94.6	92.5	79.4	79.6	80.6	79.6
BC	83.3	84.4	84.1	84.3	76.7	95.7	95.3	95.0	-	93.0	91.7	91.7	91.4	78.9	79.1	79.3	78.6
BD	83.6	84.7	84.3	84.7	77.1	96.7	95.4	94.9	97.0	-	93.4	92.8	91.2	77.5	77.8	78.7	79.4
BI	83.8	84.8	84.2	84.3	77.7	94.7	95.6	97.6	95.0	95.5	-	98.8	89.8	78.3	78.6	80.2	79.8
BL	83.4	84.3	83.9	84.7	77.1	94.5	95.1	97.1	95.4	95.7	99.1	-	89.4	77.9	78.2	79.6	79.9
BG	83.1	83.7	83.6	83.9	76.4	92.9	93.3	94.6	93.6	93.4	93.9	93.8	-	81.0	81.0	80.4	76.7
MCC	85.4	85.6	85.4	85.5	75.9	82.9	84.5	83.7	83.0	83.1	83.3	83.1	84.2	-	100.0	97.1	72.4
MCH	85.7	85.5	85.4	85.4	76.1	82.9	84.3	83.5	83.0	82.9	83.1	82.9	84.2	99.9	-	97.2	72.3
MM	85.8	86.0	86.0	85.9	76.9	84.1	85.1	83.8	83.8	83.8	83.6	83.2	84.3	97.7	97.8	-	72.8
CA	78.1	78.7	78.0	78.7	75.9	79.3	78.8	79.4	79.3	79.9	79.5	79.7	79.3	76.5	76.4	76.9	-
CI	78.4	79.0	79.1	79.1	76.6	80.7	80.5	80.0	80.5	80.7	80.1	80.2	79.3	76.8	76.7	77.5	93.3
CS	78.3	78.9	78.6	78.9	77.0	80.7	80.2	80.2	80.7	80.7	80.2	80.2	79.1	77.1	77.2	78.3	93.2
MP	77.4	77.8	77.6	78.0	81.0	76.4	76.7	76.8	76.5	77.1	76.7	76.5	75.7	76.5	76.6	76.8	75.7
MT	76.0	77.7	76.8	77.6	81.0	76.7	76.8	77.4	76.9	76.6	77.1	76.9	76.1	75.6	75.6	75.9	75.6
MV	77.2	78.2	77.8	78.3	80.7	76.7	76.9	77.2	76.7	77.0	77.2	76.8	76.0	76.5	76.7	77.2	75.8
AF	79.9	81.4	80.2	81.1	78.4	78.8	79.6	78.5	78.9	79.1	78.6	78.5	78.8	77.3	77.6	78.0	85.5
AM	81.2	82.0	81.2	82.0	79.3	79.6	80.3	79.4	79.7	79.9	79.4	79.2	79.6	78.2	78.4	79.0	86.2
AP	81.9	83.5	82.5	83.2	79.6	81.1	80.5	80.5	80.6	80.3	80.5	80.7	80.9	79.2	79.3	79.5	86.3
AR	81.3	82.9	82.4	83.0	79.0	79.8	80.0	79.6	79.7	79.1	79.6	79.8	80.0	78.9	79.1	79.1	85.4
AV	80.9	82.3	81.1	82.2	79.6	80.4	80.9	80.3	80.1	79.9	80.0	80.4	81.4	78.9	79.0	79.0	87.0
OU	80.2	81.6	80.7	81.6	79.1	80.2	80.9	80.7	79.9	80.3	79.9	79.8	80.7	78.3	78.0	78.3	89.3
LA	78.6	79.0	78.2	78.6	80.7	77.5	77.8	77.7	77.8	78.1	78.3	79.2	77.9	77.0	77.1	77.7	76.3
LC	79.4	79.7	79.2	79.6	81.4	79.1	79.1	79.2	79.0	78.8	79.0	79.1	77.9	78.5	78.7	78.8	75.6
LCa	76.0	74.7	74.9	74.9	79.1	76.2	75.4	75.0	76.2	75.2	75.2	75.2	75.8	75.5	76.1	75.5	76.3
LR	79.1	79.5	78.8	79.2	81.6	78.6	79.2	78.5	78.9	78.5	78.6	78.5	77.6	78.3	78.6	78.7	72.3
LV	77.0	76.9	76.8	76.2	79.6	76.6	76.9	77.1	75.4	76.9	77.5	76.9	76.1	76.0	76.1	75.8	76.7

	CI	CS	MP	MT	MV	AF	AM	AP	AR	AV	OU	LA	LC	LCa	LR	LV
PA	77.5	78.2	75.3	72.9	74.7	77.0	80.0	80.2	80.1	81.9	80.8	75.9	77.8	75.1	77.7	76.2
PAv	78.7	78.8	75.3	75.7	76.2	80.1	81.5	83.4	83.1	84.9	82.8	75.3	77.8	73.5	78.3	75.5
PG	79.3	79.4	74.5	73.5	74.9	79.1	81.3	82.9	82.3	83.1	81.9	76.2	78.0	73.6	77.3	74.4
PP	79.3	79.0	76.6	75.2	76.8	79.5	82.0	82.8	83.7	84.7	82.8	74.5	78.1	74.7	77.9	73.8
PAI	76.0	75.8	79.3	77.7	78.0	73.5	75.9	76.8	75.4	77.5	77.2	75.7	76.5	76.5	76.9	76.1
BAd	78.8	79.2	75.4	75.5	75.9	75.5	78.4	79.1	77.7	80.4	79.4	71.8	75.7	72.4	75.1	73.3
BB	78.5	77.4	76.3	75.9	76.2	76.0	77.8	78.7	78.5	81.0	79.8	75.6	76.6	73.3	77.8	74.8
BBr	79.1	79.3	75.7	76.9	76.5	75.8	77.9	79.6	78.4	80.3	80.7	74.7	75.7	73.3	75.0	74.6
BC	78.7	79.0	74.8	74.7	75.6	74.8	76.9	78.5	77.8	79.4	79.0	72.5	74.9	73.0	75.1	69.9
BD	78.9	78.9	75.3	75.4	75.9	75.6	77.1	78.0	76.1	79.1	79.0	73.3	74.8	72.7	74.9	74.4
BI	79.7	80.0	75.5	76.3	76.3	76.2	78.2	79.4	78.0	80.2	79.2	76.4	75.3	73.5	75.4	74.6
BL	79.6	79.9	75.1	76.5	75.1	75.8	77.9	79.8	78.8	80.2	78.5	76.6	75.8	73.9	75.4	74.3
BG	77.0	75.3	74.5	76.0	75.0	75.2	77.6	79.4	78.1	81.5	81.0	73.5	73.7	71.6	73.7	73.4
MCC	72.5	71.6	73.1	71.7	72.6	72.8	75.9	76.4	77.1	76.3	75.0	73.0	76.2	71.9	75.8	72.8
MCH	72.8	71.9	73.4	72.1	72.9	73.1	76.2	76.7	77.3	76.6	75.3	73.6	76.5	71.9	76.2	73.2
MM	73.7	74.1	74.1	72.1	74.2	73.2	77.0	76.3	76.6	75.8	73.8	75.9	70.8	75.6	72.8	72.8
CA	94.4	93.7	73.9	74.0	73.3	80.6	83.0	83.1	82.3	84.0	86.5	74.4	68.3	72.2	60.2	76.9
CI	-	97.5	75.1	74.5	75.0	81.6	84.1	84.5	83.5	85.0	88.1	71.1	73.5	73.5	67.3	73.1
CS	97.4	-	76.1	75.1	76.0	81.4	84.0	85.0	83.3	84.4	88.5	75.2	73.6	72.9	65.2	70.9
MP	76.8	76.4	-	95.1	98.8	74.8	76.5	77.8	76.0	78.6	77.0	76.7	79.8	72.4	79.9	78.6
MT	75.4	75.5	97.0	-	96.0	73.5	75.2	77.9	76.0	77.4	76.4	76.2	78.5	73.1	78.4	78.6
MV	76.5	76.0	98.5	96.9	-	73.7	75.8	77.9	76.5	78.7	77.1	76.6	78.6	73.9	79.4	78.1
AF	85.8	85.3	77.8	76.8	77.3	-	94.0	89.7	88.1	89.2	84.6	74.4	73.2	71.3	73.1	73.6
AM	86.1	85.9	78.3	77.5	77.9	97.1	-	92.5	90.5	92.6	87.6	76.4	76.5	74.4	76.7	75.3
AP	86.2	86.1	78.6	78.5	78.5	93.3	94.1	-	93.4	92.7	90.9	76.5	75.5	74.2	76.1	74.7
AR	85.4	85.4	78.4	78.1	78.4	91.9	92.5	96.4	-	92.7	88.8	74.7	77.5	74.9	77.7	73.4
AV	86.9	87.0	78.4	77.9	78.4	92.1	93.5	93.3	92.7	-	91.3	77.6	76.6	73.3	77.0	75.4
OU	89.5	89.5	77.8	76.9	77.8	90.6	91.7	92.5	91.3	93.5	-	75.8	76.4	75.5	75.6	77.1
LA	77.2	76.7	78.9	78.7	78.8	78.2	79.3	78.9	78.1	79.1	78.5	-	80.4	74.3	83.3	74.0
LC	76.5	76.8	81.0	80.4	80.3	78.8	80.3	79.3	79.6	79.1	78.8	87.5	-	75.1	97.0	77.4
LCa	76.2	76.2	75.6	76.0	75.9	75.9	77.9	77.8	77.1	77.8	77.9	79.4	78.7	-	76.8	85.2
LR	74.1	73.7	80.8	80.3	80.5	78.5	80.2	79.3	79.5	79.0	78.2	88.4	98.6	78.7	-	70.7
LV	78.0	77.4	78.3	78.6	78.1	77.2	77.8	77.2	76.5	77.5	78.6	80.1	80.9	89.4	78.4	-

The percentage similarities between the full 16S rRNA gene sequences of the species are indicated in the lower left triangle, the percentage differences between the 5' end 527-bp 16S rRNA gene sequences of the species are indicated in the upper right triangle. Percentage similarities of >97% were highlighted in gray.

Abbreviations: PA, *Propionibacterium acnes*; PAv, *Propionibacterium avidum*; PG, *Propionibacterium granulosum*; PP, *Propionibacterium propionicum*; PAI, *Pseudoramibacter alactolyticus*; BAd, *Bifidobacterium adolescentis*; BB, *Bifidobacterium bifidum*; BBr, *Bifidobacterium breve*; BC, *Bifidobacterium catenulatum*; BD, *Bifidobacterium dentium*; BI, *Bifidobacterium infantis*; BL, *Bifidobacterium longum*; BG, *Bifidobacterium globosum*; MCC, *Mobiluncus curtisii* subsp. *curtisii*; MCH, *Mobiluncus curtisii* subsp. *holmesii*; MM, *Mobiluncus mulieris*; CA, *Collinsella aerofaciens*; CI, *Collinsella intestinalis*; CS, *Collinsella stercoris*; MP, *Mogibacterium pumilum*; MT, *Mogibacterium timidum*; MV, *Mogibacterium vesicum*; AF, *Atopobium fossor*; AM, *Atopobium minutum*; AP, *Atopobium parvulum*; AR, *Atopobium rimae*; AV, *Atopobium vaginae*; OU, *Olsenella uli*; LA, *Lactobacillus acidophilus*; LC, *Lactobacillus casei*; LCa, *Lactobacillus cateniformis*; LR, *Lactobacillus rhamnosus*; LV, *Lactobacillus vitulinus*.

