



OTU	Phylum	Class	Order	Family	Genus
1	Synergistetes	Synergistia	Synergistales	Synergistaceae	Aminivibrio
2	Spirochaetae	Spirochaetes	Spirochaetales	Spirochaetaceae	Spirochaeta
3	Tenericutes	Mollicutes	NB1-n	unclassified	unclassified
4	Bacteroidetes	vadinHA17	unclassified	unclassified	unclassified
5	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	unclassified
6	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobulbaceae	Desulfobulbus
7	Synergistetes	Synergistia	Synergistales	Synergistaceae	Thermovirga
8	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	unclassified	unclassified
9	Spirochaetae	Spirochaetes	Spirochaetales	Spirochaetaceae	unclassified
10	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	RC9 gut group
11	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	vadinBC27 wastewater sludge grp
12	Firmicutes	Clostridia	Clostridiales	Family XI	unclassified
13	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Petrimonas
14	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Porphyromonas
15	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
16	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Paludibacter
17	Synergistetes	Synergistia	Synergistales	Synergistaceae	unclassified
18	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	unclassified
19	Firmicutes	Clostridia	Clostridiales	Family XI	Sedimentibacter
20	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	unclassified
21	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	Atopobium
22	Synergistetes	Synergistia	Synergistales	Synergistaceae	Aminobacterium
23	Firmicutes	Clostridia	Clostridiales	Eubacteriaceae	Pseudoramibacter
24	Firmicutes	Clostridia	Clostridiales	Family XIII	unclassified
25	Synergistetes	Synergistia	Synergistales	Synergistaceae	Pyramidobacter
26	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Fastidiosipila
27	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	Trichococcus
28	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Peptostreptococcus
29	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides

Figure S3: Dual hierarchal clustering of the bacterial communities.

The 29 OTUs detected in all digesters with the highest relative abundance, including the enrichment culture, were considered in the clustering analysis. The 29 OTUs contributed to 70-85% of the total bacterial sequences in all the biomass samples analyzed. The gradient scale ranges from 0 to 100% relative abundance. Sample names x1, x2 and x3 represent the enrichment culture. The sample names for digesters are denoted as follows: for example “nB1” – the prefix “n” represents “non-bioaugmented, the middle letter “B” represents Set-B and the suffix “1” represent the replicate number. The enrichment culture has a unique bacterial community structure as compared to the other digesters and clusters separately. Fermenters of the phyla *Firmicutes*, *Bacteroidetes* and *Synergistetes* dominated all non-bioaugmented digesters. G3 digesters (Set-H & I) were uniquely dominated by *RC9 gut group* (OTU 10), contributing 50-60% of the relative abundance.