

Table S1: Process parameters of the biogas fermenter at time of sampling. These data were kindly determined and provided by Bonalytic GmbH.

Sampling date	Water Quality Parameters																Nutrient Concentrations					
	pH	EC [mS/cm]	VOA [g HAc _{eq} /l]	TIC [g CaCO ₃ /l]	VOA/TIC ratio	NH ₄ +N [g/l]	DM [g/kg]	ODM [g/kg]	Acetic acid [g/l]	Propionic acid [g/l]	Butyric acid [g/l]	Isobutyric acid [g/l]	Valeric acid [g/l]	Isovaleric acid [g/l]	Hexanoic acid [g/l]	Ca [g/kg dm]	K [g/kg dm]	Mg [g/kg dm]	Na [g/kg dm]	P [g/kg dm]	S [g/kg dm]	
5-Mar-2013	7.9	35.6	3.28	18.7	0.18	3.14	103	78.3	0.13	< 0.03	< 0.03	< 0.03	< 0.03	< 0.03	< 0.03	20.7	47.6	7.03	4.61	10.4	5.97	
27-May-2013	8.0	34.2	3.06	17.7	0.17	2.98	87.4	65.6	0.29	< 0.03	< 0.03	< 0.03	< 0.03	< 0.03	< 0.03	16.4	41.8	5.72	2.92	9.38	4.98	
Sampling date	Heavy Metals and Trace Elements																					
	Al [mg/kg dm]	As [mg/kg dm]	B [mg/kg dm]	Ba [mg/kg dm]	Cd [mg/kg dm]	Co [mg/kg dm]	Cr [mg/kg dm]	Cu [mg/kg dm]	Fe [mg/kg dm]	Hg [mg/kg dm]	Li [mg/kg dm]	Mn [mg/kg dm]	Mo [mg/kg dm]	Nb [mg/kg dm]	Ni [mg/kg dm]	Pb [mg/kg dm]	Se [mg/kg dm]	Si [mg/kg dm]	Sn [mg/kg dm]	Sr [mg/kg dm]	V [mg/kg dm]	Zn [mg/kg dm]
5-Mar-2013	870	<15	29.1	26	0.23	2.16	3.91	66.3	4340	<4.2	3.18	313	5.82	<0.3	6.67	2.5	<15	342	<1.4	41.6	2.26	233
27-May-2013	799	<15	30.9	27.2	0.24	1.57	3.12	53.3	3400	<4.2	2.31	333	3.3	<0.3	4.19	1.48	<15	421	<1.4	39.9	1.61	285

EC: Electric conductivity
VOA: Volatile organic acids
HAc_{eq}: Acetic acid equivalent
TIC: Total inorganic carbon
NH₄+N: Ammonium nitrogen
DM: Dry matter
ODM: organic Dry matter

Table S2: Diversity and richness of biogas fermenter samples taken in March and May 2013 based on 16S rRNA gene analysis. OTUs were clustered at 99% sequence similarity level and singleton OTUs (i.e. OTUs with only one sequence assigned to them) were removed.

Sample	^{A)} Observed OTUs	^{B)} Coverage (%)	Shannon index (H')	Chao1
Bacteria biogas fermenter March 2013	994	90	6.5	1101
Archaea biogas fermenter March 2013	59	77	1.9	77
Bacteria biogas fermenter May 2013	1108	92	6.4	1206
Archaea biogas fermenter May 2013	95	97	2.2	98

A) Singleton OTUs not included B) Calculated by comparing number of observed OTUs with Chao1 index

Table S3: Shared OTUs between both biogas fermenter samples.