**Supplementary Table 1c** Comparison of 16S rRNA gene sequences of medically important *Eubacterium*, *Eggerthella*, *Bulleidia*, *Catenibacterium*, *Cryptobacterium*, *Holdemania* and *Slackia* species

	EB	EBu	ES	EC	ECt	EI	EM	EMo	EMu	EN	ENo	ESa	ESu	ET	EYM	EYS	EYY	BE	CM	CC	EL	HF	SE	SH
EB	-	81.9	78.8	82.1	81.9	86.9	83.4	82.7	81.4	81.9	81.5	84.0	84.9	86.0	79.5	79.6	79.0	76.3	72.7	72.8	73.5	75.4	71.7	73.7
EBu	82.1	-	80.2	90.5	84.2	83.4	80.7	97.2	97.0	99.6	79.3	83.1	83.2	84.8	77.3	71.3	78.3	76.7	79.2	72.7	75.6	74.3	73.3	74.9
ES	81.1	81.6	-	79.6	89.7	78.8	80.9	80.0	79.7	80.2	80.1	78.0	76.0	81.2	78.5	76.1	78.6	74.0	79.6	75.9	75.5	74.9	75.4	76.9
EC	82.8	90.8	81.4	-	82.2	84.0	80.7	90.9	90.3	90.7	79.7	82.9	82.8	86.2	75.0	71.4	75.3	76.8	79.7	72.2	74.6	76.0	73.3	74.3
ECt	82.7	84.1	89.7	83.9	-	81.4	81.5	83.2	83.1	84.3	79.3	80.4	80.5	84.1	77.7	77.2	78.3	73.9	79.6	76.2	76.8	75.1	74.2	76.4
EI	89.6	83.6	81.2	83.0	82.2	-	86.4	83.5	81.6	82.9	86.2	87.0	98.0	86.2	77.3	78.6	78.8	76.3	79.2	74.7	74.5	74.6	73.8	74.6
EM	85.9	80.9	81.4	81.0	81.8	88.8	-	82.5	81.9	80.8	91.1	85.8	85.9	84.4	78.5	72.9	77.9	75.3	79.0	73.2	74.1	74.6	72.9	74.4
EMo	82.5	98.0	81.0	91.0	83.7	82.6	80.5	-	98.8	97.0	81.7	84.3	82.9	86.5	77.6	72.1	79.6	75.3	78.5	72.6	76.3	75.6	73.0	74.0
EMu	81.7	97.8	81.4	90.5	83.5	83.1	81.6	99.2	-	96.6	80.9	83.1	81.6	85.8	78.4	73.0	79.4	77.3	77.7	71.4	75.5	75.2	72.8	73.4
EN	81.5	99.0	81.8	90.7	84.3	82.2	80.1	97.6	97.7	-	78.9	82.7	82.3	85.0	77.4	71.5	78.0	76.4	78.6	72.3	74.9	74.2	72.6	74.5
ENo	85.5	80.3	81.0	81.7	82.0	88.3	94.6	81.1	81.1	80.3	-	83.5	86.4	84.8	77.0	78.8	76.7	73.4	78.9	72.0	73.1	73.7	72.4	72.6
ESa	89.1	84.5	81.5	84.3	82.5	89.8	88.6	84.9	84.1	84.4	86.6	-	86.5	79.7	78.5	78.6	78.0	74.9	77.0	74.4	74.5	73.3	73.4	74.9
ESu	89.0	83.5	80.0	82.7	82.3	98.8	88.3	82.3	82.5	82.6	88.6	89.5	-	80.2	77.0	78.5	78.4	75.5	71.3	72.7	73.1	74.9	72.4	73.7
ET	86.9	85.2	82.7	85.0	84.8	87.7	85.1	85.6	85.7	85.2	84.6	85.2	85.3	-	82.8	77.1	83.8	77.1	80.8	76.8	76.5	77.7	75.2	75.8
EYM	82.3	80.7	80.9	79.6	81.3	80.5	81.0	80.5	80.8	80.4	80.4	82.1	80.3	82.4	-	94.0	99.2	75.6	76.3	72.2	72.4	75.2	72.5	73.4
EYS	82.3	80.5	80.2	79.8	81.2	81.1	80.8	78.4	80.8	80.2	81.1	82.2	80.9	80.3	97.9	-	88.1	69.6	70.3	65.8	65.3	75.2	72.4	66.9
EYY	81.6	80.9	80.7	79.9	81.3	81.1	80.6	81.2	81.0	80.4	80.1	81.6	80.8	82.7	99.4	97.4	-	75.9	77.2	72.6	73.4	74.3	72.6	73.3
BE	79.0	79.1	79.4	79.8	79.4	80.2	78.4	78.4	79.5	79.1	77.5	79.8	79.9	79.6	77.5	77.3	77.4	-	80.3	71.9	74.0	85.2	73.4	75.2
CM	76.4	79.6	79.1	79.4	80.0	79.3	79.6	78.0	78.5	79.0	79.7	78.2	76.6	79.3	76.3	74.1	76.4	81.2	-	75.6	78.8	81.3	76.4	77.0
CC	75.6	75.4	77.0	76.6	76.9	77.8	76.9	75.1	75.1	75.6	76.9	77.6	77.3	77.7	75.6	75.3	75.3	75.6	78.5	-	86.6	72.0	88.2	88.1
EL	76.8	78.5	76.8	77.9	77.5	78.4	78.0	78.4	78.4	78.3	77.3	78.4	77.5	78.7	74.5	71.7	74.8	76.8	78.0	89.4	-	73.6	87.7	90.1
HF	79.8	79.5	79.4	81.3	80.6	79.0	78.5	80.3	80.2	79.7	79.4	80.0	78.7	80.7	77.5	77.5	77.3	88.4	82.5	76.0	76.7	-	70.7	72.7
SE	74.5	76.0	75.8	75.5	75.7	78.4	77.0	75.2	76.0	76.0	77.1	77.4	77.4	77.7	74.4	74.5	74.3	75.6	78.6	89.9	90.0	75.6	-	92.5
SH	76.2	76.5	76.9	76.3	75.8	77.6	77.8	75.9	75.7	76.1	76.9	77.8	77.8	77.9	74.6	74.2	74.2	76.5	78.4	90.4	91.2	76.2	94.9	-

The percentage similarities between the full 16S rRNA gene sequences of the species are indicated in the lower left triangle, the percentage differences between the 5' end 527-bp 16S rRNA gene sequences of the species are indicated in the upper right triangle. Percentage similarities of >97% were highlighted in gray.

Abbreviations: EB, *Eubacterium brachy*; EBu, *Eubacterium budayi*; ES, *Eubacterium saburreum*; EC, *Eubacterium combesii*; ECt, *Eubacterium contortum*; EI, *Eubacterium infirmum*; EM, *Eubacterium minutum*; EMo, *Eubacterium moniliforme*; EMu, *Eubacterium multiforme*; EN, *Eubacterium nitritogenes*; ENo, *Eubacterium nodatum*; ESa, *Eubacterium saphenum*; ESu, *Eubacterium sulci*; ET, *Eubacterium tenue*; EYM, *Eubacterium yurii* subsp. *margaretiae*; EYS, *Eubacterium yurii* subsp. *schiitka*; EYY, *Eubacterium yurii* subsp. *yurii*; BE, *Bulleidia extracta*; CM, *Catenibacterium mitsuokai*; CC, *Cryptobacterium curtum*; EL, *Eggerthella lenta*; HF, *Holdemania filiformis*; SE, *Slackia exigua*; SH, *Slackia heliotrinireducens*.

**Supplementary Table 1d** Comparison of 16S rRNA gene sequences of medically important *Actinomyces*, *Actinobaculum* and *Arcanobacterium* species

	AB	AH	AP	APi	APy	AS	ASu	ABv	ABw	AC	ACt	AD	AE	AF	AG	AGe	AGr	AHo	AHw	AHy	AI	AM	AN	ANe	AO	AR	ARg	ASl	AT	AU	AV	
AB	-	93.0	93.6	94.1	96.6	89.5	88.7	87.1	86.4	85.7	85.3	85.6	83.9	84.7	85.3	79.9	86.9	86.6	84.2	84.0	80.7	86.9	84.7	86.3	87.6	86.8	84.6	84.2	86.6	86.8	85.3	
AH	94.6	-	97.5	94.8	91.8	89.7	88.2	86.7	86.1	86.0	85.3	86.4	82.6	84.6	85.6	80.6	85.7	84.2	85.6	85.8	82.9	87.6	86.1	85.0	87.8	88.2	83.1	85.9	87.0	86.9	86.6	
AP	95.3	97.9	-	95.3	92.7	91.3	89.4	88.0	88.1	87.8	85.7	88.0	84.6	86.7	87.5	82.8	87.0	86.4	86.2	87.3	83.7	89.5	87.0	85.8	89.5	89.6	83.4	86.9	87.9	88.4	88.0	
APi	95.2	95.6	96.7	-	93.1	90.2	89.6	88.1	86.4	85.9	86.4	86.0	82.3	85.7	86.5	81.1	87.0	84.4	83.7	85.1	83.0	88.3	84.9	86.7	87.8	86.9	83.6	84.6	87.4	87.6	85.7	
APy	97.9	94.2	95.1	95.1	-	89.2	88.4	86.6	87.4	85.3	87.1	86.6	83.9	84.4	86.5	80.3	85.8	86.3	84.3	85.1	83.0	86.4	86.7	87.3	86.2	86.9	83.2	86.3	85.8	85.7	85.9	
AS	91.4	91.5	91.9	92.0	91.6	-	89.3	87.3	87.7	85.2	85.5	87.1	83.4	85.4	87.2	80.5	86.1	85.0	86.2	84.8	83.4	87.8	86.2	84.7	87.5	87.2	83.3	85.8	86.6	88.2	86.6	
ASu	91.4	90.1	91.0	91.3	91.3	93.7	-	83.8	85.9	83.9	83.7	83.6	82.9	83.8	84.1	84.2	84.3	83.4	82.3	82.8	83.0	84.6	82.7	84.8	84.2	83.4	81.8	83.6	85.6	84.0	83.5	
ABv	89.6	90.2	90.1	90.4	89.6	89.0	87.4	-	94.0	85.3	93.9	92.1	86.9	86.9	89.8	87.2	91.2	88.4	91.3	85.5	89.5	89.2	93.0	84.4	88.4	93.7	86.3	92.0	87.6	97.0	93.3	
ABw	89.7	88.9	90.2	89.7	90.1	89.7	89.3	95.8	-	85.9	93.1	95.0	87.9	86.1	89.3	86.6	88.9	87.0	91.1	87.2	88.0	90.7	95.3	84.3	88.6	92.6	86.2	92.9	90.2	95.0	97.2	
AC	89.9	90.5	91.2	90.6	89.8	89.6	88.7	90.5	90.9	-	84.3	85.5	85.7	90.8	91.5	82.0	86.4	88.7	84.6	90.8	85.0	90.7	83.9	85.3	90.3	88.3	87.5	85.6	84.8	91.4	85.8	84.6
ACt	89.1	88.9	89.5	89.8	89.6	89.5	87.9	95.3	95.3	90.5	-	91.8	87.2	84.9	87.4	87.1	90.6	87.4	92.1	84.3	89.5	86.5	91.2	83.0	86.4	91.8	83.8	90.2	85.4	93.3	92.3	
AD	88.6	88.6	89.4	88.6	89.0	89.2	87.9	94.3	95.9	90.6	94.0	-	86.5	86.4	87.6	88.7	88.4	88.0	91.4	86.5	89.7	87.5	93.5	84.6	87.5	92.8	86.1	92.8	87.4	93.0	94.9	
AE	88.0	88.1	88.8	88.1	87.8	88.3	88.0	89.9	90.3	90.9	89.8	89.8	-	85.6	84.4	83.5	86.2	86.6	86.4	85.9	83.9	85.3	88.7	86.4	85.8	87.5	85.4	87.1	86.3	89.2	88.4	
AF	88.6	88.9	90.1	89.7	88.9	88.8	88.1	90.6	91.0	94.6	89.8	90.5	90.1	-	92.1	85.2	85.3	86.7	86.0	96.1	84.5	94.3	85.7	84.1	94.0	89.0	88.6	86.3	95.2	87.0	86.4	
AG	88.4	89.0	89.7	89.3	88.9	89.2	87.7	91.9	91.7	94.5	91.7	91.8	88.9	94.6	-	85.0	87.6	87.1	88.9	91.8	85.6	96.9	88.0	84.7	95.9	88.5	90.0	88.3	96.2	88.4	89.0	
AGe	86.5	86.9	87.5	86.9	86.5	86.8	87.5	92.7	92.5	89.0	92.8	93.2	88.4	90.1	90.8	-	84.3	81.5	89.4	82.8	91.2	84.2	88.2	81.4	83.7	84.8	83.3	92.1	88.3	85.2	89.1	
AGr	90.4	89.6	90.4	90.7	90.2	88.7	88.1	92.5	92.0	90.5	92.6	91.3	89.8	89.4	90.4	89.7	-	87.3	89.4	85.1	88.2	86.4	87.6	85.2	88.0	91.4	85.7	87.8	88.2	92.4	89.1	
AHo	90.2	90.3	91.0	90.2	89.9	89.9	87.9	90.8	89.8	92.6	90.7	89.9	90.7	91.1	91.1	87.9	90.1	-	85.5	86.8	83.9	88.8	86.3	84.6	88.4	88.8	88.5	86.9	89.7	88.5	87.5	
AHw	88.4	89.6	89.4	88.4	88.3	89.3	87.3	95.1	94.6	90.1	95.3	94.4	89.8	90.7	92.1	94.1	92.1	90.0	-	84.2	91.8	87.6	92.0	82.5	85.3	89.6	84.3	93.4	88.0	90.9	92.7	
AHy	88.4	89.3	89.9	89.5	89.2	89.2	88.2	90.5	91.7	94.3	90.3	90.8	91.0	97.1	94.7	89.9	89.6	91.4	90.4	-	85.7	93.1	84.8	85.1	92.7	87.7	89.2	85.7	94.3	86.0	85.8	
AI	85.8	86.7	87.4	86.7	87.0	87.5	87.7	92.4	92.2	89.4	92.7	93.5	88.2	89.2	90.8	95.2	90.1	87.3	93.9	90.4	-	84.3	90.1	83.2	84.2	87.5	85.6	89.3	85.0	87.6	89.5	
AM	89.1	89.9	90.6	90.3	89.1	89.6	87.8	92.0	91.8	94.1	90.9	90.8	90.2	96.0	97.5	90.5	90.2	92.4	91.9	95.5	88.8	-	88.0	85.2	97.9	89.7	90.4	88.0	99.0	89.4	88.8	
AN	88.8	89.5	89.7	89.4	89.5	89.2	87.8	94.9	96.6	89.7	95.0	95.2	91.0	90.0	91.4	93.2	92.2	90.3	95.7	90.5	93.0	91.9	-	82.8	86.8	91.7	84.2	92.2	87.1	92.7	97.1	
ANe	88.7	89.1	89.5	89.9	89.0	88.8	87.9	88.5	88.5	90.0	88.1	88.1	89.9	88.2	88.5	86.8	88.4	89.2	87.8	89.7	86.8	88.9	88.1	-	84.7	84.8	86.0	83.5	86.3	83.7	82.5	
AO	89.8	90.2	91.4	91.0	89.6	89.8	88.2	91.3	90.9	94.8	91.4	90.2	90.8	95.5	96.3	89.9	90.9	91.5	90.6	95.1	88.5	97.7	91.1	89.3	-	90.3	89.4	85.1	98.8	89.3	88.4	
AR	89.2	89.7	90.3	89.5	89.1	89.4	87.5	95.4	94.9	91.2	95.5	94.0	90.2	91.4	91.2	91.4	93.3	91.3	94.4	91.1	91.7	92.2	95.0	88.3	92.6	-	85.0	91.2	89.0	94.8	93.3	
ARg	88.8	88.4	88.8	88.8	88.5	88.6	87.8	90.3	90.2	92.1	89.2	90.0	90.5	93.2	93.6	89.0	89.4	91.9	89.4	94.3	89.1	93.6	89.7	89.9	92.9	90.2	-	85.2	90.7	85.5	84.5	
ASl	89.1	89.0	89.9	89.1	89.8	89.2	87.9	94.6	95.8	90.8	95.4	94.6	90.0	90.2	91.4	94.2	91.6	90.2	95.5	90.7	92.2	90.9	95.4	88.2	90.6	95.0	89.9	-	87.8	91.4	92.6	
AT	89.4	89.9	90.7	90.6	89.4	89.5	88.7	91.2	91.5	95.1	91.2	90.2	90.9	95.6	96.2	91.7	90.9	92.1	91.7	95.4	89.5	97.6	91.3	89.9	99.0	92.1	93.2	91.5	-	87.8	88.0	
AU	89.7	89.8	90.4	90.2	89.4	90.0	88.1	97.2	96.5	90.8	96.0	95.0	90.8	91.2	91.3	92.0	93.5	91.1	95.3	91.0	92.2	91.9	95.7	88.7	91.8	96.9	90.2	95.6	91.4	-	94.2	
AV	88.9	89.5	89.9	89.4	89.1	89.2	87.8	95.5	97.2	90.0	95.4	95.9	90.7	90.5	91.7	93.7	92.6	90.5	96.2	90.7	92.8	92.1	98.8	87.9	91.7	95.7	89.7	95.6	91.6	96.4	-	

