

**Process Parameters and changes in the microbial community patterns
during the first 240 days of an agricultural energy crop digester**

AMB Express

Authors: N.Weithmann, A.Weig, R. Freitag*

* corresponding author

Process Biotechnology, Center for Energy Technology, University of Bayreuth,
95440 Bayreuth, Germany

ruth.freitag@uni-bayreuth.de, Tel.: +49 921 557371

Taxa Summaries

Legend	Taxonomy	Total	F30	F37	F50	F178	F192	F206	P30	P37	P50	P178	P192	P206
		%	%	%	%	%	%	%	%	%	%	%	%	%
Unassigned;Other;Other;Other;Other;Other		1.6%	1.2%	2.0%	1.6%	1.1%	1.9%	1.4%	1.9%	2.1%	2.1%	1.3%	1.4%	1.4%
k_Archaea;p_Crenarchaeota;c_MCG0;p_GrFC26;f_g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Archaea;p_Euryarchaeota;c_Methanobacteria;o_Methanobacteriales;f_Methanobacteriaceae;g_Methanobacterium		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Archaea;p_Euryarchaeota;c_Methanobacteria;o_Methanobacteriales;f_VSA2;g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%
k_Archaea;p_Euryarchaeota;c_Methanomicrobia;o_Methanomicrobiales;f_Methanocorpusculaceae;g_Methanocorpusculum		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Archaea;p_Euryarchaeota;c_Methanomicrobia;o_Methanomicrobiales;f_Methanomicrobiaceae;g_Methanoculleus		0.3%	0.1%	0.2%	0.5%	0.0%	0.1%	0.2%	0.2%	0.2%	0.2%	1.9%	0.1%	0.1%
k_Archaea;p_Euryarchaeota;c_Methanomicrobia;o_Methanomicrobiales;f_Methanospirillaceae;g_Methanospirillum		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Archaea;p_Euryarchaeota;c_Methanomicrobia;o_Methanomicrobiales;f_Methanomicrobales;Other;Other		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%
k_Archaea;p_Euryarchaeota;c_Methanomicrobia;o_Methanomicrobiales;f_Methanomicrobales;g_Methanosaeta		0.8%	0.4%	0.9%	1.7%	0.0%	0.0%	0.4%	1.6%	4.3%	0.0%	0.0%	0.0%	0.0%
k_Archaea;p_Euryarchaeota;c_Methanomicrobia;o_Methanomicrobiales;f_Methanomicrobales;g_Methanosarcina		2.5%	1.0%	2.4%	2.3%	2.4%	3.5%	3.3%	1.2%	0.5%	2.1%	4.9%	2.8%	3.1%
k_Archaea;p_Euryarchaeota;c_Methanomicrobia;o_YC-E6f;g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Archaea;p_Euryarchaeota;c_Theplomastasma;o_E2f_[Methanomassiliicoccaceae];g_Methanomassiliicoccus		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.2%	0.0%	0.0%
k_Archaea;p_Euryarchaeota;c_Theplomastasma;o_E2f_[Methanomassiliicoccaceae];g_vadinCA11		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;Other;Other;Other;Other;Other		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_c_o_f_g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Acidobacteria;c_Acidobacteria-6;o_lii1-15-f_g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Acidobacteria;c_BPC102;o_MVS-40f;g		0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Acidobacteria;c_Soilbacteria;o_Soilbacteriales;f_AKIW659;g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Acidobacteria;c_Soilbacteria;o_Soilbacteriales;f_Soilbacteraceae;g_Candidatus Solibacter		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Actinobacteria;c_o_f_g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Actinobacteria;c_Acidimicrobia;o_Acidimicrobiales;f_g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Actinomyces		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Cellulomonadaceae;g_Actinotalea		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Cellulomonas		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Actinobacteria;c_Actinomycetales;f_Corynebacteriaceae;g_Corynebacterium		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Actinobacteria;c_Actinomycetales;f_Intrasporangiaceae;g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Actinobacteria;c_Actinomycetales;f_Microbacteriaceae;Other		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Actinobacteria;c_Actinomycetales;f_Microbacteriaceae;g_Salinibacterium		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Actinomycetales;f_Micromonosporaceae;g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Actinobacteriac;c_Actinobacteria;o_Actinomycetales;f_Nocardioipsaceae;g_Thermobifida		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Actinobacteriac;c_Actinobacteria;o_Actinomycetales;f_Pseudonocardiaeae;g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Actinobacteriac;c_Actinobacteria;o_Actinomycetales;f_Pseudonocardiaeae;g_Saccharomonospora		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Actinobacteriac;c_Actinobacteria;o_Actinomycetales;f_Thermomonosporaceae;g_Actinomadura		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Actinobacteriac;c_Actinobacteria;o_Bifidobacteriales;f_Bifidobacteriaceae;g_Bifidobacterium		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Actinobacteriac;c_Bacteriobacteria;o_Coriobacteriales;f_Coriobacteriaceae;g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Actinobacteriac;c_Thermoleophilia;o_f_g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Actinobacteriac;c_Thermoleophilia;o_Gaellaiales;f_g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Armatimonades;c_SJA-176;o_RB046;f_g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_BRC1;c_NPL-UPA2;o_f_g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_BRC1;c_PRR-11;o_f_g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Bacteroides;c_Bacteroidia;o_Bacteroidales;Other;Other;Other		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Bacteroides;c_Bacteroidia;o_Bacteroidales;f_g		6.4%	16.6%	6.6%	4.1%	9.5%	2.2%	3.6%	17.4%	2.8%	1.6%	7.2%	3.2%	2.3%
