Supplementary Material

to "*Criibacterium bergeronii* gen. nov., sp. nov., a new member of the family *Peptostreptococcaceae*, isolated from human clinical samples"

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Supplementary results:

Research for outer membrane marker proteins in strains CCRI-22567[T] and CCRI-24246:

The genomes of strains CCRI-22567[T] and CCRI-24246 were assessed for genes encoding 17 outer membrane marker proteins conserved in enterobacteria and diderm *Firmicutes*: early LPS synthesis (LpxACDB), Omp85, POTRA, ExbD, Secretin, TamB, TonB (C-terminal region), and lipid-A synthesis and export (KdsBACD, LptA, LptB, FabZ) [1]. We used HMMER 3.2.1 (http://hmmer.org/) [2-4] and included *Escherichia coli* and *Veillonella parvula* genomes as controls. None of the aforementioned marker proteins were detected in strains CCRI-22567[T] and CCRI-24246. Conversely, 13 genes coding for marker proteins were detected in *Escherichia coli* (KdsBACD, FabZ, LptA, LpxACB, Omp85, POTRA, Secretin, TamB) and 15 in *Veillonella parvula* (KdsBACD, FabZ, LptA, LptB, LpxACB, ExbD, Omp85, POTRA, Secretin, TamB).

Supplementary Tables:

Table S1. Cellular Fatty Acid Composition of *Criibacterium bergeronii* gen. nov., sp. nov. as compared to selected genera and species in the family *Peptostreptococcaceae*

Fatty acid*	*Criibacterium bergeronii* CCRI-22567[T]	*Romboutsia ilealis* CRIB[T]/CCRI-22875[T]	*Filifactor alocis* ATCC 35896[T]†	*Intestinibacter bartlettii* DSM 16795[T]&	*Terrisporobacter glycolicus* DSM 1288[T]&	*Asaccharospora irregularis* DSM 2635[T]&	*Peptostreptococcus anaerobius*DSM 2949[T]&
Saturated, Straight-Chain							
$C_{10:0}$ (10.000)	2.7	Nd/Nd/Nd**	5.3	Nd	Nd	Nd	Nd
$C_{12:0}$ (12.000)	2.3	1.6/2.2/Nd	5.4	0.2	1.1	1.5	2.2
$C_{14:0}$ (14.000)	2.0	3.8/3.6/4.4	11.0	1.1	2.0	4.0	6.7
$C_{15:0}$ (15.000)	Nd	6.2/7.1/Nd	Nd	1.3	3.2	2.2	0.2
$C_{16:0}$ (16.000)	5.8	31.3/21.9/18.5	15.0	4.2	15.6	26.9	9.6
$C_{17:0}$ (17.000)	Nd	10.0/10.1/Nd	Nd	2.0	7.4	1.4	Nd
$C_{18:0}$ (18.000)	3.3	6.6/4.1/14.3	2.0	1.0	1.6	2.3	0.3
Saturated, branch-chained							
$C_{12:0}$ iso (11.608)	Nd	Nd/Nd/Nd	Nd	0.2	0.4	2.0	4.7
$C_{13:0}$ anteiso (12.703)	Nd	Nd/Nd/Nd	Nd	0.3	0.3	2.4	8.4
$C_{14:0}$ iso (13.618)	Nd	Nd/Nd/Nd	Nd	3.2	2.0	0.7	11.2
$C_{13:0}$ iso 3OH (14.114)	Nd	Nd/Nd/Nd	Nd	Nd	Nd	Nd	3.5