Shared OTUs	Archaea May	Archaea March	Bacteria March	Bacteria May
Archaea May	95	52	0	0
Archaea March	52	59	0	0
Bacteria March	0	0	994	691
Bacteria May	0	0	691	1108

Table S4: Bin overview (tax. Assignment, completeness, contamination, other assembly stats)

good bins						
Bin-ID	Taxonomy (Consensus Score > 0.8)	completeness	contamination	Mb	N50 for contigs	length of largest contig (Kb)
pb121	Bacteria Fibrobacteres Acidobacteria group Fibrobacteria Fibrobacteres Fibrobacteraceae Fibrobacter Fibrobacter succinogenes	98.84	4.40	2.645	19.300	217
pb122	Bacteria Fibrobacteres Acidobacteria group Fibrobacteria Fibrobacteres Fibrobacteraceae Fibrobacter Fibrobacter succinogenes	98.74	2.36	2.117	11.850	259
pb172	Bacteria Bacteroidetes Chlorobi group Bacteroidetes	96.24	2.07	2.501	19.077	233
pb190	Bacteria Firmicutes Clostridia	98.28	6.74	2.230	16.089	234
pb192-1	Bacteria Firmicutes Clostridia	96.77	1.61	2.250	129.429	36
pb212	Bacteria	98.31	6.78	2.485	22.750	210
pb215	Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae Ruminiclostridium	100.00	8.77	3.177	45.291	144
pb31	Bacteria Spirochaetes Spirochaetia Spirochaetales Spirochaetaceae Treponema	99.30	7.23	2.150	16.062	213
pb35-2	Bacteria Firmicutes Clostridia Clostridiales Lachnospiraceae Lachnoclostridium Lachnoclostridium phytofermentans	98.30	8.68	2.710	28.326	143
pb40	Bacteria Firmicutes Clostridia	96.61	2.97	2.357	33.655	139
pb6-1	Bacteria Firmicutes Clostridia	96.00	0.13	1.469	12.735	160
pb6-1	Bacteria Firmicutes Clostridia	96.00	1.33	1.750	105.819	37
pb65	Bacteria Firmicutes Clostridia Clostridiales	98.60	7.89	2.314	66.410	77
pb69	Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Porphyromonadaceae	96.24	3.73	1.741	17.355	181
pb75-1	Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae	96.55	8.62	1.767	21.374	134
pb80	Bacteria Firmicutes	95.10	2.97	2.648	77.072	95
pb85	Archaea Euryarchaeota Methanomicrobia Methanosarcinales Methanosarcinaceae Methanosarcina Methanosarcina barkeri	99.84	0.03	3.431	70.311	111
pb88	Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales	96.24	1.08	3.549	17.475	336
pb90	Bacteria Spirochaetes Spirochaetia Spirochaetales Spirochaetaceae Treponema	99.30	9.91	2.444	22.018	215
pb97	Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae	97.09	1.43	2.143	36.708	91
nearly complete genome drafts						
Bin-ID	Taxonomy (Consensus Score > 0.8)	completeness	contamination	Mb	N50 for contigs	length of largest contig (Kb)
107	Bacteria Firmicutes Clostridia Clostridiales	91.03	1.34	2.012	67.725	71
121	Bacteria Firmicutes Clostridia	93.22	0.00	2.043	51.306	93
125	Bacteria Bacteroidetes Chlorobi group Bacteroidetes	96.24	1.34	2.340	20.117	159
145	Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Porphyromonadaceae Paludibacter Paludibacter propionigenes	98.92	0.46	1.932	88.660	96
159	Bacteria Firmicutes Clostridia Clostridiales	97.90	3.85	2.319	56.632	73
184	Bacteria Chlamydiae Verucomicrobia group Verucomicrobia	93.92	3.58	4.152	13.165	446
18	Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae Mageeibacillus Mageeibacillus indolicus	94.44	1.77	2.121	15.834	248
45	Bacteria Bacteroidetes Chlorobi group Bacteroidetes	95.59	0.81	1.986	17.036	164
96	Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae	95.40	0.00	2.004	186.963	124
pb186-2	Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae Ruminiclostridium Ruminiclostridium thermocellum	97.65	2.57	3.255	16.777	281