k_Bacteria;p_Bacteroides;c_Bacteroidia;o_Bacteroidales;f_BA008;g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Bacteroides;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;Other		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Bacteroides;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g		0.7%	0.5%	0.9%	0.5%	0.9%	0.4%	0.3%	0.8%	1.2%	1.0%	0.9%	0.4%	0.2%
k_Bacteria;p_Bacteroides;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_BF311		2.0%	2.0%	2.0%	2.0%	2.0%	2.0%	1.7%	2.5%	2.2%	2.0%	2.6%	1.7%	1.1%
k_Bacteria;p_Bacteroides;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Bacteroides;c_Bacteroidia;o_Bacteroidales;f_Marinilabiaceae;Other		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Bacteroides;c_Bacteroidia;o_Bacteroidales;f_Marinilabiaceae;g		2.2%	1.8%	2.8%	7.1%	1.6%	0.5%	1.0%	0.7%	8.5%	1.5%	0.4%	0.5%	0.3%
k_Bacteria;p_Bacteroides;c_Bacteroidia;o_Bacteroidales;f_Porphyrimonadaceae;Other		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Bacteroides;c_Bacteroidia;o_Bacteroidales;f_Porphyrimonadaceae;g		4.0%	3.4%	3.5%	2.6%	6.4%	4.1%	4.9%	4.2%	3.0%	2.7%	3.6%	5.3%	4.8%
k_Bacteria;p_Bacteroides;c_Bacteroidia;o_Bacteroidales;f_Porphyrimonadaceae;g_Paludibacter		0.3%	0.2%	0.4%	0.3%	0.8%	0.2%	0.2%	0.2%	0.7%	0.2%	0.4%	0.2%	0.1%
k_Bacteria;p_Bacteroides;c_Bacteroidia;o_Bacteroidales;f_Porphyrimonadaceae;g_Parabacteroides		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Bacteroides;c_Bacteroidia;o_Bacteroidales;f_Prevotellaceae;g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Bacteroides;c_Bacteroidia;o_Bacteroidales;f_Prevotellaceae;g_Bacteroides		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Bacteroides;c_Sphingobacteria;o_Sphingobacteriales;f_Sphingobacteriaceae;g_Sphingobacterium		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Chloroflexi;c_Anaerolineae;o_f_g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Chloroflexi;c_Sphingobacteria;o_Sphingobacteriales;f_Sphingobacteriaceae;g_Sphingobacterium		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Chloroflexi;c_Anaerolineae;o_f_g		0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Chloroflexi;c_Anaerolineae;o_Anaerolineales;f_Anaerolinaceae;g_Anaerolinea		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Chloroflexi;c_Anaerolineae;o_Anaerolineales;f_Anaerolinaceae;g_SHD-231		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Chloroflexi;c_Anaerolineae;o_Anaerolineales;f_Anaerolinaceae;g_T78		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Chloroflexi;c_Anaerolineae;o_CFB-26f;g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Chloroflexi;c_Caldilineales;o_Caldilineaceae;g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Chloroflexi;c_GCA04f;g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Chloroflexi;c_SBR1031;f_SHA-31;g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Chloroflexi;c_Anaerolineae;o_SHA-20f;g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Chloroflexi;c_Dehalococcoidetes;o_Dehalococcoidales;f_Dehalococcoidaceae;g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Chloroflexi;c_SHA-26o;f_g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Chloroflexi;c_TK10;o_f_g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Chloroflexi;c_JG30-KF-CM45;f_g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Chloroflexi;c_Thermomicrobia;o_Sphaerotilaceae;f_Sphaerotilaceales;g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Cyanobacteria;c_4C0d-2;o_YS2;f_g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Cyanobacteria;c_Chloroplasto;o_Streptophytta;f_g		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Fibrobacteres;c_Fibrobacteria;o_Fibrobacterales;f_Fibrobacteraceae;g_Fibrobacter		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Fibrobacteres;c_TG3;c_TG3-1;f_TS003-O20;g		0.2%	0.2%	0.3%	0.7%	0.0%	0.0%	0.4%	0.4%	0.4%	0.2%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;Other;Other;Other;Other		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillales;g_Bacillus		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillales;g_Bacillus		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillales;g_Bacillus</td														

