



Supplementary Figure S1. (a) Neighbor-joining (NJ) and (b) maximum parsimony (MP) 16S rRNA gene sequence phylogenetic trees for *R-7^T* and *WTE2008^T*, and *Christensenellaceae* type strains from valid species descriptions. Phylogenies were constructed in MEGA 11, under default settings: The NJ tree (a) was computed using the maximum composite likelihood method, with branch lengths scaled by the number of substitutions per site. The MP tree (b) was built using the Subtree Pruning Regrafting (SPR) algorithm, with branch lengths calculated using the average pathway method scaled by the number of changes over whole sequences. For both phylogenies, bootstrap values associated with branches are shown if $\geq 50\%$ of 500 bootstrap replications.

Supplementary Table S1. Genome characteristics of R-7^T and WTE2008^T and *Christensenellaceae* type strains.

Taxa: 1, R-7^T; 2, WTE2008^T; 3, *Christensenella minuta* YIT 12065^T; 4, *Christensenella hongkongensis* HKU16^T; 5, *Christensenella intestinhominis* AF73-05CM02^T; 6, *Christensenella tenuis* NSJ-35^T; 7, *Luoshenia tenuis* NSJ-44^T; 8, *Gehongia tenuis* NSJ-53^T; 9, *Guopingia tenuis* NSJ-63^T.

Parameter	1	2	3	4	5	6	7	8	9
GenBank accession	CP068393	CP069421-22	CP029256	GCA_004342745	GCA_001678845	GCA_014287795	GCA_014384745	GCA_014384795	GCA_014384805
No. of contigs	1	2	1	40	36	15	11	14	10
Genome size (Mb)	3.39	3.41 (0.044) ¹	2.97	3.15	3.03	3.03	2.66	2.22	2.20
G+C mol%	53.0	53.7 (39.9) ¹	51.4	48.5	52.1	48.9	57.6	56.5	53.3

¹Values in brackets represent the second contig of the WTE2008^T assembly.

Supplementary Table S2. Genome distance comparisons of R-7^T and WTE2008^T to *Christensenellaceae* type strains.

	WTE2008 ^T	<i>Christensenella minuta</i> YIT 12065 ^T	<i>C. hongkongensis</i> HKU16 ^T	<i>C. intestinhominis</i> AF73-05CM02 ^T	<i>C. tenuis</i> NSJ-35 ^T	<i>Gehongia tenuis</i> NSJ-53 ^T	<i>Guopingia tenuis</i> NSJ-63 ^T	<i>Luoshenia tenuis</i> NSJ-44 ^T
ANI (%)¹								
R-7 ^T	83.6	BT	BT	BT	BT	BT	BT	BT
WTE2008 ^T	-	BT	BT	BT	BT	BT	BT	BT
<i>is</i>DDH (%)								
R-7 ^T	25.5	23.0	25.9	26.2	25.3	19.9	22.8	20.1
WTE2008 ^T	-	25.6	25.7	26.2	25.2	24.2	22.1	20.8
AAI (%)								
R-7 ^T	80.2	43.3	43.2	43.3	43.1	44.0	44.2	44.4
WTE2008 ^T	-	43.6	43.0	43.4	43.1	44.2	44.1	44.5
POCP (%)								
R-7 ^T	77.9	24.3	24.2	24.5	24.1	26.3	26.9	26.8
WTE2008 ^T	-	23.8	22.9	23.7	23.0	26.3	26.2	27.7

¹Below threshold (BT) results could not be computed in fastANI using default settings as these comparisons had alignment fractions less than the 20% cut-off required.

Supplementary Table S3. Cellular fatty acid profiles of R-7^T and WTE2008^T.

Cellular fatty acid ¹	Relative abundance (%) ²	
	R-7 ^T	WTE2008 ^T
10:0	0.11	0.11
11:0	n.d.	0.05
11:0 anteiso	0.05	n.d.
12:0	0.78	0.82
12:0 iso	0.18	0.33
13:0	0.20	0.38
13:0 iso	0.26	0.48
13:0 anteiso	0.42	0.94
13:0 iso 3OH	0.13	0.19
14:0	3.08	3.61
14:0 iso	1.80	3.19
14:0 DMA	n.d.	0.19
15:0	3.23	3.44
15:0 iso	0.90	1.79
15:0 anteiso	8.92	7.70
15:0 iso DMA	0.43	0.67
15:0 3OH	0.17	0.67
16:0	11.54	15.17
16:0 iso	18.19	8.40
16:0 2OH	0.17	0.20
16:0 3OH	0.97	2.20
16:1 ω 7c	0.08	0.20
17:0	4.30	2.99
17:0 iso	0.48	0.70
17:0 anteiso	19.74	8.72
17:0 3OH	0.44	0.95
17:0 anteiso 3OH	0.78	2.39
18:0	9.11	19.32
18:0 iso	6.63	2.57
18:1 ω 6c	0.22	0.48
18:1 ω 9c	0.72	1.72
18:2 ω 6, 9c	0.75	1.27
19:0	0.50	0.35
19:0 anteiso	1.85	0.78
20:0	0.80	1.52
Summed feature 1	n.d.	0.10
Summed feature 2	0.26	0.62
Summed feature 3	0.61	1.09
Summed feature 4	0.77	2.25
Summed feature 5	0.20	0.66
Summed feature 6	0.23	0.43
Summed feature 7	n.d.	0.35

¹Summed features: 1, C12:0 3OH and C13:0 dimethylacetal (DMA); 2, C15:0 DMA and C14:0 3OH; 3, C13:0 anteiso 3OH and C16:1 ω 9c DMA; 4, C16:0 iso 3OH and unknown 17.157 DMA; 5, C18:1 ω 7c and unknown 17.834; 6, C17:0 iso 3OH and C18:2 DMA; 7, unknown 18.622 and C:19:0 iso.

²Values >10% are shown in bold type; n.d., not detected.

Supplementary Table S4. Fermentation end products of R-7^T and WTE2008^T on insoluble substrates.

Substrate	R-7 ^T		WTE2008 ^T	
	Ethanol ¹	SCFAs ¹	Ethanol	SCFAs
Cellulose	0	-0.3 ± 0.6	0.5 ± 0.06	-1.1 ± 0.1
Dextrin	6.6 ± 0.4	1.7 ± 2.4	2.7 ± 0.5	1.3 ± 0.5
Glycogen	0	-3.5 ± 2.5	0.5 ± 0.1	-0.1 ± 0.8
Inulin	0.8 ± 0.06	0.7 ± 0.3	0.5 ± 0.01	-0.5 ± 0.3
Pectin	1.2 ± 0.2	1.9 ± 0.2	2.3 ± 0.3	0.3 ± 0.6
Starch	3.3 ± 0.2	7.7 ± 0.5	2.1 ± 0.3	1.5 ± 0.5
Xylan	4.2 ± 0.3	7.5 ± 0.7	3.1 ± 0.06	1.3 ± 0.2
Rutin	0	0.1 ± 0.06	0.6 ± 0.06	-0.1 ± 0.2
Salicin	8.8 ± 0.5	7.3 ± 4.8	2.1 ± 0.2	0.3 ± 1

¹Values represent average ± SEM concentrations (mM) of ethanol and total short chain fatty acids (SCFAs) in 5 day-old cultures grown in BY media supplemented with 0.5% (w/v) of each substrate. Measurements were performed in triplicate and initial concentrations were subtracted from final values.

²Fermentation on the soluble substrate, cellobiose, is included as a reference.