

Supplementary material

The Supplementary file contains the following tables and figures: archaea nMDS plot (**Figure S1**), bacteria nMDS plot (**Figure S2**), DESeq2 results (**Figure S3**), long-term co-digestion functional data (**Figure S4**), and APLs organic constituents quantified by GC-FID analysis. (**Table S1**).

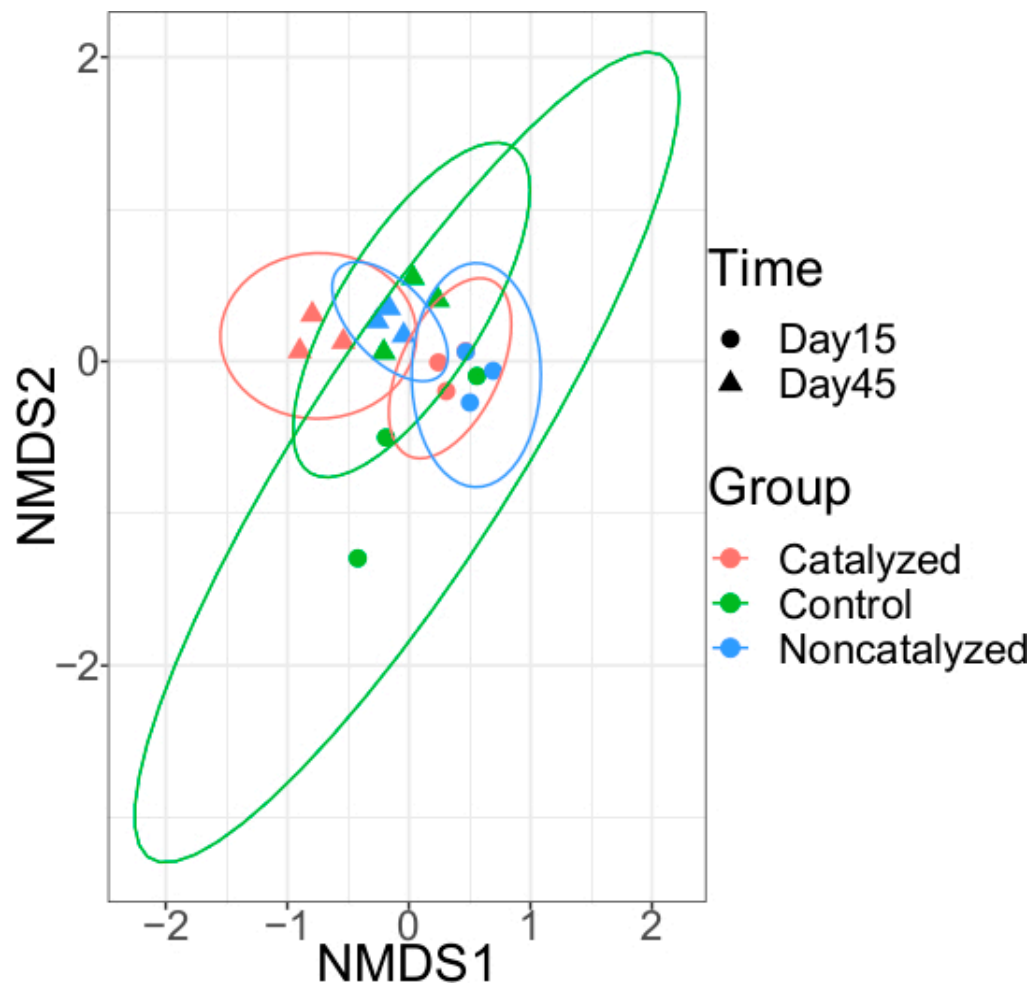


Figure S1. Archaea nMDS plot. Ellipses represent 95% confidence intervals for the three points (each group represents the three triplicate digesters). On day 15, all digester archaeal communities were similar. Exposure to catalyzed APL for 45 days altered the archaeal community compared to control digester communities, whereas the archaeal communities in digesters fed non-catalyzed APL were more similar