pb186-2	Bacteria Firmicutes Clostridia Clostridiales Lachnospiraceae Lachnoclostridium Lachnoclostridium phytofermentans	90.72	2.06	2.106	39.480	70
pb205	Bacteria Firmicutes Clostridia Clostridiales	94.38	4.20	2.087	55.007	78
pb233-1	Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae	93.96	1.69	2.090	46.118	69
pb235-2	Bacteria Firmicutes Clostridia Clostridiales	93.17	4.79	2.016	17.760	148
pb237	Bacteria Firmicutes Clostridia Clostridiales	90.03	2.82	1.655	8.072	296
pb35-1	Bacteria Firmicutes Clostridia Clostridiales Lachnospiraceae Lachnoclostridium	91.05	1.34	2.288	51.148	66
pb47	Bacteria Chlamydiae Verucomicrobia group Verucomicrobia	90.03	3.41	2.785	22.427	224
pb60-2	Bacteria Firmicutes	92.58	2.54	2.729	106.815	75
pb61-1	Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae	93.10	0.67	1.733	9.928	227
pb84	Bacteria Firmicutes Bacilli Bacillales Bacillaceae Oceanobacillus Oceanobacillus thevenesi	92.88	1.90	2.351	14.552	208
nearly complete pangenome drafts						
Bin-ID	Taxonomy (Consensus Score > 0.8)	completeness	contamination	Mb	N50 for contigs	length of largest contig (Kb)
114	Bacteria Firmicutes Clostridia	90.80	19.75	2.456	14.476	308
118	Bacteria Bacteroidetes Chlorobi group Bacteroidetes	96.55	8.62	1.717	7.488	293
120	Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales	98.57	5.86	3.371	107.165	113
122	Bacteria Firmicutes	98.28	15.52	2.756	98.798	72
128	Bacteria Firmicutes Clostridia Clostridiales	98.28	38.09	2.304	47.314	91
131	Bacteria Firmicutes Clostridia Clostridiales	98.39	27.90	2.771	42.529	119
135	Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales	92.24	28.62	3.713	8.219	565
137	Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae	96.64	17.24	2.021	32.847	109
138	Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales	100.00	50.71	3.221	14.313	376
142	Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales	98.28	36.39	3.603	19.789	334
149	Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales	100.00	91.44	5.381	11.253	648
162	Bacteria Firmicutes Clostridia	94.23	13.46	2.647	74.664	90
165	Bacteria Firmicutes Clostridia Clostridiales Peptococcaceae Pelotomaculum Pelotomaculum thermopropionicum	94.94	11.18	2.864	56.541	99
167	Bacteria Firmicutes Clostridia Clostridiales	99.30	16.08	2.243	50.875	72
16	Bacteria Firmicutes Clostridia	99.19	42.87	3.191	8.807	580
172	Bacteria Firmicutes Clostridia Clostridiales	93.71	11.89	2.446	58.832	87
179	Bacteria Actinobacteria Actinobacteria Micrococcales	100.00	61.99	5.944	12.829	692
17	Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales	100.00	98.78	6.802	50.520	301
180	Bacteria	98.67	31.39	2.400	45.126	108
188	Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales	94.05	19.03	2.278	40.215	171
200	Bacteria Actinobacteria Actinobacteria Corynebacteriales Corynebacteriaceae Corynebacterium	100.00	56.62	4.101	17.663	505
201	Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales Porphyromonadaceae Paludibacter Paludibacter propionigenes	93.10	23.28	4.195	17.714	390
204	Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae Mageeibacillus Mageeibacillus indolicus	96.34	13.65	2.387	33.234	160
23	Bacteria	96.70	19.17	24.083	226	240,613
36	Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales	100.00	25.86	3.075	48.908	106
41	Bacteria	98.56	12.00	1.999	64.174	61
43	Bacteria Firmicutes Clostridia Clostridiales	99.07	38.58	3.220	95.854	89
48	Archaea Euryarchaeota Methanobacteria Methanobacteriales Methanobacteriaceae Methanobacterium	99.07	19.63	2.241	47.585	99