The percentage similarities between the full 16S rRNA gene sequences of the species are indicated in the lower left triangle, the percentage differences between the 5' end 527-bp 16S rRNA gene sequences of the species are indicated in the upper right triangle. Percentage similarities of >97% were highlighted in gray.

Abbreviations: AB, *Arcanobacterium bernardiae*; AH, *Arcanobacterium haemolyticum*; AP, *Arcanobacterium phocae*; APi, *Arcanobacterium plurianimalium*; APy, *Arcanobacterium pyogenes*; AS, *Actinobaculum schaalii*; ASu, *Actinobaculum suis*; ABv, *Actinomyces bovis*; ABw, *Actinomyces bowdenii*; AC, *Actinomyces canis*; ACt, *Actinomyces catuli*; AD, *Actinomyces denticolens*; AE, *Actinomyces europaeus*; AF, *Actinomyces funkei*; AG, *Actinomyces georgiae*; AGe, *Actinomyces gerencseriae*; AGr, *Actinomyces graevenitzi*; AHo, *Actinomyces hordeovulneris*; AHw, *Actinomyces howellii*; AHy, *Actinomyces hyo vaginalis*; AI, *Actinomyces israelii*; AM, *Actinomyces meyeri*; AN, *Actinomyces naeslundii*; ANe, *Actinomyces neiui*; AO, *Actinomyces odontolyticus*; AR, *Actinomyces radidentis*; ARg, *Actinomyces radingae*; ASl, *Actinomyces slackii*; AT, *Actinomyces turicensis*; AU, *Actinomyces urogenitalis*; AV, *Actinomyces viscosus*.

**Supplementary Table 1e** Comparison of 16S rRNA gene sequences of medically important *Bacteroides* species

	BC	BCa	BD	BE	BF	BM	BO	BP	BS	BSt	BT	BTh	BU	BUr	BV
BC	-	71.9	82.4	89.6	89.4	84.5	90.8	86.8	83.9	90.4	87.0	91.0	90.8	69.7	85.7
BCa	75.4	-	75.5	73.1	71.1	74.7	72.0	73.4	75.1	73.5	73.0	71.2	72.3	74.3	69.3
BD	83.6	73.6	-	82.0	81.8	94.0	83.1	81.4	82.2	84.8	81.4	83.0	83.2	67.1	78.8
BE	92.9	76.3	83.3	-	90.2	84.1	89.9	86.9	81.1	92.8	87.5	90.9	92.5	69.6	88.2
BF	94.1	74.5	83.0	93.2	-	82.0	87.2	87.3	81.1	90.0	87.5	90.8	91.2	70.4	88.4
BM	87.9	75.5	90.4	87.7	86.9	-	84.0	82.9	83.8	86.4	82.5	84.8	85.3	67.4	78.9
BO	95.1	75.1	83.5	93.3	93.1	88.0	-	84.2	80.9	90.8	84.7	92.7	90.3	69.1	85.3
BP	90.2	75.3	82.3	90.3	90.3	86.5	89.7	-	82.5	88.4	99.2	86.6	91.6	68.6	85.6
BS	84.9	74.3	81.1	83.6	82.8	85.0	83.7	83.3	-	82.1	82.6	82.2	82.1	72.9	78.3
BSt	92.2	76.3	82.7	94.4	91.6	87.1	92.5	90.1	83.7	-	88.2	92.2	94.2	70.1	87.7
BT	90.2	75.0	81.4	90.4	90.1	86.1	89.8	98.8	82.9	90.2	-	87.1	91.8	69.2	86.8
BTh	95.3	74.7	83.5	93.7	94.8	88.3	96.3	90.7	84.0	92.8	90.7	-	92.2	70.9	86.6
BU	93.4	76.4	84.0	94.5	93.4	87.9	93.0	91.4	83.7	94.6	91.6	93.9	-	70.4	88.8
BUr	73.2	76.1	68.1	72.9	72.5	72.7	72.7	71.1	72.1	73.4	71.7	72.6	72.6	-	69.0
BV	90.8	74.0	81.7	90.7	91.0	85.1	89.7	88.1	81.9	89.4	88.2	90.7	91.7	72.3	-

The percentage similarities between the full 16S rRNA gene sequences of the species are indicated in the lower left triangle, the percentage differences between the 5' end 527-bp 16S rRNA gene sequences of the species are indicated in the upper right triangle. Percentage similarities of >97% were highlighted in gray.

Abbreviations: BC, *Bacteroides caccae*; BCa, *Bacteroides capillosus*; BD, *Bacteroides distasonis*; BE, *Bacteroides eggerthii*; BF, *Bacteroides fragilis*; BM, *Bacteroides merdae*; BO, *Bacteroides ovatus*; BP, *Bacteroides pyogenes*; BS, *Bacteroides splanchnicus*; BSt, *Bacteroides stercoris*; BT, *Bacteroides tectus*; BTh, *Bacteroides thetaiotaomicron*; BU, *Bacteroides uniformis*; UBr, *Bacteroides ureolyticus*; BV, *Bacteroides vulgatus*.

**Supplementary Table 1f** Comparison of 16S rRNA gene sequences of medically important *Leptotrichia*, *Prevotella*, *Porphyromonas*, *Selenomonas* and *Sneathia* species