C$_{15:0}$ iso (14.623)	Nd	Nd/Nd/Nd	Nd	12.2	2.2	2.5	0.5
C$_{15:0}$ anteiso (14.714)	Nd	Nd/Nd/Nd	Nd	7.7	1.2	1.7	7.8
C$_{16:0}$ iso (15.627)	Nd	Nd/Nd/Nd	Nd	4.7	3.2	5.3	6.5
C$_{17:0}$ iso (16.630)	Nd	Nd/Nd/Nd	Nd	3.7	1.5	4.2	0.2
C$_{17:0}$ anteiso (16.723)	Nd	Nd/Nd/Nd	Nd	3.4	1.0	3.0	0.7
Unsaturated, Straight-Chained (ECLs observed)							
C$_{14:1}$ ω5c (13.903)	1.0	Nd/Nd/Nd	Nd	Nd	Nd	Nd	Nd
C$_{16:1}$ ω9c (15.774)	Nd	6.5/7.7/Nd	2.3	1.9	5.1	8.0	Nd
C$_{16:1}$ ω7c (15.818) = Summed Feature 3[@]	4.0	9.1/9.3/6.7	9.9	2.8	6.9	17.6	0.4
C$_{16:1}$ ω5c (15.909)	Nd	Nd/Nd/Nd	Nd	Nd	0.7	1.5	Nd
C$_{17:1}$ ω6c (16.864)	Nd	3.3/5.8/Nd	Nd	Nd	Nd	Nd	Nd
C$_{18:2}$ ω6,9c (17.723)	3.1	Nd/Nd/Nd	1.9	Nd	Nd	Nd	Nd
C$_{18:1}$ ω9c (17.771)	**33.6**	3.4/2.9/46.1	3.6	1.0	1.4	2.5	0.2
C$_{18:1}$ ω5c (17.919)	Nd	0.7/1.1/Nd	Nd	Nd	ND	Nd	Nd
Dimethyl Acetal (DMA) or Aldehydes							

$C_{11:0}$ DMA (12.469)	Nd	Nd/Nd/Nd	1.7	Nd	Nd	Nd	Nd
$C_{14:0}$ DMA (14.472)	Nd	Nd/Nd/Nd	Nd	0.9	0.5	Nd	3.5
$C_{16:0}$ ALDE (14.951)	Nd	Nd/Nd/Nd	8.1	1.9	7.1	Nd	3.9
$C_{15:0}$ iso DMA (15.112)	Nd	Nd/Nd/Nd	Nd	3.5	0.3	Nd	0.2
$C_{16:1}$ ω7c DMA (16.285)	0.7	Nd/Nd/Nd	2.6	Nd	Nd	Nd	Nd
$C_{16:0}$ DMA (16.471)	1.0	Nd/Nd/Nd	17.4	10.8	9.3	0.6	9.8
$C_{17:0}$ anteiso DMA (17.196)	Nd	Nd/Nd/Nd	Nd	4.4	0.3	ND	0.3
$C_{17:0}$ DMA (17.469)	Nd	Nd/Nd/Nd	Nd	2.6	2.1	0.2	Nd
$C_{18:1}$ω9c DMA (18.224)	**21.5**	Nd/Nd/Nd	Nd	Nd	Nd	Nd	Nd
$C_{18:1}$ω7c DMA (18.285)	2.7	Nd/Nd/Nd	2.8	Nd	Nd	Nd	Nd
$C_{18:0}$ DMA (18.467)	0.7	Nd/Nd/Nd	1.4	Nd	Nd	Nd	Nd
Cyclopropanes							
$C_{19:0}$ cyclopropane 9,10 (18.870)	Nd	0.8/1.5/ Nd	Nd	Nd	Nd	Nd	Nd
Summed Features$^@$							

Summed feature 4 (14.780)	Nd	1.1/2.7/Nd	3.0	0.5	1.7	0.3	Nd
Summed feature 5 (15.472)	Nd	Nd/Nd/Nd	Nd	2.5	2.7	Nd	0.2
Summed feature 7 (16.765)	5.3	Nd/Nd/Nd	Nd	Nd	0.8	Nd	Nd
Summed feature 8 (16.794)	Nd	5.3/9.0/Nd	1.8	1.8	3.1	1.1	Nd
Summed feature 10 (17.830)	6.4	8.3/7.6/7.5	4.9	1.0	2.9	2.5	Nd
Summed Feature 12 (18.624)	4.1	Nd/Nd/2.6	Nd	Nd	Nd	Nd	Nd
Totals	100&	98.0/96.5&	100&	80.8&	87.6&	94.4&	81&