Taxa Summaries

k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Aerococcaceae;g_	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Aerococcaceae;g_Facklamia	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;g_Enterococcus	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.1%	0.1%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Pediococcus	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus	0.3%	0.3%	0.3%	0.3%	0.8%	0.4%	0.2%	0.2%	0.1%	0.3%	0.2%	0.4%	0.2%	0.2%
k_Bacteria;p_Firmicutes;c_Bacilli;o_Turicibacteriales;f_Turicibacteraceae;g_Turicibacter	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;Other;Other	0.3%	0.1%	0.2%	0.2%	0.1%	0.5%	0.4%	0.1%	0.3%	0.4%	0.5%	0.7%	0.7%	0.7%
k_Bacteria;p_Firmicutes;c_Clostridia;o_f;g_	0.2%	0.2%	0.3%	0.3%	0.1%	0.2%	0.1%	0.3%	0.3%	0.2%	0.2%	0.2%	0.2%	0.2%
k_Bacteria;p_Firmicutes;c_Clostridia;o_BSA2B-08;f_g	0.2%	0.1%	0.2%	0.1%	0.1%	0.2%	0.2%	0.1%	0.1%	0.2%	0.2%	0.2%	0.2%	0.2%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;Other;Other	0.2%	0.2%	0.2%	0.2%	0.2%	0.2%	0.2%	0.2%	0.2%	0.2%	0.2%	0.2%	0.2%	0.2%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_g	0.6%	0.6%	0.8%	0.8%	0.5%	0.4%	0.8%	0.8%	0.7%	0.6%	0.3%	0.2%	0.2%	0.2%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Caldicoprobacteraceae;g_Caldicoprobacter	2.7%	3.6%	2.9%	2.9%	4.1%	2.6%	1.9%	3.8%	2.8%	2.2%	2.0%	2.4%	1.6%	1.6%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Christensenellaceae;g_	0.2%	0.3%	0.3%	0.2%	0.4%	0.2%	0.3%	0.2%	0.2%	0.1%	0.2%	0.3%	0.2%	0.2%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;Other	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_	0.8%	1.0%	0.9%	0.7%	1.8%	1.1%	1.3%	0.8%	0.6%	0.4%	0.5%	0.5%	0.5%	0.5%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_02d06	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Alkaliphilus	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Clostridium	7.4%	15.8%	9.7%	8.3%	11.1%	6.4%	4.8%	9.5%	6.5%	4.3%	3.8%	5.2%	3.5%	3.5%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Geoprotobacter_Thermotalea	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Natronincola_Anaerovirgula	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Dehalobacteriaceae;g_Dehalobacterium	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.0%	0.0%	0.1%	0.1%	0.1%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_EtOHg	0.6%	0.8%	1.7%	0.6%	0.7%	0.6%	0.5%	0.4%	0.4%	0.3%	0.2%	0.3%	0.3%	0.3%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Eubacteriaceae;g_	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Eubacteriaceae;g_Anaerofustis	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Eubacteriaceae;g_Garcilla	0.1%	0.1%	0.1%	0.2%	0.0%	0.0%	0.0%	0.2%	0.1%	0.1%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Eubacteriaceae;g_Pseudomambacter_Eubacterium	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Gracilibacteraceae;Other	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Gracilibacteraceae;g_	0.1%	0.1%	0.0%	0.2%	0.0%	0.0%	0.0%	0.1%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Gracilibacteraceae;g_Gracilbacter	0.0%	0.1%	0.1%	0.2%	0.2%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.2%	0.1%	0.1%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Glutispora	0.1%	0.1%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;Other	0.0%	0.1%	0.1%	0.0%	0.0%	0.1%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_	