	LB	PA	PC	PCo	PCs	PCt	PCi	PE	PG	PGu	PL	PM	PB	PBu	PBl	PCp	PD	PDe	PDi
LB	-	68.5	71.2	71.5	68.9	74.9	66.3	71.0	74.0	73.3	71.0	71.8	70.9	71.8	67.7	71.8	69.6	70.4	71.6
PA	71.8	-	82.1	82.2	83.5	81.2	84.6	83.9	82.7	83.2	82.8	82.2	81.4	79.5	78.0	81.1	77.7	77.6	79.9
PC	73.2	86.0	-	87.9	86.9	85.4	85.9	86.9	85.7	86.0	89.8	87.0	77.5	75.7	76.4	77.6	76.7	76.5	77.1
PCo	72.2	85.6	91.8	-	85.5	85.5	84.5	83.7	85.9	86.2	84.6	86.6	78.0	76.0	76.5	76.0	77.6	77.4	75.8
PCs	73.1	85.5	89.5	89.5	-	83.9	83.9	85.1	86.7	86.4	84.8	86.0	78.2	76.6	76.6	76.0	75.8	76.3	77.2
PCt	74.8	84.3	88.6	88.3	87.8	-	85.0	86.2	89.0	90.4	84.1	86.3	77.8	77.1	77.1	77.5	79.1	76.4	77.8
PCi	72.8	87.7	87.3	86.0	86.1	86.0	-	92.8	86.9	85.3	83.3	87.9	80.0	78.7	76.4	77.5	78.0	75.3	78.2
PE	73.7	87.7	88.7	86.3	87.3	86.9	94.2	-	86.5	87.4	84.1	87.7	79.3	78.7	77.8	80.0	78.5	77.4	79.1
PG	74.0	85.6	89.3	88.3	89.4	89.3	87.3	87.8	-	96.2	83.8	89.4	80.2	79.2	80.9	79.2	79.1	77.6	81.1
PGu	74.2	85.9	89.8	88.6	89.5	90.1	86.9	88.3	98.0	-	84.2	88.8	79.6	78.2	79.3	79.1	79.6	77.0	80.5
PL	73.2	85.1	91.3	89.2	87.3	87.0	86.2	86.6	87.0	87.0	-	83.9	78.6	75.7	76.5	78.9	75.8	76.6	78.0
PM	73.4	85.4	88.8	88.6	88.0	89.1	87.9	87.7	88.6	88.6	87.2	-	80.5	80.8	79.0	79.9	79.4	77.9	79.0
PB	72.2	80.6	80.5	79.4	79.6	80.5	80.2	80.0	81.0	80.9	79.8	79.5	-	86.7	88.6	89.0	86.2	87.3	88.2
PBu	72.7	79.3	79.1	78.0	78.2	79.8	79.8	79.3	79.9	79.7	78.3	80.3	87.9	-	87.5	88.7	88.4	89.6	83.1
PBl	71.8	78.3	79.2	78.3	78.2	80.1	78.4	78.2	80.4	79.9	79.1	79.3	90.1	88.7	-	90.0	85.7	87.2	86.2
PCp	72.5	79.7	79.7	78.2	79.3	80.8	79.3	80.0	80.8	80.8	80.3	79.9	90.8	88.7	90.6	-	86.2	89.7	89.7
PD	70.7	78.9	79.8	79.2	78.2	81.2	78.6	78.5	79.2	79.9	78.7	79.0	89.5	89.5	88.2	89.3	-	83.8	82.6
PDe	71.3	78.0	79.5	78.5	78.4	79.8	78.2	78.4	79.1	79.4	78.6	78.4	89.1	90.7	88.5	90.7	89.3	-	86.2
PDi	72.7	79.5	79.5	77.7	79.4	80.0	79.9	80.1	81.0	80.9	80.2	79.6	91.8	86.7	89.4	92.1	87.1	89.1	-
PEn	70.8	78.5	78.8	77.9	78.1	79.3	78.7	78.6	79.9	79.6	78.6	78.9	88.4	87.5	88.9	88.7	87.7	87.6	87.7
PH	71.6	80.6	83.1	81.8	81.1	83.5	82.7	81.8	83.4	83.2	83.4	82.6	84.7	84.1	84.4	84.5	83.5	84.6	83.3
PI	72.5	78.3	79.2	78.2	79.6	80.7	79.5	79.9	80.6	80.9	79.2	78.4	90.9	87.1	88.2	92.6	88.1	89.7	93.7
PLo	71.6	79.3	80.7	79.7	78.7	81.4	80.5	79.8	80.8	81.2	79.9	80.5	89.7	90.3	90.2	89.8	90.5	89.7	88.0
PMe	72.1	79.1	81.5	79.7	79.8	80.9	79.3	79.6	79.9	80.8	80.9	79.2	91.8	88.2	89.0	92.4	89.1	93.5	91.8
PN	71.6	77.6	78.2	77.4	78.5	79.9	78.0	78.6	80.0	80.1	78.8	77.9	89.4	87.6	88.8	92.7	88.1	90.7	91.1
PO	70.4	77.6	79.9	79.3	79.1	80.4	78.1	77.8	78.9	79.8	79.0	78.8	88.4	88.3	89.9	87.8	89.0	88.0	86.3
POr	72.3	79.0	79.7	78.1	78.8	81.0	78.8	78.7	80.1	79.8	80.0	79.1	91.1	89.6	91.3	90.7	89.6	91.0	89.1
POu	72.9	79.6	80.7	79.3	79.8	81.3	80.1	80.1	80.4	80.5	80.0	80.5	91.3	88.1	89.6	91.3	89.2	90.2	91.8
PP	72.0	79.0	79.0	78.4	79.3	79.7	80.1	79.9	80.6	80.5	79.4	79.5	91.1	86.0	88.2	93.0	87.4	89.1	93.7
PT	70.5	76.9	79.1	77.9	79.0	79.9	77.1	77.7	79.6	79.7	78.7	78.5	83.6	84.1	83.1	83.1	83.1	84.2	82.1
PV	71.8	79.6	80.7	78.8	79.3	80.3	79.5	79.9	79.7	80.2	79.5	79.2	91.8	88.7	89.4	92.3	89.3	92.3	91.6
PZ	71.7	81.0	82.6	81.4	80.8	82.6	82.8	81.3	83.0	83.1	82.2	82.5	84.7	83.9	83.6	83.9	83.9	84.6	82.4
SD	79.3	70.7	72.5	70.9	72.9	72.8	70.8	72.5	73.0	73.4	71.7	72.4	71.7	71.3	72.1	71.8	71.2	72.1	71.7
SF	77.9	71.1	72.0	70.7	72.0	72.1	69.7	72.1	72.6	73.3	71.4	71.4	72.2	72.0	71.8	71.2	71.0	72.0	72.0
SI	78.6	70.4	72.2	71.1	72.8	72.5	70.2	71.7	72.1	73.0	71.3	71.9	72.2	71.4	71.2	70.9	71.4	71.8	71.6
SN	77.0	71.2	72.0	71.3	72.4	72.6	70.5	72.3	72.7	72.8	71.3	71.8	72.1	70.8	71.1	71.2	71.0	71.0	71.5
SS	76.4	71.0	71.7	70.4	71.6	72.4	70.9	72.6	72.9	72.3	71.3	72.6	71.9	72.3	72.3	72.4	72.2	72.2	71.4
SSa	85.9	70.0	71.8	71.1	71.5	71.0	70.1	70.2	70.4	71.4	74.2	72.4	71.0	67.6	69.1	69.3	67.7	68.5	70.3

	PEn	PH	PI	PLo	PMe	PN	PO	POr	POu	PP	PT	PV	PZ	SD	SF	SI	SN	SS	SSa
LB	70.0	67.6	71.8	66.7	69.8	71.5	68.3	67.3	70.8	71.9	70.8	70.6	67.4	77.9	75.7	75.9	73.5	73.6	85.2
PA	79.0	77.1	77.8	79.5	79.6	77.4	75.9	79.1	80.2	79.4	74.2	81.3	78.8	69.4	69.8	68.9	70.0	70.5	65.3
PC	76.8	80.0	76.8	78.6	79.1	74.5	76.6	76.4	77.4	77.9	75.1	78.1	79.6	69.7	69.1	68.4	68.8	68.3	68.3
PCo	76.5	79.1	76.3	78.5	78.2	75.0	75.9	75.6	76.3	76.6	73.8	77.2	80.1	70.0	69.6	68.9	70.1	67.5	67.5
PCs	76.2	77.5	77.0	77.3	77.7	75.0	77.1	77.0	77.6	77.7	76.8	78.1	78.5	72.3	70.6	71.3	71.3	69.6	69.0
PCt	78.9	79.9	78.7	80.3	77.4	77.5	78.3	79.3	78.1	78.3	75.5	76.6	79.9	73.4	70.6	71.7	72.3	72.5	68.7
PCi	78.5	81.3	78.8	80.0	77.5	76.8	76.7	76.9	78.9	79.5	73.7	78.1	81.3	71.1	68.6	69.2	69.8	68.8	65.6
PE	79.6	79.6	80.0	79.6	79.2	77.6	77.0	77.4	80.4	80.3	74.1	80.0	79.3	71.0	70.9	70.0	71.1	70.6	67.5
PG	80.0	80.1	79.4	80.7	78.4	78.1	77.2	80.0	80.1	81.1	76.6	78.2	80.5	75.0	73.5	72.3	72.8	73.8	68.4
PGu	78.8	79.0	78.4	81.2	79.0	76.4	78.6	78.5	78.6	80.1	76.4	78.6	79.9	74.5	73.8	72.2	72.2	72.1	69.4
PL	77.1	80.4	77.0	78.1	80.4	77.4	77.8	78.4	77.9	77.8	73.9	76.0	80.6	70.7	69.8	69.9	69.4	68.6	73.9
PM	79.8	80.9	78.0	81.4	79.1	77.2	78.1	79.1	80.8	79.9	77.9	79.3	81.9	73.3	71.0	72.4	71.6	72.4	70.9
PB	88.7	83.4	88.0	88.3	90.3	88.2	86.1	89.0	88.3	87.6	82.5	89.9	84.0	72.5	72.7	73.7	73.3	71.9	69.2
PBu	87.3	81.6	85.1	91.5	86.8	86.0	88.0	88.1	85.9	83.9	82.1	87.8	82.2	72.3	71.1	71.1	70.7	72.9	64.9
PBl	88.6	82.5	85.6	89.9	87.6	87.5	87.6	92.5	88.9	86.3	81.6	88.8	82.3	73.1	71.8	70.9	70.1	72.4	67.6
PCp	87.6	80.4	89.1	90.0	90.5	91.0	87.1	90.1	89.5	90.8	80.3	90.3	82.4	72.5	70.3	70.3	70.2	71.7	65.6
PD	85.5	79.8	83.9	90.0	84.6	85.3	87.1	84.8	84.2	84.3	78.1	85.2	80.8	71.5	71.2	71.2	70.4	71.1	64.2
PDe	87.3	81.3	86.8	87.9	93.9	89.1	86.5	89.0	87.1	88.6	80.4	90.7	82.5	72.3	71.5	70.9	69.1	71.5	65.1
PDi	86.7	79.2	91.0	85.3	90.6	89.7	82.7	85.6	88.4	91.7	78.5	90.0	80.0	72.2	72.1	72.7	72.2	71.4	68.5
PEn	-	79.8	87.5	89.5	88.9	87.1	90.3	89.0	87.5	88.2	80.4	87.7	80.6	71.2	70.9	69.1	68.6	69.1	67.2
PH	82.8	-	80.9	83.4	83.1	81.9	82.0	82.1	82.4	80.9	81.8	81.5	97.4	71.9	69.7	70.5	69.5	71.3	66.7
PI	87.8	84.1	-	86.6	89.3	91.5	84.8	86.6	86.5	90.6	78.8	87.5	80.9	73.3	70.4	71.5	70.8	70.9	68.2
PLo	89.1	84.9	89.2	-	87.4	88.7	91.3	88.6	86.5	87.3	81.3	87.2	84.2	71.0	69.9	69.9	69.3	71.2	68.9
PMe	89.0	84.8	91.6	89.5	-	89.3	86.9	88.8	89.3	89.4	80.8	92.7	84.2	72.1	70.2	70.9	70.9	71.8	67.2
PN	87.2	84.1	93.7	89.2	90.3	-	85.0	88.5	86.3	92.6	80.8	87.7	83.3	71.7	71.1	70.1	70.0	70.3	66.4
PO	89.7	83.9	86.7	90.3	88.5	87.0	-	85.7	84.6	84.5	78.5	84.5	82.8	69.2	67.7	69.1	68.5	70.0	66.5
POr	89.1	84.3	89.8	90.5	91.3	89.7	88.1	-	90.6	87.1	81.1	89.0	82.9	73.5	70.3	72.1	69.9	72.1	67.1
POu	88.2	84.4	90.5	89.1	92.5	88.8	87.9	92.4	-	88.2	82.6	89.9	84.2	74.3	71.4	72.7	72.8	73.4	68.6
PP	87.9	84.0	94.1	88.4	91.8	93.2	87.2	89.4	91.3	-	79.9	89.4	82.4	72.0	68.4	69.4	69.4	70.1	68.7
PT	82.4	84.2	81.8	82.7	83.0	83.2	83.1	83.2	83.5	81.9	-	81.9	83.0	68.7	69.3	68.8	68.2	69.0	68.3
PV	88.3	84.0	90.9	89.3	96.8	89.8	87.2	91.3	92.6	91.8	83.5	-	81.5	73.2	71.7	72.7	71.9	73.3	68.8
PZ	83.2	96.7	83.2	85.0	84.4	84.6	84.3	84.1	84.2	83.0	84.3	83.4	-	72.7	69.9	71.7	69.8	71.8	67.7
SD	71.9	73.2	72.4	71.8	72.0	71.5	70.9	71.9	72.5	72.2	72.3	72.2	72.7	-	95.0	97.0	94.5	88.6	76.1
SF	72.4	72.9	71.5	71.9	71.7	71.2	70.6	71.5	71.4	71.0	72.1	72.0	72.4	97.0	-	95.4	95.7	86.3	72.7
SI	71.0	72.6	71.8	71.2	72.0	71.0	71.6	71.3	72.0	70.2	71.3	71.9	72.7	98.4	97.3	-	96.1	87.3	73.8
SN	71.0	72.5	71.6	71.0	71.7	70.7	70.9	70.5	71.5	71.4	71.5	71.8	71.8	96.1	96.7	96.8	-	87.0	72.7
SS	72.4	73.1	71.9	71.8	71.9	71.5	71.2	72.2	71.9	71.0	72.2	72.5	73.1	91.8	90.3	89.8	90.7	-	71.0
SSa	69.4	70.1	69.8	70.4	70.4	68.9	69.2	69.1	69.9	70.6	69.6	70.7	70.9	77.0	75.5	75.7	75.3	74.4	-

The percentage similarities between the full 16S rRNA gene sequences of the species are indicated in the lower left triangle, the percentage differences between the 5' end 527-bp 16S rRNA gene sequences of the species are indicated in the upper right triangle. Percentage similarities of >97% were highlighted in gray.