* Values shown are the percent of CFA from total CFAs detected; data generated from this study for the type strain of *Criibacterium bergeronii, Romboutsia ilealis* CCRI-22875[T], and *Filifactor alocis* ATCC 35896[T] based on an average from 2 runs of the bacterium. ECL, equivalent chain lengths as described the peak naming table found in Moore 6.0 method; Nd, not detected. No species shown here contained CFAs [name, (ECL)]: $C_{18:1}\omega6c$ (17.864), $C_{17:0}$cyclopropane (16.889), nor $C_{19:0}$cyclopropane 11,12 (18.904)

** value1/value2/value3: The first two values are the amount of fatty acids from Gerritsen *et al.*, 2014 and Gerritsen *et al.*, 2018 respectively [5, 6]. The third value has been generated by our analysis of CRIB[T] /CCRI-22875[T]

@ Summed Features represent two or more CFAs that are grouped together by the MIDI system which have identical or nearly identical Equivalent Chain lengths (ECLs) but chemically differ as described in the Sherlock system using the method Moore 6.0. Summed features detected: Summed Feature 3 (cited in some versions of the library) included $C_{16:1}\omega7c$ (15.820) and $C_{16:1}$ $\omega6c$; Summed

Feature 4 included $C_{15:1}\omega 8c$, $C_{15:2}$ and /or an unknown $C_{15:2}$; Summed Feature 5 included $C_{15:0}DMA$ and/or $C_{14:0}3OH$; Summed Feature 7 included $C_{17:1}\omega 9c$ and/or $C_{17:2}$; Summed Feature 8 included $C_{17:1}\omega 8c$ and/or $C_{17:2}$; Summed Feature 10 includes $C_{18:1}\omega 7c$ and / or an unknown CFA; Summed Feature 12 included unknown CFA ECL 18.622 and $C_{19:0}$ iso.

from reference Gerritsen *et al.*, 2018 [6].

& Data adapted from Supplemental Table 2 of Gerritsen *et al.*, 2014 [5]. However, data alluded to there as unknown CFA compounds that did not correlate to ECLs in Moore6 Peak naming table, were not included in our table. Data for *R. ilealis* CCRI 22875^T from this study. For strains DSM 16795^T and DSM 2949^T the remaining percentages (~19%) represent CFAs that were absent or different from work done at the DSMZ.

† From testing of *F. alocis* ATCC 35896^T, which had the same results as cited in Moore *et al.*, 1994 [7].

Table S2: Characteristics of *Criibacterium* and other genera from the family *Peptostreptococcaceae*.

Property		Criibacterium	Acetoanaerobium [8]	Asaccharospora [5]	Clostridioides [8, 9]	Filifactor* [8, 9]	Intestinibacter [8]	Paeniclostridium [8]	Paraclostridium [8]	Peptacetobacter [10]	Peptoanaerobacter [11]	Peptoclostridium [8]	Peptostreptococcus [8, 9]	Proteocatella [8]	Romboutsia [5,6, 8]	Sporacetigenium [8]	Tepidibacter [8, 9, 12]	Terrisporobacter [5,9]
										Organisms								
GenBank accession No. (16S rRNA)		MF547661.1	GU562448.1	AB971797.1	HM245939.1	AF537211.1	AY438672.1	AB542933.1	HM245932.1	MK144347.1	HM120213.1	X77845.1	D14150.1	AF450134.1	JN381505.1	AY682207.1	AY158079.1	HM245942.1
Genome size, Mb (type species)		2.18	2.1	2.62	4.2	1.93	2.9	3.51	3.5	2.14	2.5	3	2.11	2.4	2.58	ND	2.2	3.21
G+C (mol%)		32.9-33.8	33.3-35.7	30.3	28.8	28-35.4	29.8	30.2	27-30.2	31.1–32.8	30.0-30.07	41.3-44.0	28-46	39.5	27-28.1	53.9-54.3	24-29.8	25.6-29
Cell size, Width μm (type species)		0.63	0.8	0.8-1.6	0.5-1.9	0,4-0,7	1.0–1.5	0.5–1.5	0.5–0.9	0.7-1	0.4-0.8	0.5–1.5	0.5-1.8	0.7–0.8	1.0–2.0	0.9–1.0	0.7-1.6	0.3-1.3
Cell size, Length μm (type species)		1.75	1-5	3.5-12.6	3-16.9	1,5-7,0	5.0–50	2–10	2–4	3.2-8	1.2-2.5	2–8	0.5-1.8	3.0–5.0	1.0–5.3	3.6–7.3	2.3-6.0	1.8-15.4
Cell shape		rods	rods	rods	rods	rods	rods	rods	rods	rods	rods	rods	cocci	rods	rods	rods	rods	rods
Gram staining		variable	-	+	+	variable	variable	+	+	+/variable	+	variable	+	+	+/variable	+	+	+/variable
Oxygen requirement		anaerobe	anaerobe	anaerobe	obligate anaerobe	obligate anaerobe	obligate anaerobe	obligate anaerobe	obligate anaerobe	anaerobe	obligate anaerobe	obligate anaerobe	obligate anaerobe	obligate anaerobe	anaerobe	anaerobe	anaerobe	anaerobe
Spore formation		-	-	+	+	variable	+	+	+	-	-	variable	-	+	+	+	+	+
Motility		+	+	+	+	+/-	-	+	+	-	+	+	-	+	-	+	+	+
Temperature range (C°)		30-42 (42)	37	37	30-37	37	37	20-45	30–35	25–45	30 – 42 (37)	15–40	30–39 (37)	29–37 (29)	30-45 (37)	20–42 (37)	28-60	15–45
Predominant fatty acids		C18:1 ω9c and C18:1ω9c DMA	ND	C16:0 C16:1ω7c	C16:0, C17:1 ISO I/C16:0 DMA	$C_{16:0}$ DMA	iso-C15 :0 and C16 :0 DMA	C12 to C18	C16 :0	C18:1ω9c C18:2ω6 9c C18:0 iso-C17:0 iso-C15:0	C14:0	ND	C16:0 C18:1 C18:1 aldehyde	C14:0 C16:0	C16 :0	C14:0	iso-C15 :0, iso-C14 :0, C16 :0 iso-C13:0	C16 :0