81	Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae	95.19	11.21	2.187	58.951	96
82	Bacteria Firmicutes Clostridia Clostridiales	95.80	11.19	3.264	29.444	199
pb15-1	Bacteria	98.31	5.93	2.451	9.604	394
pb186-2	Bacteria Bacteroidetes Chlorobi group Bacteroidetes	95.48	7.14	2.355	22.487	183
pb189	Bacteria	99.94	7.89	5.025	39.690	217
pb38-1	Bacteria Tenericutes Mollicutes Acholeplasmatales Acholeplasmataceae	92.06	6.33	1.123	24.983	80
pb70	Bacteria Firmicutes Clostridia Clostridiales Clostridiaceae Alkaliphilus Alkaliphilus oremlandii	91.13	5.20	2.413	28.556	201
pb78-1	Bacteria Firmicutes	94.07	8.47	2.097	60.316	53
pb93-2	Bacteria Firmicutes Clostridia Clostridiales Syntrophomonadaceae	97.92	5.17	2.625	69.056	80
incomplete genome drafts						
Bin-ID	Taxonomy (Consensus Score > 0.8)	completeness	contamination	Mb	N50 for contigs	length of largest contig (Kb)
109	Bacteria Firmicutes Erysipelotrichia Erysipelotrichales Erysipelotrichaceae Erysipelotricha Erysipelotricha rhusiopathiae	79.90	4.04	1.120	5.151	279
141	Bacteria Proteobacteria delta epsilon subdivisions Deltaproteobacteria	73.99	2.58	2.545	5.013	674
147	Bacteria Firmicutes Clostridia	90.25	6.79	2.117	42.492	105
175	Bacteria Spirochaetes Spirochaetia Spirochaetales Spirochaetaceae Sphaerochaeta	64.12	2.84	1.015	2.321	476
178	Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales	80.46	1.40	1.499	8.230	255
1	Bacteria Firmicutes Clostridia Clostridiales	73.48	2.62	1.283	4.246	351
20	Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae	64.22	2.35	1.547	2.173	761
2	Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae	63.64	4.80	2.007	1.864	1116
33	Archaea Euryarchaeota	71.64	2.26	1.172	2.027	615
9	Bacteria Firmicutes Clostridia Clostridiales	61.88	5.44	1.007	2.137	507
49	Bacteria Firmicutes Clostridia Halanaerobiales Halanaerobiaceae	72.10	5.26	1.233	1.959	669
72	Bacteria Fibrobacteres Acidobacteria group Acidobacteria	68.80	5.41	2.193	2.569	960
75	Bacteria Firmicutes Clostridia	71.08	3.04	1.380	2.916	553
pb108-3	Bacteria Firmicutes Clostridia	85.35	5.23	2.207	37.524	86
pb162	Bacteria Firmicutes Clostridia Clostridiales	88.36	7.07	1.811	3.318	669
pb173	Bacteria	87.77	4.39	0.826	12.005	102
pb177	Bacteria Firmicutes Clostridia	88.45	3.06	2.110	5.461	512
pb185	Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae Mageeibacillus Mageeibacillus indolicus	84.97	4.18	1.728	4.443	513
pb208-2	Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales	81.97	5.41	2.138	11.327	239
pb207	Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales	87.50	0.50	2.513	11.906	302
pb233-3	Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae Mageeibacillus Mageeibacillus indolicus	84.14	4.49	1.413	11.939	166
pb235-1	Bacteria Firmicutes Clostridia Clostridiales Lachnospiraceae Lachnoclostridium	86.35	4.36	2.336	71.225	50
pb243	Bacteria Spirochaetes Spirochaetia Spirochaetales Spirochaetaceae Sphaerochaeta Sphaerochaeta globosa	89.14	3.51	2.397	12.472	319
pb246	Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae	85.81	5.09	1.580	3.920	490
pb2	Bacteria Bacteroidetes Chlorobi group Bacteroidetes Bacteroidia Bacteroidales	82.22	5.20	2.148	3.435	757
pb30	Bacteria Planctomycetes Planctomycetia Planctomycetales Planctomycetaceae	87.12	0.99	3.035	7.797	516
pb6-2	Bacteria	88.55	1.82	1.390	8.194	254

Table S5: Blastp results and MEGAN LCA assignment of 100 ORFs with the highest numbers of mapped reads in the biogas fermenter