1.1%	2.4%	2.3%	0.8%	2.2%	1.1%	0.6%	1.0%	1.5%	0.5%	0.3%	0.5%	0.2%	0.2%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Butyribivrio	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Coprococcus	0.9%	1.2%	1.4%	1.8%	1.7%	0.7%	0.6%	0.7%	1.7%	0.5%	0.3%	0.3%	0.2%	0.2%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Defluvittalea	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Dorea	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Lachnospira	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Ruminococcus	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;Other	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_	0.4%	0.6%	0.6%	0.5%	0.5%	0.4%	0.3%	0.5%	0.4%	0.3%	0.2%	0.3%	0.2%	0.2%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Dehalobacter_Syntrophobolulus	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.0%	0.0%	0.1%	0.1%	0.1%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Desulfobifobacter	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Desulfovorusinus	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Desulfovulum	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Desulfovirovula	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Desulfurispora	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Pelotomaculum	0.3%	0.2%	0.3%	0.3%	0.5%	0.4%	0.3%	0.4%	0.2%	0.3%	0.2%	0.2%	0.3%	0.3%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Sporotomaculum	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptostreptococcaceae;g_	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;Other	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_	4.6%	5.6%	5.5%	5.6%	5.4%	3.9%	3.3%	5.8%	5.1%	3.9%	4.0%	4.0%	2.8%	2.8%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Anaerotruncus	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Cellulosibacter	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Ruminococcus	0.3%	0.9%	0.9%	0.3%	0.5%	0.2%	0.1%	0.3%	0.4%	0.1%	0.1%	0.1%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Symbiobacteriaceae;g_Symbiobacterium	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Syntrophomonadaceae;g_Syntrophomonas	2.1%	3.2%	2.6%	2.3%	3.1%	1.8%	1.3%	2.9%	1.9%	1.9%	1.5%	1.3%	1.1%	1.1%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_	0.7%	0.3%	0.2%	0.9%	1.2%	0.9%	0.1%	0.7%	0.4%	1.2%	0.9%	0.7%	0.7%	0.7%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_BS43	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Megasphaera	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Selenomonas	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Sporomusa	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Acidaminobacteraceae;g_Guggenheimella	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Mogibacteriaceae;g_Mogibacter	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Mogibacteriaceae;g_Anaerovorax	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Tissierellaceae;Other	0.1%	0.1%	0.1%	0.0%	0.2%	0.1%	0.1%	0.0%	0.1%	0.0%	0.1%	0.1%	0.1%	0.1%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Tissierellaceae;g_g	0.9%	1.0%	1.0%	0.9%	1.6%	1.2%	0.9%	1.0%	0.8%	0.6%	0.4%	0.6%	0.6%	0.6%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Tissierellaceae;g_GW-34	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Tissierellaceae;g_g	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Tissierellaceae;g_Gallicola	3.4%	4.4%	3.1%	2.7%	4.9%	3.3%	3.0%	6.8%	1.					