ND= Not Determined

*Some data are not for the type species *Filifactor villosus* but for *Filifactor alocis*

Supplementary figures:

Fig. S1. **Neighbor joining phylogenetic tree showing the relationship of** *Criibacterium bergeronii* **within the family** *Peptostreptococcaceae***.** The 16S RNA sequences were aligned using MUSCLE software [13]. The phylogenetic tree was reconstructed using neighbor joining method on 1262 sites with the Maximum Composite Likelihood substitution model implemented in MEGA software version 6.06 [14]. Only bootstrap values >50% based on 1000 replications are shown at branching points. Sequences from type strains are indicated with a superscript T. Organisms with names not validly published are presented with quotation marks. GenBank accession numbers for each 16S rRNA gene sequence are given in parentheses. Each bar indicates 0.02 substitutions per position. *Clostridium botulinum* ATCC 25763[T] and *Clostridium butyricum* DSM 10702[T] (*Clostridium sensu stricto*) were used as an outgroup.

Romboutsia ilealis DSM 25109^T (JN381505)
70
'Romboutsia maritimum' CCRI-22766^T (MF979851)
Romboutsia sedimentorum LAM201^T (KF443808)
74
73
'Romboutsia weinsteinii' CCRI-19649^T (MF537253)
63
'Clostridium dakarense' DSM 27086^T (KC517358)
Romboutsia lituseburensis JCM 1404^T (LC007106)
50
Romboutsia hominis DSM 28814^T (KT372679)
Intestinibacter bartlettii DSM 16795^T (AY438672)
Asaccharospora irregularis DSM 2635^T (X73447)
85
'Terrisporobacter othiniensis' 08-306576^T (JWHR01000141)
62
100
Terrisporobacter petrolearius LAM0A37^T (KJ000015)
77
Terrisporobacter glycolicus DSM 1288^T (X76750)
55
Terrisporobacter mayombei DSM 6539^T (FR733682)
100
Paraclostridium benzoelyticum JC272^T (LN846800)
Paraclostridium bifermentans ATCC 638^T (AB075769)
98
Paeniclostridium sordellii ATCC 9714^T (AB075771)
99
Eubacterium tenue DSM 20695^T (FR749984)
69
Paeniclostridium ghonii DSM 15049^T (AB542933)
96
Clostridioides difficile ATCC 9689^T (AB075770)
80
Clostridioides mangenotii DSM 1289^T (FR733662)
Peptoacetobacter hiranonis DSM 13275^T (AB023970)
Peptostreptococcus russellii DSM 23041^T (AY167952)
68
100
Peptostreptococcus canis DSM 27025^T (HE687281)
99
Peptostreptococcus anaerobius DSM 2949^T (AY326462)
90
Peptostreptococcus stomatis DSM 17678^T (DQ160208)
Sporacetigenium mesophilum DSM 16796^T (AY682207)
100
Clostridium paradoxum DSM 7308^T (Z69941)