Abbreviations: LB, *Leptotrichia buccalis*; PA, *Porphyromonas asaccharolytica*; PC, *Porphyromonas cangingivalis*; PCo, *Porphyromonas canoris*; PCs, *Porphyromonas cansulci*; PCt, *Porphyromonas catoniae*; PCi, *Porphyromonas circumdentaria*; PE, *Porphyromonas endodontalis*; PG, *Porphyromonas gingivalis*; PGu, *Porphyromonas gulae*; PL, *Porphyromonas levii*; PM, *Porphyromonas macacae*; PB, *Prevotella bivia*; PBU, *Prevotella buccae*; PBl, *Prevotella buccalis*; PCp, *Prevotella corporis*; PD, *Prevotella dentalis*; PDe, *Prevotella denticola*; PDi, *Prevotella disiens*; PEn, *Prevotella enoeca*; PH, *Prevotella heparinolytica*; PI, *Prevotella intermedia*; PLo, *Prevotella loescheii*; PMe, *Prevotella melaninogenica*; PN, *Prevotella nigrescens*; PO, *Prevotella oralis*; POr, *Prevotella oris*; POu, *Prevotella oulorum*; PP, *Prevotella pallens*; PT, *Prevotella tanneriae*; PV, *Prevotella veroralis*; PZ, *Prevotella zoogloformans*; SD, *Selenomonas diana*; SF, *Selenomonas flueggei*; SI, *Selenomonas infelix*; SN, *Selenomonas noxia*; SS, *Selenomonas sputigena*; SSa, *Sneathia sanguinegens*.

**Supplementary Table 1g** Comparison of 16S rRNA gene sequences of medically important *Alistipes*, *Anaerobiospirillum*, *Bilophila*, *Butyrivibrio*, *Desulfovibrio*, *Dialister*, *Faecalibacterium*, *Filifactor*, *Fusobacterium*, *Johnsonella*, *Megamonas*, *Succinivibrio*, *Sutterella*, *Tannerella* and *Tissierella* species

	AP	AS	AT	BW	BF	DP	DPn	FP	FA	FG	FM	FN	FNe	FNuA	FNuN	FNuP	FPe	FR	FU	FV	JI	MH	SD	SW	TF	TP		
AP	-	72.8	72.2	71.1	71.8	71.5	68.6	74.9	69.8	70.8	69.8	70.5	73.5	70.5	70.8	71.8	70.4	68.6	69.8	70.1	68.1	74.1	72.6	72.9	82.0	74.0		
AS	73.8	-	92.2	79.1	80.8	80.5	78.4	81.6	75.8	77.1	75.4	73.2	71.7	72.1	72.3	72.5	76.0	73.4	75.8	75.9	73.9	69.5	92.5	82.6	70.6	74.2		
AT	73.4	93.4	-	77.3	79.2	78.1	74.4	82.0	74.9	75.8	75.0	73.7	74.7	72.8	72.2	74.0	74.1	74.9	74.4	75.6	73.9	75.3	92.5	79.4	70.7	74.2		
BW	74.5	79.6	78.9	-	79.1	88.1	77.6	78.5	76.7	76.0	75.8	73.2	74.3	72.5	73.8	74.2	74.1	72.1	76.7	76.4	75.6	75.8	77.0	71.9	70.8	78.2		
BF	76.2	78.8	78.3	78.9	-	75.2	77.0	77.4	79.2	79.7	78.5	73.9	73.0	72.5	72.3	72.8	77.9	73.7	78.4	79.0	80.8	75.1	79.9	76.1	68.5	77.4		
DP	73.3	79.9	79.5	90.8	78.0	-	80.1	79.8	78.6	75.7	75.7	74.1	77.3	73.7	74.4	76.2	75.1	77.1	76.7	76.3	77.6	77.0	78.6	75.8	70.5	78.0		
DPn	72.8	77.4	76.6	79.1	78.9	79.0	-	82.0	75.2	78.7	77.9	76.3	76.7	75.8	76.2	72.1	71.0	73.4	78.4	78.5	73.5	81.1	78.2	75.8	67.8	76.7		
FP	75.7	80.2	79.4	79.2	79.6	78.9	82.1	-	76.9	78.0	78.0	76.6	76.7	75.1	75.7	77.4	78.7	77.8	78.2	78.6	77.2	82.8	82.0	78.6	70.1	78.0		
FA	75.0	76.6	77.1	76.9	82.3	77.8	78.6	79.7	-	70.5	69.8	71.8	66.5	71.5	72.2	67.7	72.8	67.0	70.2	70.3	78.3	78.6	76.7	72.7	69.9	78.5		
FG	74.0	79.2	78.2	77.6	81.5	76.8	78.8	79.5	75.8	-	93.9	91.4	97.7	91.9	92.8	92.6	93.4	93.9	94.2	93.9	94.2	93.9	74.7	77.0	75.7	74.3	70.3	74.6
FM	74.2	77.9	77.2	76.9	81.5	77.1	78.8	78.7	75.9	95.3	-	92.8	92.8	92.6	93.3	94.0	94.1	95.1	99.3	100.0	74.7	75.7	76.0	73.0	69.5	75.3		
FN	74.0	77.4	77.0	75.9	78.6	76.2	77.2	78.2	76.3	93.1	94.2	-	89.6	97.2	98.0	97.5	97.7	94.2	93.3	93.1	73.6	74.1	74.2	71.4	68.8	74.6		
FNe	74.1	76.6	76.9	76.6	78.3	76.7	77.0	78.3	73.0	98.0	94.5	92.5	-	89.9	90.9	91.8	92.2	92.8	93.0	92.8	75.3	75.8	75.3	74.7	71.7	76.2		
FNuA	73.5	74.2	73.8	75.0	77.9	75.0	77.4	77.0	75.4	94.3	94.6	98.1	92.5	-	97.3	96.3	96.9	93.7	93.0	92.8	74.0	73.6	72.9	71.0	69.0	75.8		
FNuN	74.0	77.3	76.7	76.2	78.0	76.2	77.3	77.9	76.4	93.7	94.4	99.0	93.0	98.1	-	97.8	98.8	94.2	93.7	93.5	74.8	73.5	73.9	71.5	69.5	76.2		
FNuP	74.2	77.1	77.2	76.0	78.3	76.7	75.7	78.2	74.0	93.8	94.7	98.6	93.5	97.5	98.8	-	99.1	95.3	94.2	94.2	69.4	75.3	76.1	69.2	70.8	77.0		
FPe	74.0	79.0	77.9	76.7	80.6	77.1	78.0	79.0	76.9	94.7	95.3	98.6	94.4	98.0	98.9	99.3	-	94.6	94.4	94.1	75.6	67.5	76.5	73.6	70.1	76.3		
FR	74.3	77.2	75.8	75.1	79.0	76.4	76.1	78.2	73.9	95.6	94.9	95.4	94.2	95.4	95.3	95.6	95.3	-	95.1	95.1	69.9	76.0	76.4	69.3	70.5	75.7		
FU	74.2	78.0	77.1	77.3	81.5	77.4	78.8	78.8	76.0	95.4	99.7	94.2	94.7	94.7	94.5	94.7	95.3	95.0	-	99.3	74.6	76.2	75.9	73.7	70.2	75.7		
FV	74.1	78.2	77.5	77.2	81.9	77.4	79.1	78.9	76.2	95.4	99.9	94.3	94.7	94.7	94.5	94.9	95.3	95.1	99.6	-	75.3	76.3	76.8	73.6	70.1	75.9		
JI	73.9	76.0	76.7	79.0	84.7	78.9	78.4	81.0	80.6	78.4	78.4	77.2	78.0	77.2	77.8	75.7	77.9	76.4	78.5	78.7	-	76.2	74.2	72.9	70.5	76.9		
MH	74.3	78.3	77.6	78.1	77.7	78.6	84.8	82.3	78.8	78.3	77.5	77.0	77.3	75.6	76.8	76.7	76.9	77.7	77.6	77.8	79.8	-	71.1	76.2	71.5	80.7		
SD	73.9	92.7	92.6	78.3	78.4	78.9	77.0	79.7	77.3	78.1	77.9	77.0	77.0	74.9	77.0	77.7	77.9	77.9	77.8	78.2	75.9	77.5	-	81.2	71.9	76.3		
SW	74.2	81.8	80.9	76.6	77.9	77.8	76.3	78.0	76.4	76.1	76.0	74.9	76.1	72.6	75.0	74.2	76.4	74.5	76.2	76.3	76.6	75.9	81.1	-	73.5	73.4		
TF	84.4	72.7	72.5	73.8	73.0	72.1	71.4	73.9	73.2	72.2	72.5	72.7	73.0	71.7	72.9	72.3	72.1	72.1	72.8	72.8	73.4	72.1	73.1	72.5	-	74.9		
TP	76.7	76.7	76.1	78.4	81.4	78.4	79.7	79.2	82.8	77.8	78.1	77.9	77.6	78.7	78.4	78.4	78.5	78.0	78.3	78.4	80.8	80.5	75.6	77.4	75.8	-		

The percentage similarities between the full 16S rRNA gene sequences of the species are indicated in the lower left triangle, the percentage differences between the 5' end 527-bp 16S rRNA gene sequences of the species are indicated in the upper right triangle. Percentage similarities of >97% were highlighted in gray.

Abbreviations: AP, *Alistipes putredinis*; AS, *Anaerobiospirillum succiniciproducens*; AT, *Anaerobiospirillum thomasi*; BW, *Bilophila wadsworthia*; BF, *Butyrivibrio fibrisolvens*; DP, *Desulfovibrio piger*; DPn, *Dialister pneumosintes*; FP, *Faecalibacterium prausnitzii*; FA, *Filifactor alocis*; FG, *Fusobacterium gonidiaformans*; FM, *Fusobacterium mortiferum*; FN, *Fusobacterium naviforme*; FNe, *Fusobacterium necrophorum*; FNuA, *Fusobacterium nucleatum* subsp. *animalis*; FNuN, *Fusobacterium nucleatum* subsp. *nucleatum*; FNuP, *Fusobacterium nucleatum* subsp. *polymorphum*; FPe, *Fusobacterium periodonticum*; FR, *Fusobacterium russii*; FU, *Fusobacterium ulcerans*; FV, *Fusobacterium varium*; JI, *Johnsonella ignava*; MH, *Megamonas hypermegale*; SD, *Succinivibrio dextrinosolvens*; SW, *Sutterella wadsworthensis*; TF, *Tannerella forsythensis*; TP, *Tissierella praeacuta*.