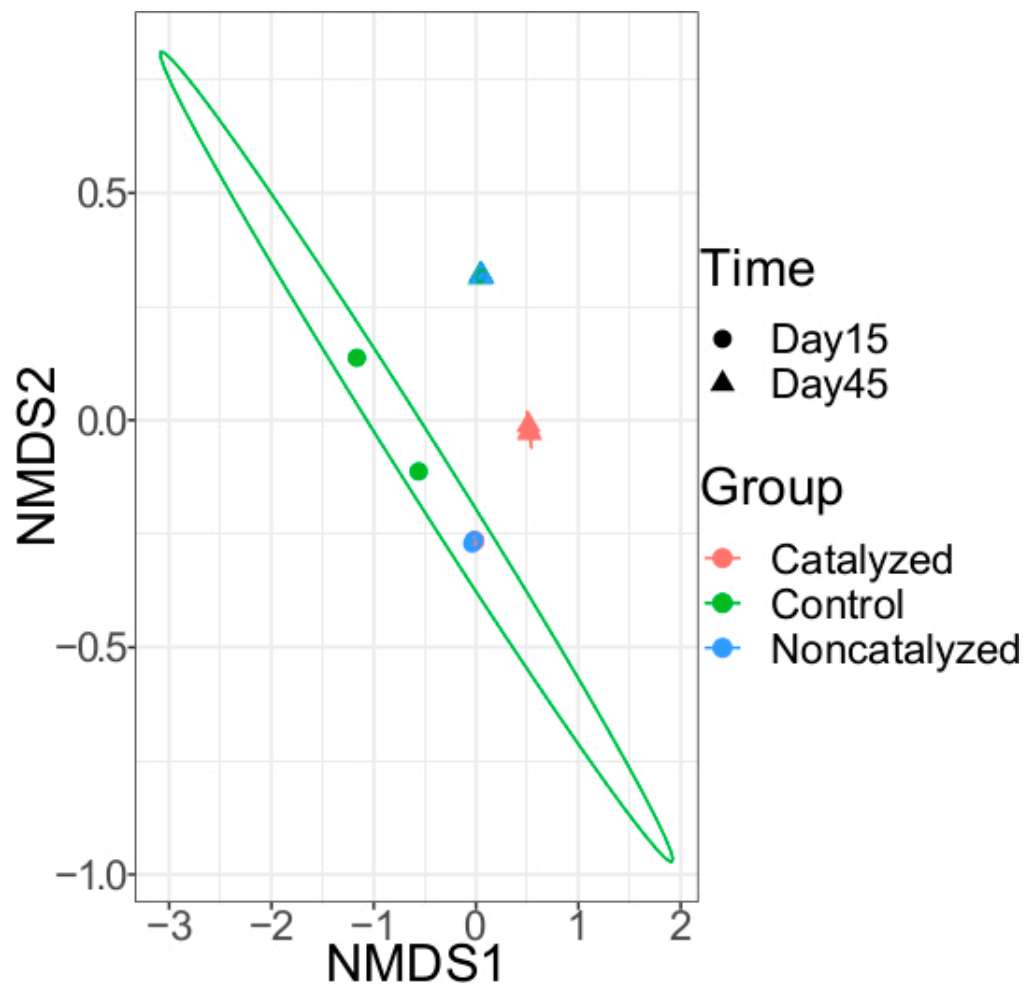
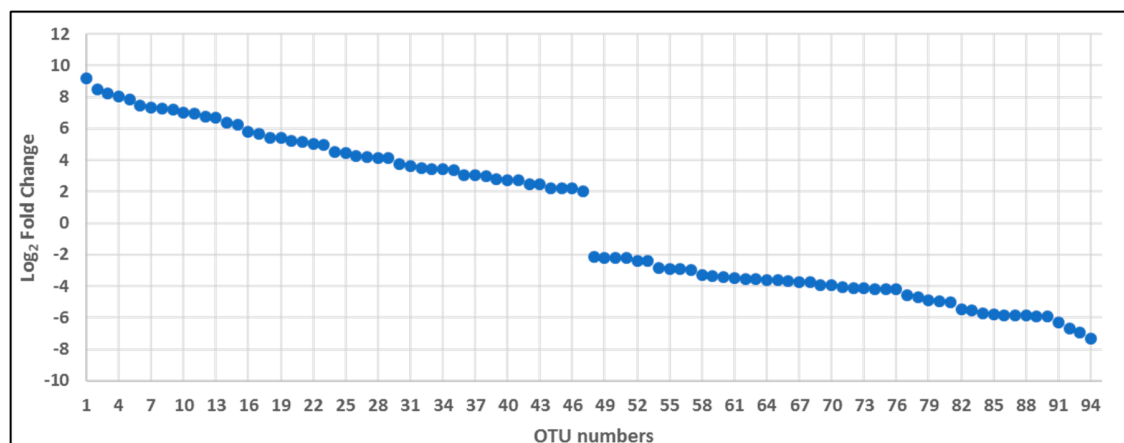