ORF	Numer of mapped RNA reads	Top hit description	Hit Length	Max Score	Total Score	Query coverage (in %)	E-Value	Max. Identity	MEGAN 5 LCA taxonomic assignment	
contig-80_19653_7	1072827	methyl-coenzyme M reductase subunit B [uncultured archaeon]	434	748.043	748.043	100	0	99	environmental samples -<Archaea>	
contig-80_13866_1	930872	hypothetical protein [Methanoculleus bourgensis] >gi 396938205 emb CCJ35460.1	518	615.15	615.15	103	0	67	Methanoculleus	
contig-80_13497_1	856474	hypothetical protein AA931_10905 [Peptococcaceae bacterium 1109]	818	603.979	603.979	99	0	69	Peptococcaceae	
contig-80_21488_7	820923	PTS mannitol IIC component [Enterococcus pallens] >gi 486865160 gb EOH97972.1	586	725.702	725.702	100	0	62	Lactobacillales	
contig-80_168684_1	795758	No hit							No hits	
contig-80_58347_5	718705	methyl-coenzyme M reductase subunit A [uncultured archaeon]	568	752.281	752.281	100	0	100	Archaea	
contig-80_23290_4	684024	extracellular solute-binding protein family 5 [Firmicutes bacterium CAG-449]	860	413.305	413.305	82	9.79E-127	37	environmental samples <clostridial firmicutes>	
contig-80_2468_2	560253	ABC transporter substrate-binding protein [Limnochorda pilosa]	576	482.256	482.256	94	5.37E-160	45	Halanaerobium	
contig-80_89734_2	448685	formate dehydrogenase subunit alpha [Methanoculleus bourgensis] >gi 396939866 emb CCJ37121.1	689	1335.09	1335.09	99	0	90	Methanoculleus	
contig-80_71905_1	448196	hypothetical protein AA931_11200 [Peptococcaceae bacterium 1109]	555	957.592	957.592	99	0	81	Peptococcaceae	
contig-80_58347_4	439480	methyl-coenzyme M reductase subunit G [uncultured archaeon]	253	525.783	525.783	97	0	99	Archaea	
contig-80_21426_21	426197	hypothetical protein AA931_00620 [Peptococcaceae bacterium 1109]	461	157.147	157.147	105	6.77E-39	29	Peptococcaceae	
contig-80_3861_2	397581	hypothetical protein UP_1185 [Limnochorda pilosa]	3410	2801.16	3385.0382	95	0	51	Not assigned	
contig-80_33291_1	396617	hypothetical protein AA931_00290 [Peptococcaceae bacterium 1109]	818	139.043	139.043	109	1.26E-31	30	Peptococcaceae	
contig-80_201192_1	378635	methyleneletrahydromethanopterin reductase [Methanoculleus bourgensis] >gi 396939342 emb CCJ3659	330	623.624	623.624	99	0	95	Methanomicrobiaceae	
contig-80_11213_1	370600	sugar ABC transporter substrate-binding protein [Limnochorda pilosa]	401	408.297	408.297	94	3.25E-136	54	Not assigned	
contig-80_82829_2	355530	F420-dependent NADP reductase [Methanosphaelaera palustris] >gi 219547574 gb ACL18024.1	226	316.62	316.62	99	1.21E-105	76	Methanosphaelaera	
contig-80_32942_2	353487	hypothetical protein AA931_11200 [Peptococcaceae bacterium 1109]	555	967.992	967.992	100	0	83	Peptococcaceae	
contig-80_23686_1	346915	hypothetical protein AA931_10905 [Peptococcaceae bacterium 1109]	818	460.299	460.299	99	4.40E-152	64	Peptococcaceae	
contig-80_201084_1	343033	hypothetical protein AA931_10905 [Peptococcaceae bacterium 1109]	818	408.297	408.297	99	2.28E-132	60	Peptococcaceae	
contig-80_3956_1	337076	pyruvate flavodoxin oxidoreductase [Clostridiales bacterium mt11]	1176	1831.61	1831.61	99	0	72	Clostridia	
contig-80_183577_1	313105	hypothetical protein AA931_00290 [Peptococcaceae bacterium 1109]	818	164.851	164.851	106	6.48E-42	39	Firmicutes	
contig-80_226378_1	306822	hypothetical protein [Erysipelotrichaceae bacterium NK30112]	646	352.058	352.058	100	5.90E-112	52	Firmicutes	
contig-80_8571_8	272301	hypothetical protein AA931_10905 [Peptococcaceae bacterium 1109]	818	1228.77	1228.77	99	0	71	Peptococcaceae	