66
Clostridium thermoalcaliphilum DSM 7309^T (NR 117154 FR749954)
66
Tepidibacter mesophilus B1^T (GQ231514)
59
Tepidibacter formicigenes DSM 15518^T (AY245527)
99
Tepidibacter thalassicus DSM 15285^T (AY158079)
Proteocatella sphenisci DSM 23131^T (AF450134)
95
Acetoanaerobium noterae ATCC 35199^T (GU562448)
98
100
Acetoanaerobium sticklandii DSM 519^T (FP565809)
Peptoclostridium acidaminophilum DSM 3953^T (CP007452.1:48659-50174)
100
Peptoclostridium litorale DSM 5388^T (X77845)
100
Filifactor alocis ATCC 35896^T (CP002390:719666..721206)
81
Filifactor villosus DSM 1645^T (AF537211)
100
Criibacterium bergeronii CCRI-24246 (MN153816)
Criibacterium bergeronii CCRI-22567^T (NR_164617)
100
Peptoanaerobacter stomatis ACC19a^T (HM120213)
100
Eubacterium yurii subsp. schtitka ATCC 43716 (AY533382)
100
Eubacterium yurii subsp. margaretiae ATCC 43715 (AY533381)
73
Eubacterium yurii subsp. yurii ATCC 43714^T (GU269551)
62
Finegoldia magna DSM 20470^T (AF542227)
100
Anaerococcus prevotii DSM 20548^T (CP001708)
Clostridium botulinum ATCC 25763^T (L37585)
100
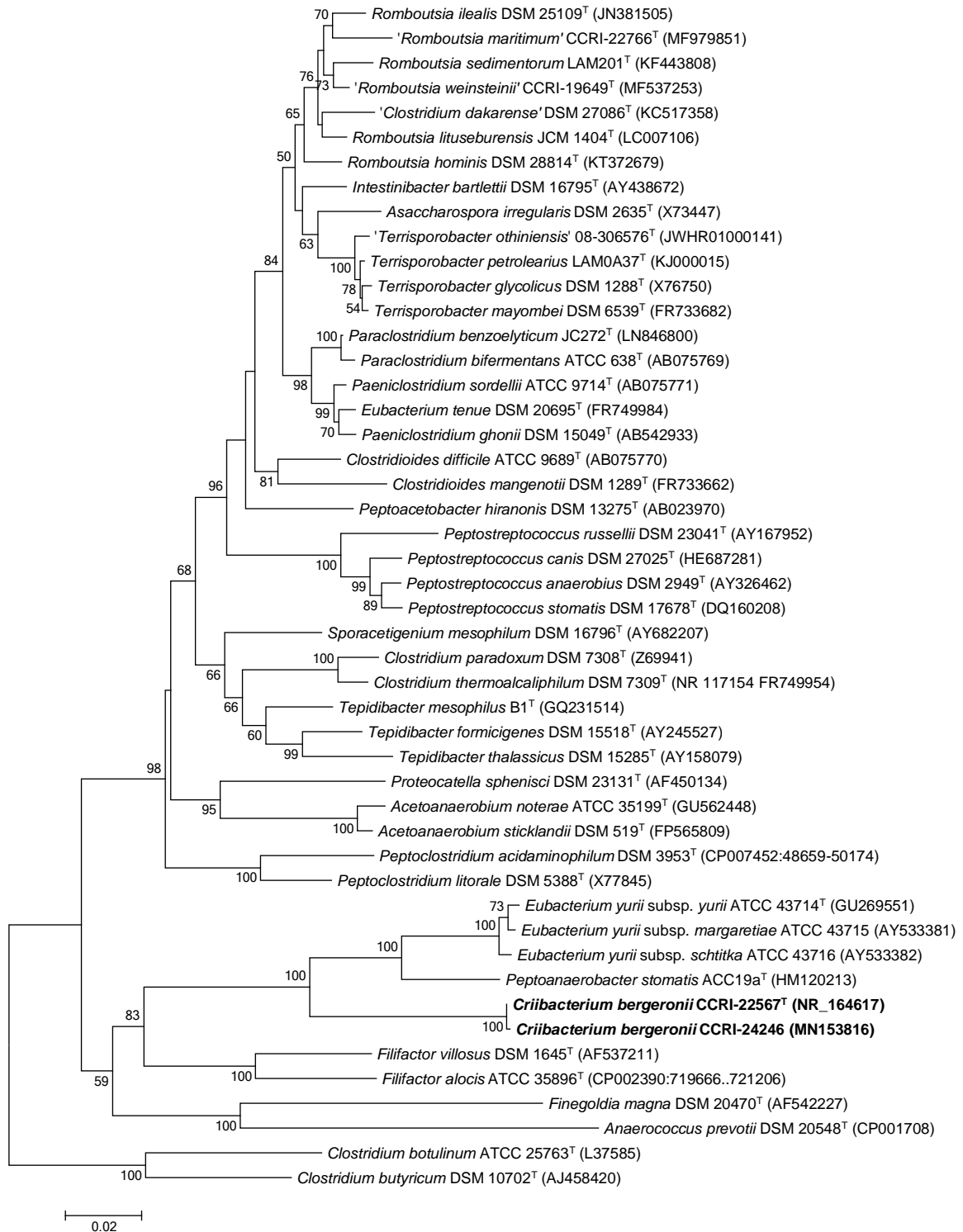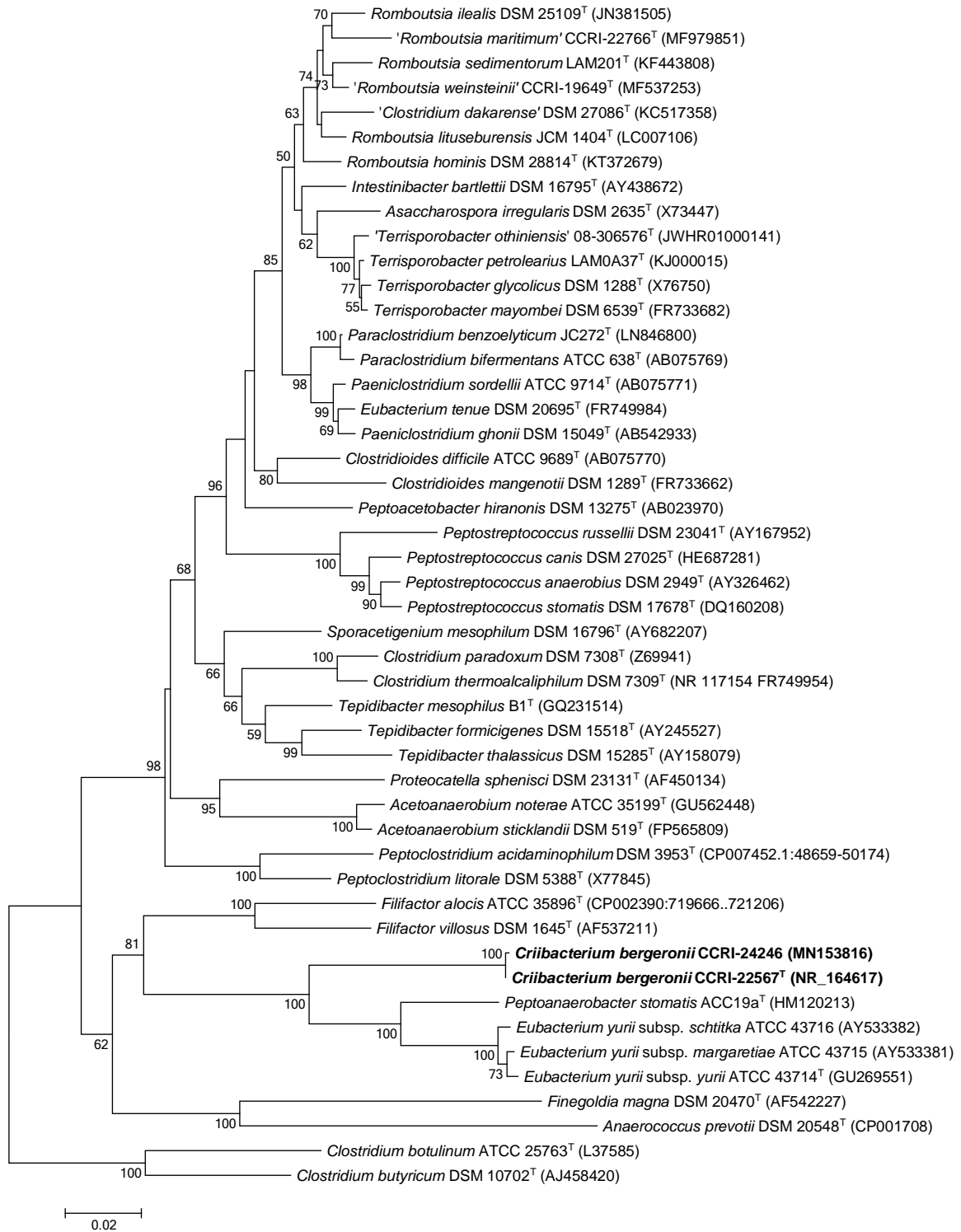Clostridium butyricum DSM 10702^T (AJ458420)