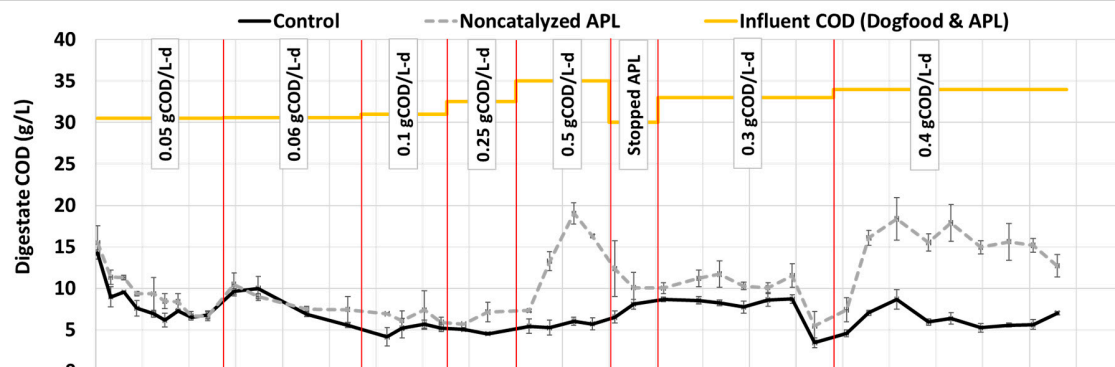
Figure S2. Bacteria nMDS plot. Ellipses represent 95% confidence intervals for triplicate digesters (each group represents the three triplicate digesters). Some ellipses are small and not visible. On day 15, all digester bacterial communities were similar. On day 45, bacterial communities in digesters fed catalyzed APL was significantly different from bacterial communities control digesters and digesters fed non-catalyzed APL. The points representing catalyzed digesters on day 15 and non-catalyzed digesters on day 15 overlap. Also, the points representing control digesters on day 45 and non-catalyzed digesters on day 45 overlap.