**Supplementary Table 1h** Comparison of 16S rRNA gene sequences of medically important anaerobic cocci

	AF	AH	AL	AO	AP	AT	AV	CP	FM	GB	ME	PN	PAs	PHa	PIn	PIv	PL	PA	PM	RP	VA	VD	VP
AF	-	74.3	73.1	73.2	70.6	69.0	73.7	84.4	72.4	70.0	83.2	78.0	75.6	77.8	74.5	77.6	73.0	77.3	71.4	81.5	83.7	84.2	83.8
AH	78.8	-	89.8	91.0	90.8	89.1	95.9	73.9	81.7	80.0	75.7	69.7	81.7	82.3	82.3	79.5	81.0	79.5	82.3	78.8	69.6	73.2	72.8
AL	80.0	92.4	-	93.0	93.7	92.7	92.0	70.0	79.4	79.9	70.1	76.8	83.8	81.5	83.2	81.1	83.2	76.6	81.9	77.6	71.2	72.7	72.2
AO	79.5	91.7	93.9	-	94.2	93.1	93.0	70.7	78.8	77.7	76.4	70.2	81.6	81.3	82.1	80.7	83.2	79.6	82.2	78.5	69.3	72.0	72.0
AP	78.7	92.7	95.2	94.7	-	94.3	91.8	67.4	78.8	78.5	69.8	73.0	83.2	81.7	82.9	81.2	82.5	78.1	82.4	78.5	71.9	70.5	69.9
AT	78.2	92.6	95.1	94.2	96.3	-	91.5	69.9	80.5	78.5	73.2	73.2	82.1	81.3	82.1	82.1	82.1	79.4	82.4	78.1	72.0	72.7	72.7
AV	79.0	95.7	92.5	92.6	92.5	92.5	-	69.9	81.3	79.6	77.7	70.2	82.3	82.8	82.7	81.3	82.7	79.3	84.9	78.6	72.0	72.6	72.1
CP	86.4	78.2	78.0	78.2	77.9	77.9	76.7	-	79.0	63.4	80.9	76.1	73.6	75.5	74.5	74.4	72.0	79.0	78.6	79.0	80.7	80.7	80.4
FM	80.7	83.3	83.4	83.0	82.6	83.6	83.7	80.5	-	81.8	80.2	76.6	85.1	83.6	84.3	83.7	82.4	80.3	86.2	77.3	69.9	77.1	77.8
GB	79.8	81.8	83.2	82.5	83.1	83.1	81.7	77.0	87.1	-	63.3	63.8	76.9	76.7	76.9	81.9	76.5	75.9	80.9	72.1	64.7	66.2	67.1
ME	85.9	79.0	78.0	77.9	78.1	79.0	77.9	85.9	81.2	76.2	-	76.2	74.4	77.7	74.4	76.5	74.1	78.7	78.8	78.0	87.0	88.9	88.5
PN	82.6	79.6	81.1	80.1	81.2	80.5	80.0	80.9	81.0	79.3	82.5	-	77.2	74.6	76.1	76.8	75.1	76.3	74.7	79.0	77.2	76.1	76.0
PAs	78.7	84.1	85.8	84.8	85.4	85.3	84.5	77.9	86.4	83.4	77.3	83.0	-	87.3	97.0	88.1	87.8	80.4	83.4	77.1	75.1	72.5	72.2
PHa	78.9	84.7	85.3	84.2	85.2	85.2	84.6	78.7	85.0	81.6	78.7	79.4	88.6	-	86.7	85.2	92.9	80.9	82.3	81.2	73.6	76.4	76.3
PIn	78.0	83.7	85.3	84.3	84.9	84.6	84.0	78.8	85.9	83.1	77.9	82.3	98.1	87.8	-	87.3	86.7	81.0	83.8	77.1	75.8	71.3	72.7
PIv	79.8	82.5	84.4	85.1	84.7	85.0	83.5	78.5	86.1	85.5	79.4	82.2	89.0	86.4	88.5	-	86.7	80.3	85.0	79.8	76.3	76.1	76.3
PL	77.3	83.1	85.3	85.3	84.8	85.3	84.3	76.6	83.9	82.0	77.7	79.9	89.1	92.1	88.4	87.7	-	77.5	81.7	78.4	74.3	73.9	73.8
PA	79.8	81.6	79.6	82.3	80.7	81.6	81.1	80.2	82.2	79.7	79.4	81.9	82.8	81.8	82.6	83.0	80.4	-	79.9	81.1	77.5	77.8	77.7
PM	80.4	83.8	83.9	84.6	84.0	84.3	84.8	79.7	87.8	85.7	80.1	81.2	86.4	84.0	85.9	87.4	84.0	83.0	-	80.1	70.5	78.7	78.6
RP	81.5	80.7	79.9	80.5	80.7	80.7	80.2	79.9	80.6	78.4	80.4	82.6	81.3	81.6	80.9	82.3	80.6	83.6	82.3	-	78.1	80.1	79.7
VA	86.7	78.0	79.0	78.2	79.3	79.7	77.9	84.9	79.9	77.8	89.1	81.3	78.3	78.6	78.5	79.6	78.8	78.6	79.9	80.2	-	97.0	96.4
VD	86.7	78.9	79.4	79.0	78.8	80.0	78.1	85.1	80.2	78.1	89.7	80.9	77.4	79.5	77.0	79.7	78.4	79.3	80.0	80.2	98.3	-	99.8
VP	86.2	78.9	79.2	78.9	78.6	79.9	78.0	84.8	80.6	78.3	89.4	80.7	77.5	79.9	77.6	79.8	78.4	78.8	80.1	80.5	98.5	99.3	-

The percentage similarities between the full 16S rRNA gene sequences of the species are indicated in the lower left triangle, the percentage differences between the 5' end 527-bp 16S rRNA gene sequences of the species are indicated in the upper right triangle. Percentage similarities of >97% were highlighted in gray.

Abbreviations: AF, *Acidaminococcus fermentans*; AH, *Anaerococcus hydrogenalis*; AL, *Anaerococcus lactolyticus*; AO, *Anaerococcus octavius*; AP, *Anaerococcus prevotii*; AT, *Anaerococcus tetradius*; AV, *Anaerococcus vaginalis*; CP, *Centipeda periodontii*; FM, *Fingoldia magna*; GB, *Gallicola barnesae*; ME, *Megasphaera elsdenii*; PN, *Peptococcus niger*; PAs, *Peptoniphilus asaccharolyticus*; PHa, *Peptoniphilus harei*; PIn, *Peptoniphilus indolicus*; PIv, *Peptoniphilus ivorii*; PL, *Peptoniphilus lacrimalis*; PA, *Peptostreptococcus anaerobius*; PM, *Peptostreptococcus micros*; RP, *Ruminococcus productus*; VA, *Veillonella atypical*; VD, *Veillonella dispar*; VP, *Veillonella parvula*.

**Supplementary Table 2** Usefulness of full 16S rRNA gene sequence, 5' end 527-bp 16S rRNA gene sequence and the existing MicroSeq 16S rDNA bacterial identification system databases for identification of medically important anaerobic Gram-positive rods

Bacteria	Full 16S rRNA gene sequence			5' end 527-bp 16S rRNA gene sequence		
	Usefulness for species identification	Medically important bacteria with similar (<3% difference) full 16S rRNA gene sequence	Usefulness of existing Microseq full 16S rDNA bacterial identification system database	Usefulness for species identification	Medically important bacteria with similar (<3% difference) 5' end 527-bp 16S rRNA gene sequence	Usefulness of existing Microseq 500 16S rDNA bacterial identification system database
<i>Actinobaculum schaalii</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Actinobaculum suis</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Actinomyces bovis</i>	?	<i>A. urogenitalis</i>	? <sup>c</sup>	?	<i>A. urogenitalis</i>	? <sup>f</sup>
<i>Actinomyces bowdenii</i>	?	<i>A. viscosus</i>	× <sup>a</sup>	?	<i>A. viscosus</i>	× <sup>d</sup>
<i>Actinomyces canis</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Actinomyces catuli</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Actinomyces denticolens</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Actinomyces europaeus</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Actinomyces funkei</i>	?	<i>A. hyovaginalis</i>	× <sup>a</sup>	√		× <sup>d</sup>
<i>Actinomyces georgiae</i>	?	<i>A. meyeri</i>	× <sup>a</sup>	√		× <sup>d</sup>
<i>Actinomyces gerencseriae</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Actinomyces graevenitzii</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Actinomyces hordeovulneris</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Actinomyces howellii</i>	√		√	√		√
<i>Actinomyces hyovaginalis</i>	?	<i>A. funkei</i>	× <sup>a</sup>	√		× <sup>d</sup>
<i>Actinomyces israelii</i>	√		× <sup>a</sup>	√		√
<i>Actinomyces meyeri</i>	?	<i>A. georgiae, A. odontolyticus, A. turicensis</i>	? <sup>c</sup>	×	<i>A. odontolyticus, A. turicensis</i>	× <sup>c</sup>
<i>Actinomyces naeslundii</i>	×	<i>A. viscosus</i>	× <sup>a</sup>	?	<i>A. viscosus</i>	? <sup>f</sup>
<i>Actinomyces neuui</i>	√		√	√		√
<i>Actinomyces odontolyticus</i>	×	<i>A. meyeri, A. turicensis</i>	× <sup>a</sup>	×	<i>A. meyeri, A. turicensis</i>	× <sup>d</sup>
<i>Actinomyces radidentis</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Actinomyces radingae</i>	√		√	√		√
<i>Actinomyces slackii</i>	√		√	√		√
<i>Actinomyces turicensis</i>	×	<i>A. meyeri, A. odontolyticus</i>	× <sup>a</sup>	×	<i>A. meyeri, A. odontolyticus</i>	× <sup>d</sup>
<i>Actinomyces urogenitalis</i>	?	<i>A. bovis</i>	× <sup>a</sup>	?	<i>A. bovis</i>	× <sup>d</sup>
<i>Actinomyces viscosus</i>	×	<i>A. bowdenii, A. naeslundii</i>	× <sup>b</sup>	?	<i>A. bowdenii, A. naeslundii</i>	? <sup>f</sup>
<i>Arcanobacterium bernardiae</i>	?	<i>A. pyogenes</i>	? <sup>c</sup>	√		√
<i>Arcanobacterium haemolyticum</i>	?	<i>A. phocae</i>	? <sup>c</sup>	?	<i>A. phocae</i>	? <sup>f</sup>
<i>Arcanobacterium phocae</i>	?	<i>A. haemolyticum</i>	× <sup>a</sup>	?	<i>A. haemolyticum</i>	× <sup>d</sup>
<i>Arcanobacterium pluranimalium</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Arcanobacterium pyogenes</i>	?	<i>A. bernardiae</i>	? <sup>c</sup>	√		√
<i>Atopobium fossor</i>	?	<i>A. minutum</i>	× <sup>a</sup>	√		√
<i>Atopobium minutum</i>	?	<i>A. fossor</i>	? <sup>c</sup>	√		√
<i>Atopobium parvulum</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Atopobium rimae</i>	√		√	√		√
<i>Atopobium vaginae</i>	√		× <sup>a</sup>	√		× <sup>d</sup>

<i>Bifidobacterium adolescentis</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Bifidobacterium bifidum</i>	√		× <sup>a</sup>	√		√
<i>Bifidobacterium breve</i>	?	<i>B. infantis</i> , <i>B. longum</i>	× <sup>a</sup>	√		× <sup>d</sup>
<i>Bifidobacterium catenulatum</i>	?	<i>B. dentium</i>	? <sup>c</sup>	√		√
<i>Bifidobacterium dentium</i>	?	<i>B. catenulatum</i>	× <sup>a</sup>	√		× <sup>d</sup>
<i>Bifidobacterium globosum</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Bifidobacterium infantis</i>	×	<i>B. longum</i> , <i>B. breve</i>	× <sup>b</sup>	×	<i>B. longum</i>	× <sup>e</sup>
<i>Bifidobacterium longum</i>	×	<i>B. infantis</i> , <i>B. breve</i>	× <sup>b</sup>	×	<i>B. infantis</i>	× <sup>e</sup>
<i>Bulleidia extracta</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Catenibacterium mitsuokai</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Clostridium aminovalericum</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Clostridium argentinense</i>	×	<i>C. subterminale</i>	× <sup>b</sup>	×	<i>C. subterminale</i>	× <sup>e</sup>
<i>Clostridium baratii</i>	√		√	√		√
<i>Clostridium beijerinckii</i>	×	<i>C. butyricum</i>	× <sup>b</sup>	×	<i>C. celatum</i> , <i>C. butyricum</i>	× <sup>e</sup>
<i>Clostridium bifermentans</i>	?	<i>C. ghonii</i> , <i>C. sordellii</i>	? <sup>c</sup>	?	<i>C. ghonii</i> , <i>C. sordellii</i>	? <sup>f</sup>
<i>Clostridium botulinum</i>	×	<i>C. sporogenes</i>	× <sup>b</sup>	×	<i>C. sporogenes</i>	× <sup>e</sup>
<i>Clostridium butyricum</i>	×	<i>C. beijerinckii</i>	× <sup>a</sup>	×	<i>C. beijerinckii</i>	× <sup>d</sup>
<i>Clostridium cadaveris</i>	√		√	√		√
<i>Clostridium carnis</i>	×	<i>C. chauvoei</i> , <i>C. septicum</i> , <i>C. tertium</i>	× <sup>a</sup>	×	<i>C. chauvoei</i> , <i>C. septicum</i> , <i>C. tertium</i>	× <sup>d</sup>
<i>Clostridium celatum</i>	×	<i>C. disporicum</i>	× <sup>a</sup>	?	<i>C. beijerinckii</i> , <i>C. disporicum</i> , <i>C. paraputrificum</i>	× <sup>d</sup>
<i>Clostridium chauvoei</i>	×	<i>C. septicum</i> , <i>C. tertium</i> , <i>C. carnis</i>	× <sup>a</sup>	×	<i>C. septicum</i> , <i>C. tertium</i> , <i>C. carnis</i>	× <sup>e</sup>
<i>Clostridium clostridioforme</i>	√		√	√		√
<i>Clostridium coccoides</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Clostridium cochlearium</i>	×	<i>C. tetani</i>	× <sup>b</sup>	×	<i>C. tetani</i>	× <sup>e</sup>
<i>Clostridium difficile</i>	√		√	√		√
<i>Clostridium disporicum</i>	×	<i>C. celatum</i>	× <sup>a</sup>	√	<i>C. celatum</i>	× <sup>d</sup>
<i>Clostridium fallax</i>	√		√	√		√
<i>Clostridium ghonii</i>	×	<i>C. sordellii</i> , <i>C. bifermentans</i>	× <sup>b</sup>	×	<i>C. sordellii</i> , <i>C. bifermentans</i>	× <sup>e</sup>
<i>Clostridium glycolicum</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Clostridium haemolyticum</i>	×	<i>C. novyi</i>	× <sup>a</sup>	×	<i>C. novyi</i>	× <sup>d</sup>
<i>Clostridium hiranonis</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Clostridium histolyticum</i>	?	<i>C. limosum</i>	? <sup>c</sup>	√		√
<i>Clostridium hylemonae</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Clostridium indolis</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Clostridium innocuum</i>	√		√	√		√
<i>Clostridium limosum</i>	?	<i>C. histolyticum</i>	? <sup>c</sup>	√		√
<i>Clostridium malenominatum</i>	√		√	√		√
<i>Clostridium manganotii</i>	√		√	√		√
<i>Clostridium novyi</i>	×	<i>C. haemolyticum</i>	× <sup>a</sup>	×	<i>C. haemolyticum</i>	× <sup>e</sup>
<i>Clostridium paraputrificum</i>	√		√	?	<i>C. celatum</i>	? <sup>f</sup>
<i>Clostridium perfringens</i>	√		√	√		√
<i>Clostridium ramosum</i>	√		√	√		√
<i>Clostridium septicum</i>	×	<i>C. chauvoei</i> , <i>C. carnis</i> , <i>C. tertium</i>	× <sup>a</sup>	×	<i>C. chauvoei</i> , <i>C. carnis</i> , <i>C. tertium</i>	× <sup>d</sup>
<i>Clostridium sordellii</i>	×	<i>C. ghonii</i> , <i>C.</i>	× <sup>b</sup>	×	<i>C. ghonii</i> , <i>C.</i>	× <sup>e</sup>