contig-80_38211_5	268888	hypothetical protein AA931_00290 [Peptococcaceae bacterium 1109]	818	161.77	161.77	100	8.97E-41	37	Peptococcaceae	
contig-80_16430_1	259914	sugar ABC transporter substrate-binding protein [Peptococcaceae bacterium 1109]	329	572.392	572.392	99	0	87	Peptococcaceae	
contig-80_48157_1	259564	hypothetical protein UP_1185 [Limnochorda pilosa]	3410	1344.33	2128.1125	100	0	54	Not assigned	
contig-80_4093_10	245182	ABC transporter substrate-binding protein [Limnochorda pilosa]	576	475.322	475.322	101	3.09E-157	43	Halanaerobium	
contig-80_52000_1	227685	aldehyde oxidoreductase [Ruminococcus gauvreaui]	911	1488.01	1488.01	99	0	76	Clostridiales	
contig-80_22025_2	218182	sugar ABC transporter substrate-binding protein [Limnochorda pilosa]	401	402.134	402.134	94	6.71E-134	53	Not assigned	
contig-80_121403_1	208772	No hit							No hits	
contig-80_58347_3	206726	methyl-coenzyme M reductase subunit C [uncultured archaeon]	207	410.223	410.223	99	4.06E-143	99	Archaea	
contig-80_23408_1	203675	hypothetical protein AA931_12550 [Peptococcaceae bacterium 1109]	630	1219.91	1219.91	99	0	92	Peptococcaceae	
contig-80_9517_9	194115	stage V sporulation protein S1 [Peptococcaceae bacterium 1109]	86	153.68	153.68	98	6.09E-46	89	Firmicutes	
contig-80_25669_1	191007	ABC transporter solute-binding protein [Peptostreptococcaceae bacterium oral taxon 113] >gi 543981515	445	523.472	523.472	92	7.65E-180	61	Bacteria	
contig-80_61065_2	189587	hypothetical protein UP_1185 [Limnochorda pilosa]	3410	288.5	1069.2004	88	1.10E-78	48	Not assigned	
contig-80_21488_5	184607	mannitol-1-phosphate 5-dehydrogenase [Enterococcus raffinosus] >gi 486844990 gb EOH78181.1	379	520.776	520.776	98	0	63	Lactobacillales	
contig-80_312444_1	171786	Multiple sugar-binding periplasmic receptor ChvE [Herbinix sp. S01D]	359	330.102	330.102	102	1.12E-108	63	Firmicutes	
contig-80_55234_3	170774	Multiple sugar-binding periplasmic receptor ChvE [Herbinix sp. S01D]	359	478.404	478.404	99	1.28E-165	70	Firmicutes	
contig-80_11579_1	169839	hypothetical protein [Bacillus sp. ICE]	3124	487.649	3527.844	27	1.20E-134	34	Bacillales	
contig-80_608665_1	168866	hypothetical protein AA931_00620 [Peptococcaceae bacterium 1109]	461	48.1358	48.1358	68	7.96E-04	36	Not assigned	
contig-80_896734_1	168691	methyl CoM reductase alpha subunit, partial [uncultured methanogenic archaeon]	155	213.772	213.772	100	2.64E-68	100	Archaea	
contig-80_52247_3	167803	ABC transporter substrate-binding protein [Anoxybacillus flavithermus]	558	397.897	397.897	97	2.08E-128	44	Bacteria	
contig-80_58347_2	166943	methyl-coenzyme M reductase [Methanoculleus bourgensis] >gi 396939403 emb CCJ36658.1	158	278.485	278.485	99	1.14E-92	84	Methanoculleus	
contig-80_52115_2	165024	membrane protein [Orbacterium parvum] >gi 394704654 gb EFJ2189.1	401	443.736	443.736	93	1.33E-150	65	Firmicutes	
contig-80_602_19	162919	sugar ABC transporter substrate-binding protein [Thermotoga maritima] >gi 15643361 ref NP_228405.1	419	252.292	252.292	102	3.44E-75	36	Bacteria	
contig-80_90256_3	161415	hypothetical protein AA931_10905 [Peptococcaceae bacterium 1109]	818	244.202	244.202	98	1.35E-72	71	Peptococcaceae	
contig-80_390436_1	156123	No hit							No hits	
contig-80_61822_1	155928	ABC transporter substrate-binding protein [Peptococcaceae bacterium 1109]	408	661.759	661.759	95	0	78	Peptococcaceae	
contig-80_39128_3	155666	aldehyde oxidoreductase [Ruminococcus gauvreaui]	911	1476.84	1476.84	99	0	76	Clostridiales	