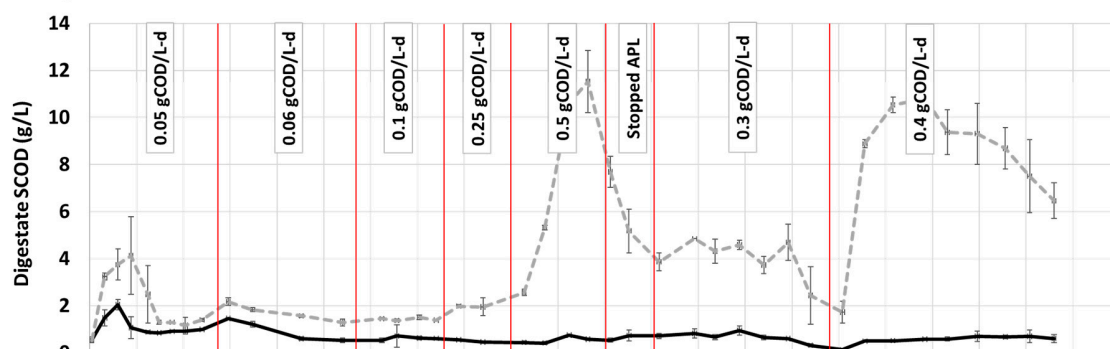
OTU	Family	Genus	Log ₂ Fold change	OTU	Family	Genus	Log ₂ Fold change
1	Enterococcaceae	Enterococcus	9.2	48	Rikenellaceae	Rikenella	-2.1
2	Rikenellaceae	Rikenella	8.5	49	Syntrophomonadaceae	Syntrophomonas	-2.2
3	Porphyromonadaceae	Proteiniphilum	8.3	50	Cloacimonetes	Cloacimonas	-2.2
4	Porphyromonadaceae	Proteiniphilum	8.0	51	Puniceicoccaceae	Puniceicoccus	-2.2
5	Ruminococcaceae	Ruminiclostridium	7.8	52	Verrucomicrobiaceae	Verrucomicrobium	-2.4
6	Desulfovibrionaceae	Desulfovibrio	7.5	53	Endomicrobia	Endomicrobium	-2.4
7	Enterococcaceae	Enterococcus	7.4	54	Rikenellaceae	Rikenella	-2.9
8	Porphyromonadaceae	Proteiniphilum	7.3	55	Deferribacteraceae	Deferribacter	-2.9
9	Ruminococcaceae	Acetivibrio	7.2	56	Methanosaetaceae	Methanosaeta	-2.9
10	Ruminococcaceae	Sporobacter	7.0	57	Deferribacteraceae	Deferribacter	-3.0
11	Syntrophomonadaceae	Syntrophomonas	7.0	58	Eubacteriaceae	Acetobacterium	-3.3
12	Ruminococcaceae	Ruminiclostridium	6.8	59	Rikenellaceae	Rikenella	-3.3
13	Ruminococcaceae	Soleaferrea	6.7	60	Geobacteraceae	Geobacter	-3.4
14	Ruminococcaceae	Ruminiclostridium	6.4	61	Syntrophobacteraceae	Syntrophobacter	-3.5
15	Enterococcaceae	Enterococcus	6.3	62	Eubacteriaceae	Acetobacterium	-3.5
16	Eubacteriaceae	Eubacterium	5.8	63	Thermotogaceae	Kosmotoga	-3.5
17	Eubacteriaceae	Eubacterium	5.7	64	Syntrophorhabdaceae	Syntrophorhabdus	-3.6
18	Ruminococcaceae	Acetivibrio	5.4	65	Eubacteriaceae	Acetobacterium	-3.6
19	Prevotellaceae	Prevotella	5.4	66	Verrucomicrobiaceae	Verrucomicrobium	-3.7
20	Clostridiaceae	Clostridium	5.2	67	Desulfobacteraceae	Desulfofaba	-3.7
21	Mycoplasmataceae	Mycoplasma	5.2	68	Syntrophaceae	Syntrophus	-3.8
22	Erysipelotrichaceae	Turicibacter	5.0	69	Bacteroidaceae	Bacteroides	-3.9
23	Ruminococcaceae	Ruminococcus	4.9	70	Clostridiaceae	Clostridium	-4.0
24	Clostridiaceae	Proteiniclasticum	4.6	71	Methanosaetaceae	Methanosaeta	-4.1
25	Bacillaceae	Terribacillus	4.4	72	Desulfobacteraceae	Desulfofaba	-4.1
26	Porphyromonadaceae	Parabacteroides	4.2	73	Leptospiraceae	Leptospira	-4.1
27	Ruminococcaceae	Acetivibrio	4.2	74	Bacteroidaceae	Bacteroides	-4.2
28	Enterococcaceae	Enterococcus	4.2	75	Synergistaceae	Synergistes	-4.2
29	Synergistaceae	Synergistes	4.1	76	Syntrophaceae	Smithella	-4.2
30	Campylobacteraceae	Campylobacter	3.8	77	Ruminococcaceae	Ruminococcus	-4.6
31	Bacteroidaceae	Anaerorhabdus	3.6	78	Clostridiaceae	Clostridium	-4.7
32	Peptoniphilaceae	Gallicola	3.5	79	Rubrobacteraceae	Rubrobacter	-4.9
33	Clostridiaceae	Clostridium	3.5	80	Desulfobacteraceae	Desulfofaba	-4.9
34	Verrucomicrobiaceae	Verrucomicrobium	3.4	81	Ruminococcaceae	Ruminococcus	-5.0
35	Bacteroidaceae	Bacteroides	3.4	82	Bacillaceae	Bacillus	-5.5
36	Clostridiales Family XI.	Tissierella	3.1	83	Syntrophaceae	Syntrophus	-5.6
37	Clostridiales Family XI.	Tissierella	3.0	84	Lachnospiraceae	Hespellia	-5.7
38	Syntrophomonadaceae	Syntrophomonas	3.0	85	Ruminococcaceae	Ruminococcus	-5.8
39	Anaerolineaceae	Leptolinea	2.8	86	Clostridiaceae	Clostridium	-5.9
40	Anaerolineaceae	Bellilinea	2.7	87	Synergistaceae	Aminomonas	-5.9
41	Synergistaceae	Cloacibacillus	2.7	88	Holophagaceae	Geothrix	-5.9
42	Clostridiales Family XI.	Sedimentibacter	2.5	89	Ruminococcaceae	Ruminococcus	-5.9
43	Clostridiales Family XI.	Sedimentibacter	2.4	90	Eubacteriaceae	Eubacterium	-5.9
44	Dehalococcoidaceae	Dehalococcoides	2.2	91	Thermotogaceae	Geotoga	-6.3
45	Spirochaetaceae	Treponema	2.2	92	Thermotogaceae	Geotoga	-6.7
46	Clostridiaceae	Clostridium	2.2	93	Clostridiaceae	Clostridium	-6.9
47	Synergistaceae	Synergistes	2.0	94	Eubacteriaceae	Eubacterium	-7.3

