

Table S1. List of type species of validly published genera within the *Ruminococcaceae* family and their 16S similarity with *Negativibacillus massiliensis*.

Species	Accession Number	Coverage %	Identity %
<i>Harryflintia acetispora</i>	KU999999	90%	93.52%
<i>Tepidibaculum saccharolyticum</i>	MH200617	92%	91.14%
<i>Clostridium methylpentosum</i>	Y18181	96%	90.60%
<i>Anaerotruncus colihominis</i>	AJ315980	93%	90.57%
<i>Hydrogenoanaerobacterium saccharovorans</i>	EU158190	99%	90.41%
<i>Massiliimalia massiliensis</i>	LT576408	100%	90.31%
<i>Ruminococcus champanellensis</i>	AJ515913	90%	90.10%
<i>Ruminococcus callidus</i>	NR_029160	92%	89.93%
<i>Ruminococcus albus</i>	AB538438	99%	89.33%
<i>Paludicola psychrotolerans</i>	KY777734	99%	89.24%
<i>Acetanaerobacterium elongatum</i>	AY487928	99%	89.15%
<i>Caproiciproducens galactitolivorans</i>	FJ805840	97%	89.06%
<i>Ethanoligenens harbinense</i>	AY675965	100%	88.72%
<i>Clostridium cellulosi</i>	L09177	99%	88.50%
<i>Hydrogeniiclostridium mannosilyticum</i>	MH043116	100%	88.43%
<i>Eubacterium siraeum strain</i>	L34625	98%	88.32%
<i>Ruthenibacterium lactatiformans</i>	KM098109	100%	88.13%
<i>Caproicibacter fermentans</i>	MN851263	100%	88.08%
<i>Intestinimonas butyriciproducens</i>	KC311367	93%	87.55%
<i>Acutalibacter muris</i>	KR364749	100%	87.52%
<i>Subdoligranulum variabile</i>	AJ518869	91%	87.51%
<i>Fournierella massiliensis</i>	LN846908	100%	87.43%
<i>Anaerofilum pentosovorans</i>	X97852	97%	87.34%
<i>Clostridium leptum</i>	M59095	91%	87.18%
<i>Butyricicoccus pullicaecorum</i>	EU410376	98%	86.98%
<i>Agathobaculum butyriciproducens</i>	KP889099	93%	86.90%
<i>Ruminococcus flavefaciens</i>	KP689131	93%	86.87%
<i>Faecalibacterium prausnitzii</i>	AJ413954	99%	86.71%
<i>Pseudoflavonifractor capillosus</i>	AY136666	98%	86.66%
<i>Lawsonibacter asaccharolyticus</i>	LC371917	99%	86.64%
<i>Petroclostridium xylanilyticum</i>	KT630605	99%	86.45%
<i>Sporobacter termitidis</i>	Z49863	100%	86.39%
<i>Flavonifractor plautii</i>	AY724678	97%	86.18%
<i>Acetivibrio cellulolyticus</i>	L35516	98%	85.65%
<i>Papillibacter cinnamivorans</i>	AF167711	99%	85.62%
<i>Dysosmobacter welbionis</i>	MG963288	94%	85.24%
<i>Monoglobus pectinilyticus</i>	KY978733	99%	85.10%
<i>Magaeibacillus indolicus</i>	GQ900632	98%	85.09%
<i>Oscillibacter valericigenes</i>	AB238598	97%	85.04%
<i>Ruminiclostridium cellobioparum</i>	X71856	99%	85.00%
<i>Saccharofermentans acetigenes</i>	AB910750	99%	85.00%

<i>Fastidiosipila sanguinis</i>	AJ575187	89%	84.83%
<i>Pseudobacteroides cellulosolvens</i>	L35517	98%	84.59%
<i>Cellulosibacter alkalithermophilus</i>	FJ815191	90%	84.36%
<i>Clostridium stercorarium</i>	AJ310082	96%	84.20%
<i>Thermoclostridium stercorarium</i>	AJ310082	96%	84.20%
<i>Anaerobacterium chartisolvens</i>	AB793710	97%	84.11%