contig-80_5424_6	154426	Alcohol dehydrogenase, zinc-binding domain protein [Methanocorpusculum labreanum Z]	357	638.262	638.262	99	0	84	Methanocorpusculum	
contig-80_1019865_1	152781	hypothetical protein AA931_10905 [Peptococcaceae bacterium 1109]	818	66.2402	66.2402	92	1.04E-10	64	Peptococcaceae	
contig-80_6460_7	152727	sugar ABC transporter substrate-binding protein [Peptococcaceae bacterium 1109]	527	795.423	795.423	98	0	71	Clostridiales	
contig-80_33866_4	150932	hypothetical protein BN140_0535 [Methanoculleus bourgensis MS2]	355	462.996	462.996	101	3.24E-159	64	Methanoculleus	
contig-80_184701_1	149566	methyl-coenzyme M reductase [Methanoculleus bourgensis] >gi 396939402 emb CCJ36657.1	434	614.379	614.379	100	0	91	Archaea	
contig-80_14342_7	144760	ABC transporter substrate-binding protein [Limnochorda pilosa]	576	479.174	479.174	101	9.41E-159	43	Halanaerobium	
contig-80_6425_10	143590	sugar ABC transporter substrate-binding protein [Peptococcaceae bacterium 1109]	353	592.423	592.423	97	0	84	Clostridiales	
contig-80_76725_1	140566	hypothetical surface-anchored protein [Coprobaillus sp. CAG-698]	1559	162.155	162.155	81	3.03E-37	28	Coprobaillales	
contig-80_58347_1	139161	methyl-coenzyme M reductase subunit B [uncultured archaeon]	434	191.045	191.045	98	2.37E-56	100	environmental samples -<Archaea>	
contig-80_517402_1	138608	hypothetical protein AA931_00620 [Peptococcaceae bacterium 1109]	461	58.151	58.151	102	3.05E-07	41	Peptococcaceae	
contig-80_10299_6	135002	No hit							No hits	
contig-80_72398_1	134486	peptidase S8 [Halanaerobium hydrogeniformans] >gi 311903494 gb ADQ13935.1	619	206.838	206.838	58	6.84E-55	40	Halanaerobiales	
contig-80_7871_10	131473	pyruvate phosphate dikinase [Peptococcaceae bacterium 1109]	876	1468.37	1468.37	99	0	79	Peptococcaceae	
contig-80_629047_1	129364	peptidase S8 [Halanaerobium hydrogeniformans] >gi 311903494 gb ADQ13935.1	619	97.0561	97.0561	90	2.48E-20	38	Halanaerobium	
contig-80_179236_2	128304	transposase [[Clostridium] cellulolyticum] >gi 219999295 gb ACL75896.1	424	375.555	375.555	95	1.14E-124	62	Clostridiales	
contig-80_213664_2	127979	No hit							No hits	
contig-80_1058524_1	127279	hypothetical protein AA931_10905 [Peptococcaceae bacterium 1109]	818	102.449	102.449	100	5.31E-23	59	cellular organisms	
contig-80_6458_4	126414	dipeptide-binding ABC transporter substrate-binding protein (TC 3.A.1.5.2) [Halanaerobium saccharolyticum]	603	523.472	523.472	95	2.61E-175	45	Bacteria	
contig-80_2203_3	125589	predicted solute binding protein [Beilinia caldissitulae]	853	879.396	879.396	96	54	0	54	Bacteria3
contig-80_507757_1	124932	peptidase S8 [Halanaerobium hydrogeniformans] >gi 311903494 gb ADQ13935.1	619	139.043	139.043	100	5.35E-35	46	Halanaerobiales	
contig-80_29131_3	123233	lipoprotein [Deffluvitoga tunisiensis] >gi 762220813 emb CEP78642.1	372	412.92	412.92	101	6.19E-139	55	Bacteria	
contig-80_5759_12	121826	lipoprotein [Deffluvitoga tunisiensis] >gi 762220813 emb CEP78642.1	372	414.846	414.846	98	8.18E-140	54	Bacteria	
contig-80_4230_3	121584	sugar ABC transporter substrate-binding protein [Paenibacillus sp. VT-400] >gi 835055943 gb KLU54630.1	551	390.963	390.963	95	1.75E-125	41	Bacteria	
contig-80_650971_1	121172	No hit							No hits	
contig-80_29649_6	119889	Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OppA (TC 3.A.1.5.1) [[Clostridium]	573	383.645	383.645	98	3.59E-124	46	Clostridiaceae	