0.02

10

Fig. S2.   **Minimum evolution phylogenetic tree showing the relationship of** *Criibacterium bergeronii* **within the family** *Peptostreptococcaceae***.** The 16S RNA sequences were aligned using MUSCLE software [13]. The phylogenetic tree was reconstructed using the minimum evolution method on 1262 sites with the Maximum Composite Likelihood substitution model implemented in MEGA software version 6.06 [14]. Only bootstrap values >50% based on 1000 replications are shown at branching points. Sequences from type strains are indicated with a superscript T. Organisms with names not validly published were presented with quotation marks. GenBank accession numbers for each 16S rRNA gene sequence are given in parentheses. Each bar indicates 0.02 substitutions per position. *Clostridium botulinum* ATCC 25763[T] and *Clostridium butyricum* DSM 10702[T] (*Clostridium sensu stricto*) were used as an outgroup.

Fig. S3. **TYGS genome-based phylogeny of *Criibacterium bergeronii*.** 16S

RNA sequences from genome projects were initially used in TYGS pipeline [15] for a

BLAST comparison with other type strain sequences. The closest relative species

were then submitted to an intergenomic distances calculation using the Genome

BLAST Distance Phylogeny (GBDP) method [16, 17]. A genome tree was inferred

with software FastME 2.1.4 [18] from GBDP distances, including 100 pseudo-

bootstrap replicates placed at the tree nodes. Shared color in column "Species cluster"

and "Subspecies cluster" indicated affiliation to the same species and/or subspecies.

Strain *Criibacterium bergeronii* CCRI-22567[T] is represented in the tree by

'Cbergeronii_CCRI-22567_GCA_001693775.2_ASM169377v2_genomic' genome

assembly. Strain *Criibacterium bergeronii* CCRI-24246 is represented by

'Cbergeronii-CCRI-24246-SPAdes2-2019' genome assembly.

References

1.   **Taib N, Megrian D, Witwinowski J, Adam P, Poppleton D** *et al.* Genome-wide analysis of the Firmicutes illuminates the diderm/monoderm transition. *Nat Ecol Evol* 2020;4:1661-1672.

2.   **Aramaki T, Blanc-Mathieu R, Endo H, Ohkubo K, Kanehisa M** *et al.* KofamKOALA: KEGG Ortholog assignment based on profile HMM and adaptive score threshold. *Bioinformatics* 2020;36:2251-2252.

3.   **Haft DH, Selengut JD, White O**. The TIGRFAMs database of protein families. *Nucleic Acids Res* 2003;31:371-373.

4.   **El-Gebali S, Mistry J, Bateman A, Eddy SR, Luciani A** *et al.* The Pfam protein families database in 2019. *Nucleic Acids Res* 2019;47:D427-D432.

