Supporting information for

Efficient biorefinery of waste activated sludge and vinegar residue into volatile fatty acids: Effect of feedstock conditioning on performance and microbiology

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Supporting tables

Table S1 One-way ANOVA and post hoc analysis on VFAs production in different treatment systems.

Dependent Variable	Treatment	Treatment	Mean Difference	*p* values
VFAs production	Control	TA	-1286.3464*	0.000
		AH	-321.0596	0.542
		SA	-612.5522	0.066
	TA	AH	965.2868*	0.001
		SA	673.7942*	0.036
	AH	SA	-291.4926	0.618

* Different notation indicates a significant difference from post hoc analysis.

Table S2 Genera (relative abundance >1% in at least one samples)

	Control	AH	TA	SA
Levilinea	3.11	4.15	7.45	5.79
Proteiniclasticum	0.32	0.7	7.4	0.95
Acetoanaerobium	3.29	2.79	4.91	5
Gemmobacter	1.25	1.25	2.67	0.98
Cloacibacillus	0.23	0.76	2.47	0.42
Methylocystis	0.29	0.37	2.14	0.47
Hyphomicrobium	0.4	0.29	2.02	0.44
Acinetobacter	1.11	2.16	1.92	1.38
Solibacillus	0	0	1.83	0
Ottowia	5.92	5.75	1.83	4.52
Defluviimonas	0.63	0.67	1.62	1.23
Anderseniella	0.24	0.21	1.6	0.29
Ilumatobacter	0.93	0.91	1.49	1.33
Thermomonas	1.17	1.34	1.33	0.92
Saccharibacteria_genera_incertae_sedis	1.33	1.53	1.32	1.16
Papillibacter	0	0.04	1.25	0.02
Catabacter	0.16	0.35	1.19	0.38
Petrimonas	0.04	0.06	1.1	0.07
Aquihabitans	0.86	0.32	1.06	0.48
Rhodopseudomonas	0.53	0.68	1.05	0.85
Ferrimicrobium	0.01	0	1.03	0
Litorilinea	1.12	0.74	1.02	0.8
Rhodobacter	0.23	0.15	0.99	1.65
Youngiibacter	0.14	0.71	0.91	1.53
Mariniphaga	1.12	3.03	0.63	2.3
Novosphingobium	1.3	1.23	0.56	1.06
Aridibacter	1.26	1.36	0.53	0.99
Clostridium sensu stricto	0.69	1.61	0.48	2.38
Limnobacter	1.58	1.48	0.46	1.14
Ornatilinea	1.1	0.89	0.35	1.32
Thermogutta	0.83	0.73	0.33	1.04
Ferruginibacter	1.91	1.91	0.28	1.33
Thauera	1.9	0.77	0.21	1.41
Gp10	3.78	2.58	0.2	2.35
Povalibacter	1.09	0.93	0.19	0.63
Sulfurovum	0.36	0.22	0.16	2.4
Rhodopirellula	1.34	1.19	0.09	1.32
Comamonas	6.31	5.55	0.06	5.27

Terrimonas	4.38	4.46	0.05	2.84
Parasegetibacter	1.58	1.59	0.02	0.93
Parachlamydia	0.56	0.99	0.01	1.38
Ignavibacterium	1.1	0.58	0.01	0.38
Telmatospirillum	1.31	1.04	0	0.87
Arenimonas	1.85	1.73	0	1.23
unclassified	14.23	13.63	17.45	11.71
Others	27.11	26.57	26.33	25.06

Table S3 Alpha diversity parameters

Name	Barcode	Seq num*[1]	OTU num*1	Shannon index	Chao1 index	Simpson
TA	CGCCAT	87006	2979	5.12	2263.35	0.01
SA	GAAACC	55392	1658	5.31	2341.28	0.01
AH	TCTATT	49258	1598	5.35	2231.57	0.01
Control	AGGCGG	36924	1493	5.36	2069.51	0.02

*[1]: "Seq num" indicated the sequence numbers obtained from the high-throughput sequencing analysis;

*[2]: "OTU num" indicated the classified OTU numbers obtained from the gene sequences with the identity of over 97 %.

Table S4 The eigenvalues of first two canonical axes and their relationships with each environmental factor

	Axis 1	Axis 2
Eigenvalues	0.2950	0.0540
Cumulative percentage variance	80.1%	94.8%
Spr	0.9428	0.2278
Sca	0.9374	0.2637
Methane	0.9593	-0.1203
VFAs	0.9480	-0.0814
HAc	0.5660	0.7499
HPr	0.8590	-0.3427
pH	-0.2392	0.3294