contig-80_3672_3	117120	NADH:ubiquinone oxidoreductase [Eubacterium acidaminophilum] >gi 595612498 gb AHM56143.1	582	820.846	820.846	99	0	66	Bacteria	
contig-80_13664_7	115796	ABC transporter substrate-binding protein [Limnochorda pilosa]	422	585.874	585.874	88	0	73	root	
contig-80_91792_2	113864	hypothetical protein [Ruminococcus] torques] >gi 145848012 gb EDK24930.1	390	338.191	338.191	99	2.35E-111	67	Clostridiales	
contig-80_9933_1	111172	formate transporter [Methanoculleus bourgensis] >gi 396938507 emb CCJ35762.1	290	413.305	413.305	99	1.46E-142	86	Methanoculleus	
contig-80_18652_2	109324	hypothetical protein [Kosmotoga pacifica]	1364	1205.66	2140.482	96	0	57	Thermotogaceae	
contig-80_2215_4	102178	hypothetical protein AA931_02620 [Peptococcaceae bacterium 1109]	706	954.51	954.51	99	0	65	Peptococcaceae	
contig-80_40526_3	101789	ABC transporter substrate-binding protein [Bacillus sp. FIAT-27997] >gi 899711270 gb KMY48284.1	447	266.159	266.159	95	3.14E-80	39	Bacteria	
contig-80_1684_11	100527	MULTISPECIES: NADP-dependent alcohol dehydrogenase [Butyrivibrio]	355	561.992	561.992	98	0	75	Bacteria	
contig-80_17330_4	100441	ABC transporter substrate-binding protein [Geobacillus sp. C56-T3] >gi 297253216 gb ADI26662.1	556	399.053	399.053	86	2.74E-128	44	Bacteria	
contig-80_1410_4	100129	hypothetical protein AA931_10905 [Peptococcaceae bacterium 1109]	818	1189.48	1189.48	99	0	68	Peptococcaceae	
contig-80_57905_5	99665	methyl-coenzyme M reductase [Methanoculleus bourgensis] >gi 396939406 emb CCJ36661.1	568	717.227	717.227	100	0	91	Archaea	
contig-80_3672_2	99558	putative PAS/PAC sensor protein [Clostridium sp. CAG-1013]	557	592.808	592.808	99	0	49	Bacteria	
contig-80_110_94	98888	methyl-coenzyme M reductase [Methanosarcina sp. E03.2] >gi 931612420 gb KPI45056.1	571	1186.02	1186.02	99	0	99	Methanosarcina	
contig-80_57603_3	97671	hypothetical protein [Thermogemmatipora carboxidivorans]	412	206.453	206.453	82	1.47E-57	32	Bacteria	
contig-80_11012_2	96689	LacI family transcriptional regulator [Peptococcaceae bacterium 1109]	311	554.673	554.673	100	0	87	Peptococcaceae	
contig-80_1090054_1	94753	hypothetical protein AA931_10905 [Peptococcaceae bacterium 1109]	818	104.76	104.76	100	5.34E-24	66	Peptococcaceae	
contig-80_8113_19	94574	translation elongation factor Tu [Treponema leathinolyticum] >gi 543988696 gb ERJ91832.1	395	727.628	727.628	99	0	87	Treponema	
contig-80_65396_1	91677	hypothetical protein UP_1185 [Limnochorda pilosa]	3410	607.446	715.6588	95	0	61	Not assigned	
contig-80_373348_1	91642	hypothetical protein [Levella massiliensis]	457	293.893	293.893	96	6.19E-93	66	Firmicutes	
contig-80_2420_8	91492	DNA-binding protein [Peptococcaceae bacterium 1109]	92	142.895	142.895	98	1.82E-41	78	Peptococcaceae	
contig-80_1										

Table S6: Results of an iterative protein sequence search using Jackhmmer (hmmer 3.1 package) to identify potential cellulosomal scaffoldin proteins in the metagenomic datasets using a score cutoff of 700

ORF	Cellulosomal scaffoldin query	E-value	score	Assigned to bin ID	
contig-80_10910_2	CipC_[Clostridium_cellulolyticum -	0	2112.4	pb35-1	Biogas fermenter dataset
contig-80_24290_1	CipC_[Clostridium_cellulolyticum -	1.2e-221	745.4	pb235-1	
contig-80_7156_9	CipA_[Clostridium_thermocellum] -	0	3156.8	96	
No Hits					Elephant feces dataset
rumenHiSeq_NODE_1839379_len_402040_cov_3_588501_369	ScaB_[Ruminococcus_flavefaciens_17] -	0	1996		Cow rumen dataset
rumenHiSeq_NODE_2071562_len_94063_cov_3_802749_50	ScaB_[Ruminococcus_flavefaciens_17] -	0	1978		