		<i>bifermentans</i>		<i>bifermentans</i>	
<i>Clostridium sphenoides</i>	√		√		√
<i>Clostridium spiroforme</i>	√		× <sup>a</sup>		× <sup>d</sup>
<i>Clostridium sporogenes</i>	×	<i>C. botulinum</i>	× <sup>b</sup>	<i>C. botulinum</i>	× <sup>e</sup>
<i>Clostridium sporosphaeroides</i>	√		√		√
<i>Clostridium subterminale</i>	×	<i>C. argentinense</i>	× <sup>b</sup>	<i>C. argentinense</i>	× <sup>e</sup>
<i>Clostridium symbiosum</i>	√		× <sup>a</sup>		× <sup>d</sup>
<i>Clostridium tertium</i>	×	<i>C. chauvoei, C. carnis, C. septicum</i>	× <sup>b</sup>	<i>C. chauvoei, C. carnis, C. septicum</i>	× <sup>e</sup>
<i>Clostridium tetani</i>	×	<i>C. cochlearium</i>	× <sup>b</sup>	<i>C. cochlearium</i>	× <sup>e</sup>
<i>Collinsella aerofaciens</i>	√		× <sup>a</sup>		× <sup>d</sup>
<i>Collinsella intestinalis</i>	?	<i>C. stercoris</i>	× <sup>a</sup>	<i>C. stercoris</i>	× <sup>d</sup>
<i>Collinsella stercoris</i>	?	<i>C. intestinalis</i>	× <sup>a</sup>	<i>C. intestinalis</i>	× <sup>d</sup>
<i>Cryptobacterium curtum</i>	√		× <sup>a</sup>		× <sup>d</sup>
<i>Eggerthella lenta</i>	√		√		√
<i>Eubacterium brachy</i>	√		× <sup>a</sup>		× <sup>d</sup>
<i>Eubacterium budayi</i>	×	<i>E. moniliforme, E. multiforme, E. nitritogenes</i>	× <sup>a</sup>	<i>E. moniliforme, E. multiforme, E. nitritogenes</i>	× <sup>d</sup>
<i>Eubacterium saburreum</i>	√		× <sup>a</sup>		× <sup>d</sup>
<i>Eubacterium combesii</i>	√		× <sup>a</sup>		× <sup>d</sup>
<i>Eubacterium contortum</i>	√		√		√
<i>Eubacterium infirmum</i>	×	<i>E. sulci</i>	× <sup>a</sup>	<i>E. sulci</i>	× <sup>d</sup>
<i>Eubacterium minutum</i>	√		× <sup>a</sup>		× <sup>d</sup>
<i>Eubacterium moniliforme</i>	×	<i>E. budayi, E. multiforme, E. nitritogenes</i>	× <sup>a</sup>	<i>E. budayi, E. nitritogenes</i>	× <sup>d</sup>
<i>Eubacterium multiforme</i>	×	<i>E. budayi, E. moniliforme, E. nitritogenes</i>	× <sup>b</sup>	<i>E. budayi</i>	× <sup>e</sup>
<i>Eubacterium nitritogenes</i>	×	<i>E. budayi, E. moniliforme, E. multiforme</i>	× <sup>a</sup>	<i>E. budayi, E. moniliforme</i>	× <sup>d</sup>
<i>Eubacterium nodatum</i>	√		× <sup>a</sup>		× <sup>d</sup>
<i>Eubacterium saphenum</i>	√		× <sup>a</sup>		× <sup>d</sup>
<i>Eubacterium sulci</i>	×	<i>E. infirmum</i>	× <sup>a</sup>	<i>E. infirmum</i>	× <sup>d</sup>
<i>Eubacterium tenue</i>	√		√		√
<i>Eubacterium yurii</i> subsp. <i>margaretiae</i>	×	<i>E. yurii</i> subsp. <i>schtitka, E. yurii</i> subsp. <i>yurii</i>	× <sup>a</sup>	<i>E. yurii</i> subsp. <i>yurii</i>	× <sup>d</sup>
<i>Eubacterium yurii</i> subsp. <i>schtitka</i>	?	<i>E. yurii</i> subsp. <i>margaretiae, E. yurii</i> subsp. <i>yurii</i>	× <sup>a</sup>		× <sup>d</sup>
<i>Eubacterium yurii</i> subsp. <i>yurii</i>	×	<i>E. yurii</i> subsp. <i>margaretiae, E. yurii</i> subsp. <i>schtitka</i>	× <sup>a</sup>	<i>E. yurii</i> subsp. <i>margaretiae</i>	× <sup>d</sup>
<i>Holdemania filiformis</i>	√		× <sup>a</sup>		× <sup>d</sup>
<i>Lactobacillus acidophilus</i>	√		√		√
<i>Lactobacillus casei</i>	×	<i>L. rhamnosus</i>	× <sup>b</sup>	<i>L. rhamnosus</i>	? <sup>f</sup>
<i>Lactobacillus catenaformis</i>	√		× <sup>a</sup>		× <sup>d</sup>
<i>Lactobacillus rhamnosus</i>	×	<i>L. casei</i>	× <sup>b</sup>	<i>L. casei</i>	? <sup>f</sup>
<i>Lactobacillus vitulinus</i>	√		× <sup>a</sup>		× <sup>d</sup>
<i>Mobiluncus curtisii</i> subsp. <i>curtisii</i>	×	<i>M. curtisii</i> subsp. <i>holmesii, M. mulieris</i>	× <sup>b</sup>	<i>M. mulieris, M. curtisii</i> subsp. <i>holmesii</i>	× <sup>e</sup>
<i>Mobiluncus curtisii</i> subsp. <i>holmesii</i>	×	<i>M. mulieris, M. curtisii</i> subsp. <i>curtisii</i>	× <sup>b</sup>	<i>M. curtisii</i> subsp. <i>curtisii, M. mulieris</i>	× <sup>e</sup>
<i>Mobiluncus mulieris</i>	?	<i>M. curtisii</i> subsp.	? <sup>c</sup>	<i>M. curtisii</i> subsp.	? <sup>f</sup>

		<i>holmesii</i> , <i>M. curtisii</i> subsp. <i>curtisii</i>			<i>curtisii</i> , <i>M. curtisii</i> subsp. <i>holmesii</i>	
<i>Mogibacterium pumilum</i>	×	<i>M. timidum</i> , <i>M. vescum</i>	× <sup>a</sup>	×	<i>M. vescum</i>	× <sup>d</sup>
<i>Mogibacterium timidum</i>	?	<i>M. pumilum</i>	× <sup>a</sup>	√		× <sup>d</sup>
<i>Mogibacterium vescum</i>	×	<i>M. pumilum</i>	× <sup>a</sup>	×	<i>M. pumilum</i>	× <sup>d</sup>
<i>Olsenella uli</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Propionibacterium acnes</i>	√		√	√		√
<i>Propionibacterium avidum</i>	√		√	√		√
<i>Propionibacterium granulosum</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Propionibacterium propionicum</i>	√		√	√		√
<i>Pseudoramibacter alactolyticus</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Slackia exigua</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Slackia heliotrinireducens</i>	√		× <sup>a</sup>	√		× <sup>d</sup>

√, >3% difference between the 16S rRNA gene sequence of the species and those of other medically important bacteria

?, 2-3% difference between the 16S rRNA gene sequence of the species and that of a closely related medically important bacterium

×, <2% difference between the 16S rRNA gene sequence of the species and that of a closely related medically important bacterium

×<sup>a</sup>, the species is not included in the existing MicroSeq full 16S rDNA bacterial identification system database

×<sup>b</sup>, although the species is included in the existing MicroSeq full 16S rDNA bacterial identification system database, the high 16S rRNA gene sequence similarity (>98% nucleotide identity) between the species and a closely related species does not allow them to be distinguished confidently

?<sup>c</sup>, although the species is included in the existing MicroSeq full 16S rDNA bacterial identification system database, 2-3% difference is observed between the 16S rRNA gene of the species and a closely related species

×<sup>d</sup>, the species is not included in the existing MicroSeq 500 16S rDNA bacterial identification system database

×<sup>e</sup>, although the species is included in the existing MicroSeq 500 16S rDNA bacterial identification system database, the high 16S rRNA gene sequence similarity (>98% nucleotide identity) between the species and a closely related species does not allow them to be distinguished confidently

?<sup>f</sup>, although the species is included in the existing MicroSeq 500 16S rDNA bacterial identification system database, 2-3% difference is observed between the 16S rRNA gene of the species and a closely related species

**Supplementary Table 3** Usefulness of full 16S rRNA gene sequence, 5' end 527-bp 16S rRNA gene sequence and the existing MicroSeq 16S rDNA bacterial identification system databases for identification of medically important anaerobic Gram-negative rods