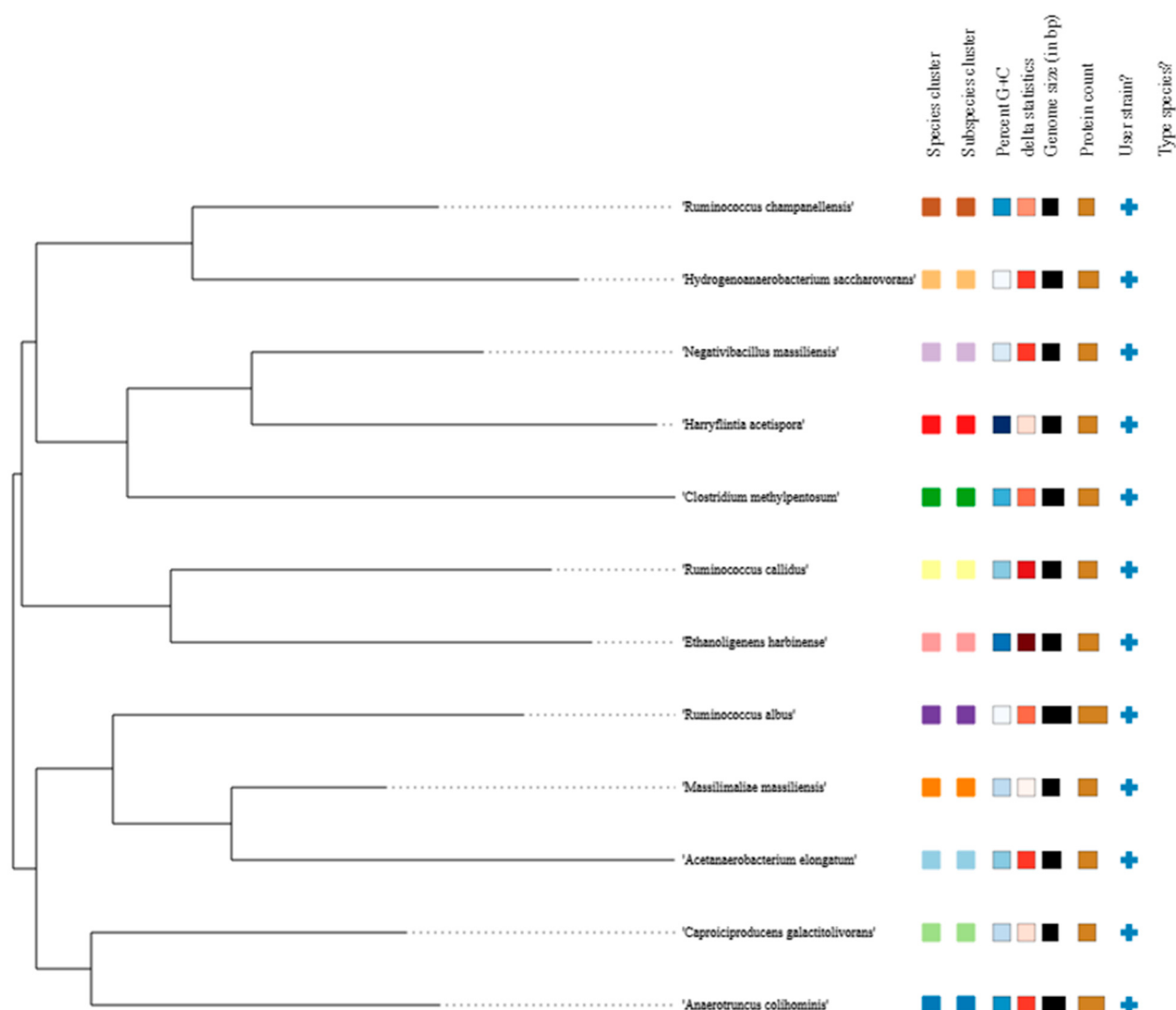


Figure S1. Phylogenetic tree based on the genomic sequences of closely related species with available genomes. Tree inferred with FastME 2.1.6.1 from GBDP distances calculated from genome sequences. The branch lengths are scaled in terms of GBDP distance formula d5. The numbers above branches are GBDP pseudo-bootstrap support values > 60 % from 100 replications, with an average branch support of 19.8 %. The tree was rooted at the midpoint.