Figure S3. DESeq2 results to identify statistically different ($p < 0.001$) OTUs between control digesters and digesters fed catalyzed APL. OTUs with greater/less than ± 2 fold changes are shown. OTUs greater than 2-fold change are more abundant in digesters fed catalyzed APL compared to control digesters.

A



B



C

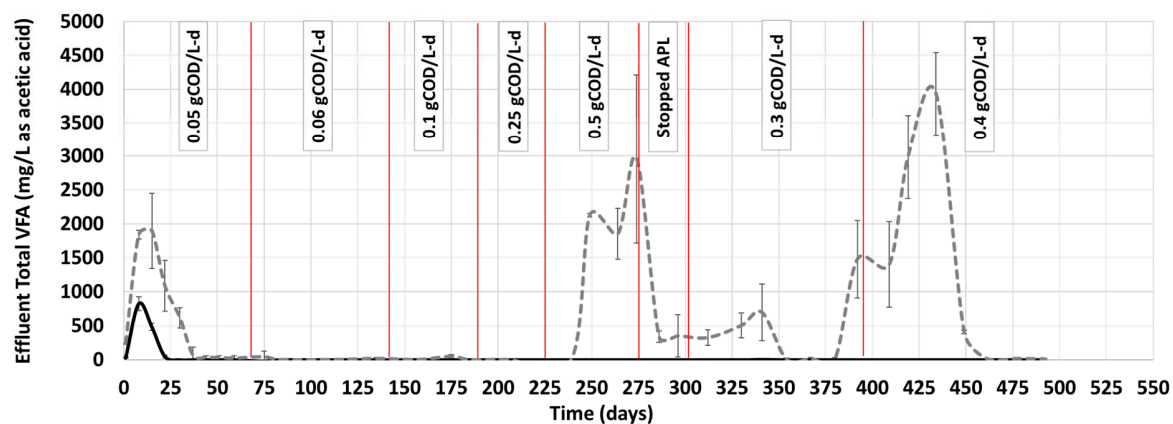


Figure S4. Long-term co-digestion functional data. Average and standard deviation values are from triplicate systems. (A) Digestate COD concentration, (B) Digestate SCOD concentration, (C) Digestate total VFA concentration as mg/L acetic acid. Error bars represent one standard deviation above and below the mean. Some whiskers are small and may not be visible.