Supporting figures

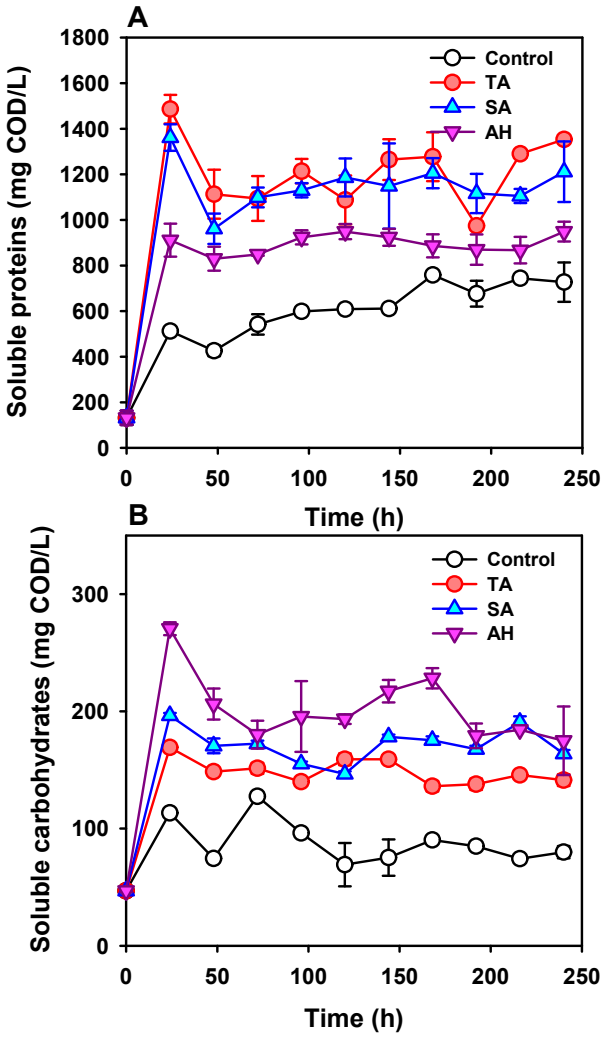

Figure S1 Time-course profiles of soluble proteins (A) and carbohydrates (B) (Note: error bars represent standard deviation).

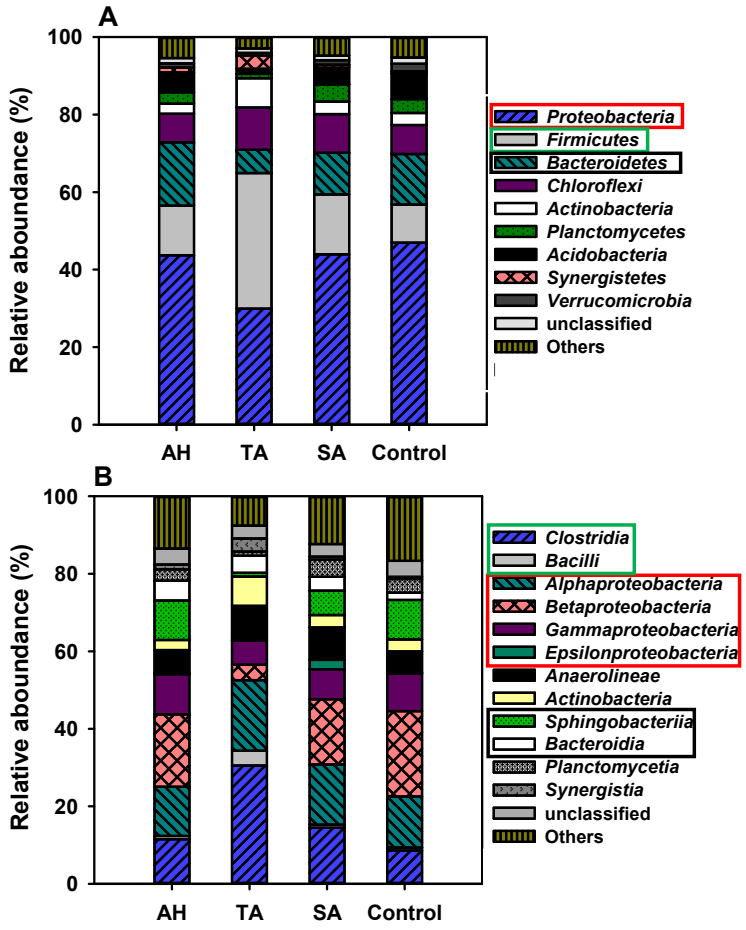

Figure S2 Taxonomic classification of pyrosequences from bacterial communities of five samples at the phyla (A) and class (B) levels.

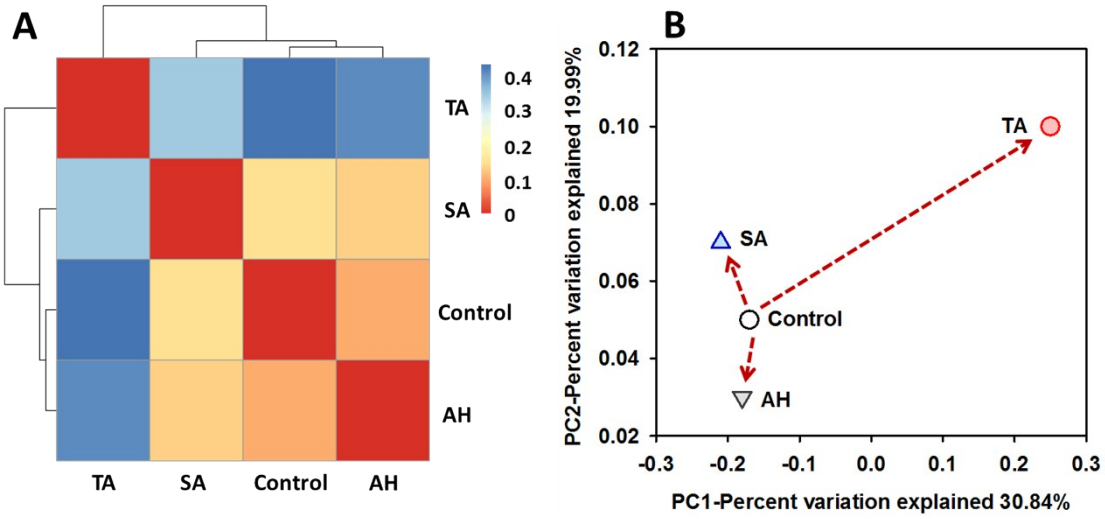

Figure S3 Principal component analysis (A) and distance heatmap analyses (B) of bacterial communities from WAS and VR co-digestion based on pyrosequencing of 16S rRNA gene.