5.   **Gerritsen J, Fuentes S, Grievink W, van Niftrik L, Tindall BJ** *et al.* Characterization of *Romboutsia ilealis* gen. nov., sp. nov., isolated from the gastro-intestinal tract of a rat, and proposal for the reclassification of five closely related members of the genus *Clostridium* into the genera *Romboutsia* gen. nov., *Intestinibacter* gen. nov., *Terrisporobacter* gen. nov. and *Asaccharospora* gen. nov. *Int J Syst Evol Microbiol* 2014;64:1600-1616.

6.   **Gerritsen J, Umanets A, Staneva I, Hornung B, Ritari J** *et al.* Romboutsia hominis sp. nov., the first human gut-derived representative of the genus Romboutsia, isolated from ileostoma effluent. *Int J Syst Evol Microbiol* 2018;68:3479-3486.

7.   **Moore LV, Bourne DM, Moore WE**. Comparative distribution and taxonomic value of cellular fatty acids in thirty-three genera of anaerobic gram-negative bacilli. *Int J Syst Bacteriol* 1994;44:338-347.

8.   **Galperin MY, Brover V, Tolstoy I, Yutin N**. Phylogenomic analysis of the family *Peptostreptococcaceae* (Clostridium cluster XI) and proposal for reclassification of *Clostridium litorale* (Fendrich *et al.* 1991) and *Eubacterium acidaminophilum* (Zindel *et al.*

1989) as *Peptoclostridium litorale* gen. nov. comb. nov. and *Peptoclostridium acidaminophilum* comb. nov. *Int J Syst Evol Microbiol* 2016;66:5506-5513.

9.   **Wade WG**. Family II. *Eubacteriaceae*, Genus I. *Eubacterium*. In: de Vos P, Garrity GM, Jones D, Krieg NR, Ludwig W et al. (editors). *Bergey's Manual of Systematic Bacteriology, Volume 3: The Firmicutes*. New York: Springer; 2009. pp. 865-891.

10.   **Chen XJ, Wang ZQ, Zhou ZY, Zeng NY, Huang QF *et al.*** Characterization of *Peptacetobacter hominis* gen. nov., sp. nov., isolated from human faeces, and proposal for the reclassification of *Clostridium hiranonis* within the genus *Peptacetobacter*. *Int J Syst Evol Microbiol* 2020;70:2988-2997.

11.   **Sizova MV, Chilaka A, Earl AM, Doerfert SN, Muller PA *et al.*** High-quality draft genome sequences of five anaerobic oral bacteria and description of *Peptoanaerobacter stomatis* gen. nov., sp. nov., a new member of the family *Peptostreptococcaceae*. *Stand Genomic Sci* 2015;10:37.

12.   **Ezaki T**. Family VII. *Peptostreptococcaceae* fam. nov. In: de Vos P, Garrity GM, Jones D, Krieg NR, Ludwig W et al. (editors). *Bergey's Manual of Systematic Bacteriology, Volume 3: The Firmicutes*. New York: Springer; 2009. pp. 1008-1015.

13.   **Edgar RC**. MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res* 2004;32:1792-1797.

14.   **Tamura K, Stecher G, Peterson D, Filipski A, Kumar S**. MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. *Mol Biol Evol* 2013;30:2725-2729.

15.   **Meier-Kolthoff JP, Göker M**. TYGS is an automated high-throughput platform for state-of-the-art genome-based taxonomy. *Nat Commun* 2019;10:2182.

16.   **Henz SR, Huson DH, Auch AF, Nieselt-Struwe K, Schuster SC**. Whole-genome prokaryotic phylogeny. *Bioinformatics* 2005;21:2329-2335.

17.   **Meier-Kolthoff JP, Auch AF, Klenk HP, Göker M**. Genome sequence-based species

delimitation with confidence intervals and improved distance functions. *BMC Bioinformatics*

2013;14:60.

18.   **Lefort V, Desper R, Gascuel O**. FastME 2.0: A Comprehensive, Accurate, and Fast

Distance-Based Phylogeny Inference Program. *Mol Biol Evol* 2015;32:2798-2800.