Table S1. Organic compounds observed in catalyzed and non-catalyzed APL with and without air stripping, quantified by GC-FID and IC₅₀ values

Compounds quantified by GC-FID (1701 Capillary)		Non-catalyzed APL	Non-catalyzed air-stripped APL	Catalyzed APL	Catalyzed air-stripped APL	IC ₅₀ value
Compound	Molecular weight (g/mol)	% w/w (raw basis) ^a (Average ± Standard deviation)				mg/L
phenol	94.1	0.22 ± 0.13	0.21 ± 0.12	-	-	2100 ^b
styrene	104	0.06 ± 0.03	-	0.05 ± 0.03	-	150 ^c
m-xylene	106	0.21 ± 0.12	0.2 ± 0.12	-	-	250 ^b
o-xylene	106	0.19 ± 0.11	0.18 ± 0.1	-	-	-
ethylbenzene	106	0.22 ± 0.12	-	0.2 ± 0.12	-	160 ^b
m,p-cresol	108	0.44 ± 0.25	0.43 ± 0.25	-	-	890 ^b , 91 ^b
o-cresol	108	0.19 ± 0.11	-	-	-	-
anisole	108	0.09 ± 0.05	0.08 ± 0.05	-	-	720 ^b
4-vinylphenol	120	-	0.75 ± 0.43	-	-	
3-ethylphenol	122	-	0.19 ± 0.11	-	-	
3,4-dimethylphenol	122	-	0.15 ± 0.08	-	-	
3,5-dimethylphenol	122	0.32 ± 0.18	0.3 ± 0.17	-	-	-
2,5-dimethylphenol	122	0.22 ± 0.13	0.21 ± 0.12	-	-	-
2-methylanisole	122	0.16 ± 0.09	0.11 ± 0.06	-	-	-
3-methylanisole	122	0.13 ± 0.08	0.11 ± 0.06	-	-	-
3-methoxy-5-methylphenol	138	0.31 ± 0.18	0.29 ± 0.17	-	-	-
2-methoxy-4-methylphenol	138	0.27 ± 0.16	0.26 ± 0.15	-	-	-
4-ethoxystyrene	148	0.11 ± 0.06	0.1 ± 0.06	-	-	-
4-ethyl-2-methoxyphenol	152	0.12 ± 0.07	0.21 ± 0.12	-	-	-
3,4-dimethoxytoluene	152	0.12 ± 0.07	0.11 ± 0.06	-	-	-
4'-hydroxy-3'-methoxyacetophenone	166	0.33 ± 0.19	0.23 ± 0.13	-	-	-
2-methoxy-4-propylphenol	166	0.11 ± 0.06	0.11 ± 0.07	-	-	-
1,2,3-trimethoxybenzene	168	0.15 ± 0.09	0.16 ± 0.1	-	-	-
2,5-dimethoxybenzylalcohol	168	-	-	0.22 ± 0.13	0.22 ± 0.13	
2',4'-dimethoxyacetophenone	180	0.02 ± 0.01	-	-	-	-
3,5-dimethoxy-4-hydroxybenzaldehyde	182	0.43 ± 0.25	0.25 ± 0.15	0.27 ± 0.15	0.27 ± 0.16	-
3',5'-dimethoxy-4'-hydroxyacetophenone	196	0.54 ± 0.31	0.47 ± 0.27	-	-	-
Total of known compounds	-	4.96	5.11	0.74	0.49	-

^a [1], ^b [2], ^c [3]

References

1. Liu, Z.; McNamara, P.; Zitomer, D. Autocatalytic Pyrolysis of Wastewater Biosolids for Product Upgrading. *Environ. Sci. Technol.* **2017**, *51*, 9808–9816.
2. Blum, D.J.W.; Speece, R.E. A database environmental interspecies of chemical bacteria to toxicity in and its use and correlations comparisons. *Water Environ. Fed.* **1991**, *63*, 198–207.
3. Araya, P.; Chamy, R.; Mota, M.; Alves, M. Biodegradability and toxicity of styrene in the anaerobic digestion process. *Biotechnol. Lett.* **2000**, *22*, 1477–1481.