Bacteria	Full 16S rRNA gene sequence			5' end 527-bp 16S rRNA gene sequence		
	Usefulness for species identification	Medically important bacteria with similar (<3% difference) full 16S rRNA gene sequence	Usefulness of existing Microseq full 16S rDNA bacterial identification system database	Usefulness for species identification	Medically important bacteria with similar (<3% difference) 5' end 527-bp 16S rRNA gene sequence	Usefulness of existing Microseq 500 16S rDNA bacterial identification system database
<i>Alistipes putredinis</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Anaerobiospirillum succiniciproducens</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Anaerobiospirillum thomasi</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Bacteroides caccae</i>	√		√	√		√
<i>Bacteroides capillosus</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Bacteroides distasonis</i>	√		√	√		√
<i>Bacteroides eggerthii</i>	√		√	√		√
<i>Bacteroides fragilis</i>	√		√	√		√
<i>Bacteroides merdae</i>	√		√	√		√
<i>Bacteroides ovatus</i>	√		√	√		√
<i>Bacteroides pyogenes</i>	×	<i>B. tectus</i>	× <sup>a</sup>	×	<i>B. tectus</i>	× <sup>d</sup>
<i>Bacteroides splanchnicus</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Bacteroides stercoris</i>	√		√	√		√
<i>Bacteroides tectus</i>	×	<i>B. pyogenes</i>	× <sup>a</sup>	×	<i>B. pyogenes</i>	× <sup>d</sup>
<i>Bacteroides thetaiotaomicron</i>	√		√	√		√
<i>Bacteroides uniformis</i>	√		√	√		√
<i>Bacteroides ureolyticus</i>	√		√	√		√
<i>Bacteroides vulgatus</i>	√		√	√		√
<i>Bilophila wadsworthia</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Butyrivibrio fibrisolvens</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Desulfovibrio piger</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Dialister pneumosintes</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Faecalibacterium prausnitzii</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Filifactor alocis</i>	√		× <sup>a</sup>	√		√
<i>Fusobacterium gonidiaformans</i>	?	<i>F. necrophorum</i>	? <sup>c</sup>	?	<i>F. necrophorum</i>	? <sup>f</sup>
<i>Fusobacterium mortiferum</i>	×	<i>F. ulcerans</i> , <i>F. varium</i>	× <sup>b</sup>	×	<i>F. ulcerans</i> , <i>F. varium</i>	× <sup>e</sup>
<i>Fusobacterium naviforme</i>	×	<i>F. nucleatum</i> subsp. <i>animalis</i> , <i>F. nucleatum</i> subsp. <i>nucleatum</i> , <i>F. nucleatum</i> subsp. <i>polymorphum</i> , <i>F. periodonticum</i>	× <sup>a</sup>	×	<i>F. nucleatum</i> subsp. <i>animalis</i> , <i>F. nucleatum</i> subsp. <i>nucleatum</i> , <i>F. nucleatum</i> subsp. <i>polymorphum</i> , <i>F. periodonticum</i>	× <sup>d</sup>
<i>Fusobacterium necrophorum</i>	?	<i>F. gonidiaformans</i>	? <sup>c</sup>	?	<i>F. gonidiaformans</i>	? <sup>f</sup>
<i>Fusobacterium nucleatum</i> subsp. <i>animalis</i>	×	<i>F. naviforme</i> , <i>F. nucleatum</i> subsp. <i>nucleatum</i> , <i>F. nucleatum</i> subsp. <i>polymorphum</i> , <i>F. periodonticum</i>	× <sup>b</sup>	?	<i>F. naviforme</i> , <i>F. nucleatum</i> subsp. <i>nucleatum</i>	? <sup>f</sup>

<i>Fusobacterium nucleatum</i> subsp. <i>nucleatum</i>	×	<i>F. naviforme</i> , <i>F. nucleatum</i> subsp. <i>animalis</i> , <i>F. nucleatum</i> subsp. <i>polymorphum</i> , <i>F. periodonticum</i>	× <sup>b</sup>	×	<i>F. naviforme</i> , <i>F. nucleatum</i> subsp. <i>animalis</i> , <i>F. nucleatum</i> subsp. <i>polymorphum</i> , <i>F. periodonticum</i>	× <sup>e</sup>
<i>Fusobacterium nucleatum</i> subsp. <i>polymorphum</i>	×	<i>F. naviforme</i> , <i>F. nucleatum</i> subsp. <i>animalis</i> , <i>F. nucleatum</i> subsp. <i>periodonticum</i>	× <sup>a</sup>	×	<i>F. naviforme</i> , <i>F. nucleatum</i> subsp. <i>nucleatum</i> , <i>F. periodonticum</i>	× <sup>d</sup>
<i>Fusobacterium periodonticum</i>	×	<i>F. naviforme</i> , <i>F. nucleatum</i> subsp. <i>animalis</i> , <i>F. nucleatum</i> subsp. <i>nucleatum</i> , <i>F. nucleatum</i> subsp. <i>polymorphum</i>	× <sup>b</sup>	×	<i>F. naviforme</i> , <i>F. nucleatum</i> subsp. <i>nucleatum</i> , <i>F. nucleatum</i> subsp. <i>polymorphum</i>	× <sup>e</sup>
<i>Fusobacterium russii</i>	√		√	√		√
<i>Fusobacterium ulcerans</i>	×	<i>F. mortiferum</i> , <i>F. varium</i>	× <sup>b</sup>	×	<i>F. mortiferum</i> , <i>F. varium</i>	× <sup>e</sup>
<i>Fusobacterium varium</i>	×	<i>F. mortiferum</i> , <i>F. ulcerans</i>	× <sup>b</sup>	×	<i>F. mortiferum</i> , <i>F. ulcerans</i>	× <sup>e</sup>
<i>Johnsonella ignava</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Leptotrichia buccalis</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Megamonas hypermegale</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Porphyromonas asaccharolytica</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Porphyromonas cangingivalis</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Porphyromonas canoris</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Porphyromonas cansulci</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Porphyromonas catoniae</i>	√		√	√		√
<i>Porphyromonas circumdentaria</i>	√		√	√		√
<i>Porphyromonas endodontalis</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Porphyromonas gingivalis</i>	×	<i>P. gulae</i>	× <sup>a</sup>	√		× <sup>d</sup>
<i>Porphyromonas gulae</i>	×	<i>P. gingivalis</i>	× <sup>a</sup>	√		× <sup>d</sup>
<i>Porphyromonas levii</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Porphyromonas macacae</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Prevotella bivia</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Prevotella buccae</i>	√		√	√		√
<i>Prevotella buccalis</i>	√		√	√		√
<i>Prevotella corporis</i>	√		√	√		√
<i>Prevotella dentalis</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Prevotella denticola</i>	√		√	√		√
<i>Prevotella disiens</i>	√		√	√		√
<i>Prevotella enoeca</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Prevotella heparinolytica</i>	√		√	?	<i>P. zooglyphiformans</i>	? <sup>f</sup>
<i>Prevotella intermedia</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Prevotella loescheii</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Prevotella melaninogenica</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Prevotella nigrescens</i>	√		× <sup>a</sup>	√		√
<i>Prevotella oralis</i>	√		√	√		√
<i>Prevotella oris</i>	√		√	√		√
<i>Prevotella oulorum</i>	√		√	√		√
<i>Prevotella pallens</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Prevotella tanneriae</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Prevotella veroralis</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Prevotella zooglyphiformans</i>	√		√	?	<i>P. heparinolytica</i>	? <sup>f</sup>

<i>Selenomonas diana</i>	×	<i>S. flueggei</i> , <i>S. infelix</i>	× <sup>a</sup>	?	<i>S. infelix</i>	× <sup>d</sup>
<i>Selenomonas flueggei</i>	?	<i>S. diana</i> , <i>S. infelix</i>	× <sup>a</sup>	√		× <sup>d</sup>
<i>Selenomonas infelix</i>	×	<i>S. diana</i> , <i>S. flueggei</i>	× <sup>a</sup>	?	<i>S. diana</i>	× <sup>d</sup>
<i>Selenomonas noxia</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Selenomonas sputigena</i>	√		√	√		√
<i>Sneathia sanguinegens</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Succinivibrio dextrinosolvens</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Sutterella wadsworthensis</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Tannerella forsythensis</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Tissierella praeacuta</i>	√		√	√		√

√, >3% difference between the 16S rRNA gene sequence of the species and those of other medically important bacteria

?, 2-3% difference between the 16S rRNA gene sequence of the species and that of a closely related medically important bacterium

×, <2% difference between the 16S rRNA gene sequence of the species and that of a closely related medically important bacterium

×<sup>a</sup>, the species is not included in the existing MicroSeq full 16S rDNA bacterial identification system database

×<sup>b</sup>, although the species is included in the existing MicroSeq full 16S rDNA bacterial identification system database, the high 16S rRNA gene sequence similarity (>98% nucleotide identity) between the species and a closely related species does not allow them to be distinguished confidently

?<sup>c</sup>, although the species is included in the existing MicroSeq full 16S rDNA bacterial identification system database, 2-3% difference is observed between the 16S rRNA gene of the species and a closely related species

×<sup>d</sup>, the species is not included in the existing MicroSeq 500 16S rDNA bacterial identification system database

×<sup>e</sup>, although the species is included in the existing MicroSeq 500 16S rDNA bacterial identification system database, the high 16S rRNA gene sequence similarity (>98% nucleotide identity) between the species and a closely related species does not allow them to be distinguished confidently

?<sup>f</sup>, although the species is included in the existing MicroSeq 500 16S rDNA bacterial identification system database, 2-3% difference is observed between the 16S rRNA gene of the species and a closely related species

**Supplementary Table 4** Usefulness of full 16S rRNA gene sequence, 5' end 527-bp 16S rRNA gene sequence and the existing MicroSeq 16S rDNA bacterial identification system databases for identification of medically important anaerobic cocci

Bacteria	Full 16S rRNA gene sequence		5' end 527-bp 16S rRNA gene sequence			
	Usefulness for species identification	Medically important bacteria with similar (<3% difference) full 16S rRNA gene sequence	Usefulness of existing Microseq full 16S rDNA bacterial identification system database	Usefulness for species identification	Medically important bacteria with similar (<3% difference) 5' end 527-bp 16S rRNA gene sequence	Usefulness of existing Microseq 500 16S rDNA bacterial identification system database
<i>Acidaminococcus fermentans</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Anaerococcus hydrogenalis</i>	√		√	√		√
<i>Anaerococcus lactolyticus</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Anaerococcus octavius</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Anaerococcus prevotii</i>	√		√	√		√
<i>Anaerococcus tetradius</i>	√		√	√		√
<i>Anaerococcus vaginalis</i>	√		√	√		√
<i>Centipeda periodontii</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Finegoldia magna</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Gallicola barnesae</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Megasphaera elsdenii</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Peptococcus niger</i>	√		√	√		√
<i>Peptoniphilus asaccharolyticus</i>	×	<i>P. indolicus</i>	× <sup>a</sup>	?	<i>P. indolicus</i>	× <sup>d</sup>
<i>Peptoniphilus harei</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Peptoniphilus indolicus</i>	×	<i>P. asaccharolyticus</i>	× <sup>a</sup>	?	<i>P. asaccharolyticus</i>	× <sup>d</sup>
<i>Peptoniphilus ivorii</i>	√		× <sup>a</sup>	√		× <sup>d</sup>
<i>Peptoniphilus lacrimalis</i>	√		√	√		√
<i>Peptostreptococcus anaerobius</i>	√		√	√		√
<i>Peptostreptococcus micros</i>	√		√	√		√
<i>Ruminococcus productus</i>	√		√	√		√
<i>Veillonella atypica</i>	×	<i>V. dispar</i> , <i>V. parvula</i>	× <sup>b</sup>	?	<i>V. dispar</i>	? <sup>f</sup>
<i>Veillonella dispar</i>	×	<i>V. atypical</i> , <i>V. parvula</i>	× <sup>b</sup>	×	<i>V. atypical</i> , <i>V. parvula</i>	× <sup>e</sup>
<i>Veillonella parvula</i>	×	<i>V. dispar</i> , <i>V. atypica</i>	× <sup>b</sup>	×	<i>V. dispar</i>	× <sup>e</sup>

√, >3% difference between the 16S rRNA gene sequence of the species and those of other medically important bacteria  
 ?, 2-3% difference between the 16S rRNA gene sequence of the species and that of a closely related medically important bacterium  
 ×, <2% difference between the 16S rRNA gene sequence of the species and that of a closely related medically important bacterium  
 ×<sup>a</sup>, the species is not included in the existing MicroSeq full 16S rDNA bacterial identification system database  
 ×<sup>b</sup>, although the species is included in the existing MicroSeq full 16S rDNA bacterial identification system database, the high 16S rRNA gene sequence similarity (>98% nucleotide identity) between the species and a closely related species does not allow them to be distinguished confidently  
 ?<sup>c</sup>, although the species is included in the existing MicroSeq full 16S rDNA bacterial identification system database, 2-3% difference is observed between the 16S rRNA gene of the species and a closely related species  
 ×<sup>d</sup>, the species is not included in the existing MicroSeq 500 16S rDNA bacterial identification system database  
 ×<sup>e</sup>, although the species is included in the existing MicroSeq 500 16S rDNA bacterial identification system database, the high 16S rRNA gene sequence similarity (>98% nucleotide identity) between the species and a closely related species does not allow them to be distinguished confidently  
 ?<sup>f</sup>, although the species is included in the existing MicroSeq 500 16S rDNA bacterial identification system database, 2-3% difference is observed between the 16S rRNA gene of the species and a closely related species