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Supplementary Materials

Enhanced Acetogenesis of Waste Activated Sludge by Conditioning with Brewing Industry Processing Wastes: Kinetics, Process Assessment and Key Microbiomes

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Supporting Tables

Table S1. α-diversity parameters.

Sample	Shannon Index	Chao1 Index	Coverage	Simpson
Control	5.36	2070	0.9856	0.0131
VR	5.12	2263	0.9941	0.0193
SR	5.25	2314	0.9870	0.0136
SSR	4.75	2200	0.9891	0.0365

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

	Control	VR	SR	SSR
Acetoanaerobium	3.29	4.91	2.75	3.08
Acinetobacter	1.11	1.92	3.38	0.70
Anderseniella	0.24	1.60	1.66	2.55
Aquihabitans	0.86	1.06	0.56	4.17
Arenimonas	1.85	0.00	0.00	0.01
Aridibacter	1.26	0.53	0.81	0.44
Catabacter	0.16	1.19	1.74	1.19
Cloacibacillus	0.23	2.47	2.41	1.20
Comamonas	6.31	0.06	0.07	0.05
Defluviimonas	0.63	1.62	0.44	0.46
Exiguobacterium	0.40	0.88	1.55	0.79

Ferrimicrobium	0.01	1.03	0.77	0.40
Ferruginibacter	1.91	0.28	0.50	0.27
Gemmobacter	1.25	2.67	1.08	0.39
Gp10	3.78	0.20	0.84	0.05
Hyphomicrobium	0.40	2.02	1.30	1.16
Ignavibacterium	1.10	0.01	0.03	0.00
Ilumatobacter	0.93	1.49	1.71	0.79
Levilinea	3.11	7.45	9.07	7.10
Limnobacter	1.58	0.46	0.41	0.28
Litorilinea	1.12	1.02	0.42	0.69
Longilinea	0.76	0.81	1.14	0.18
Macellibacteroides	0.04	0.90	1.22	2.02
Mariniphaga	1.12	0.63	1.44	0.07
Methylocystis	0.29	2.14	0.98	1.18
Novosphingobium	1.30	0.56	0.85	0.24
Ornatilinea	1.10	0.35	0.69	0.38
Ottowia	5.92	1.83	3.60	0.48
Papillibacter	0.00	1.25	1.83	1.78
Parasegetibacter	1.58	0.02	0.02	0.01
Petrimonas	0.04	1.10	1.66	1.99
Povalibacter	1.09	0.19	0.24	0.22
Proteiniclasticum	0.32	7.40	3.20	1.88
Rhodopirellula	1.34	0.09	0.38	0.81
Rhodopseudomonas	0.53	1.05	0.88	1.17
Romboutsia	0.93	0.33	0.66	1.24
Saccharibacteria_genera_incertae_sedis	1.33	1.32	1.21	1.59
Solibacillus	0.00	1.83	0.44	6.47
Telmatospirillum	1.31	0.00	0.00	0.00
Terrimonas	4.38	0.05	0.09	0.02
Thauera	1.90	0.21	0.24	0.09
Thermogutta	0.83	0.33	0.91	1.53
Thermomonas	1.17	1.33	3.53	1.10
Trichococcus	0.15	0.16	0.39	1.10
unclassified	14.23	17.45	15.96	26.59
Others	26.81	25.80	26.94	22.09

Table S3. The eigenvalues of first two canonical axes and their relationships with each environmental factor.

	Axis 1	**Axis 2**
Eigenvalues	0.312	0.089
Cumulative percentage variance	68.8%	88.4%
Spr	−0.9521	0.3005
Sca	−0.8081	0.5633
Hydrolysis constant (HC)	−0.8398	0.3533
VFAs	−0.9367	0.3403
HAc	−0.8032	0.5954
HPr	−0.8969	−0.1895
pH	0.8991	−0.3532

Supporting Figures

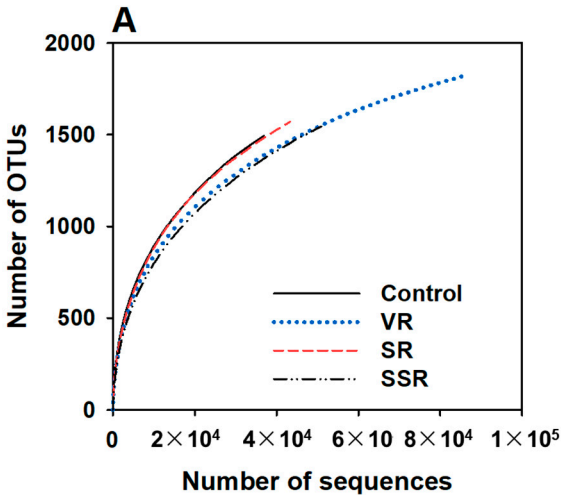

Figure S1. Rarefaction curves of bacterial communities obtained from the co-digesting WAS and three PWs based on sequencing of 16S rRNA gene.

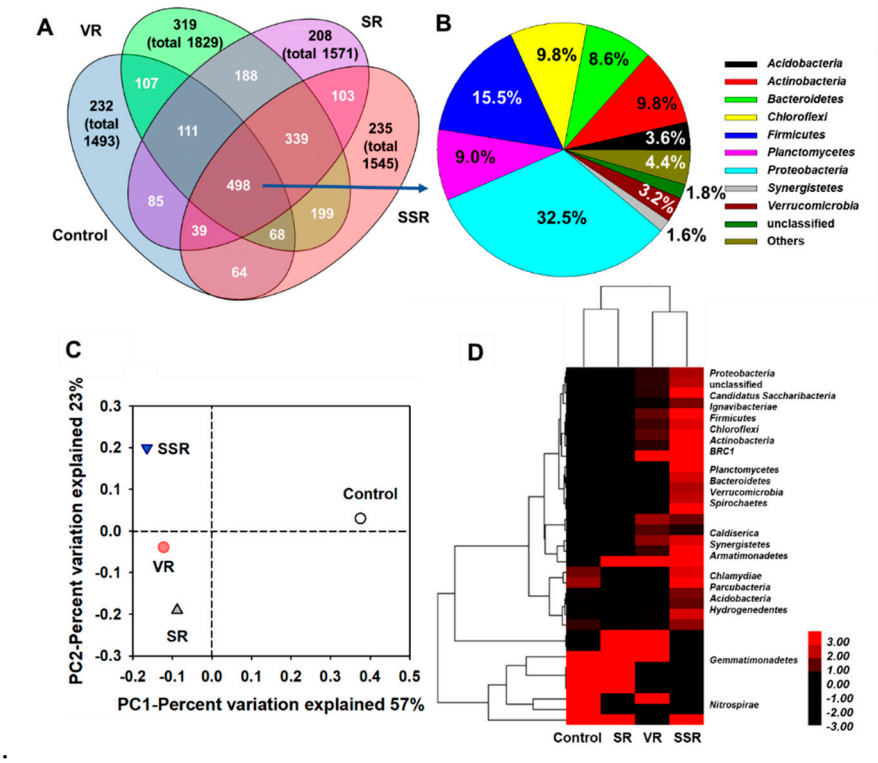

Figure S2. Chatacteristics of OTUs and bacterial communities obtained from the co-digesting WAS and three PWs based on sequencing of 16S rRNA gene, A for overlap of the four bacterial communities based on OTU (3% distance) ; B for the shared OTUs at phylum level; C for principal component analysis and D for hierarchical cluster analysis.

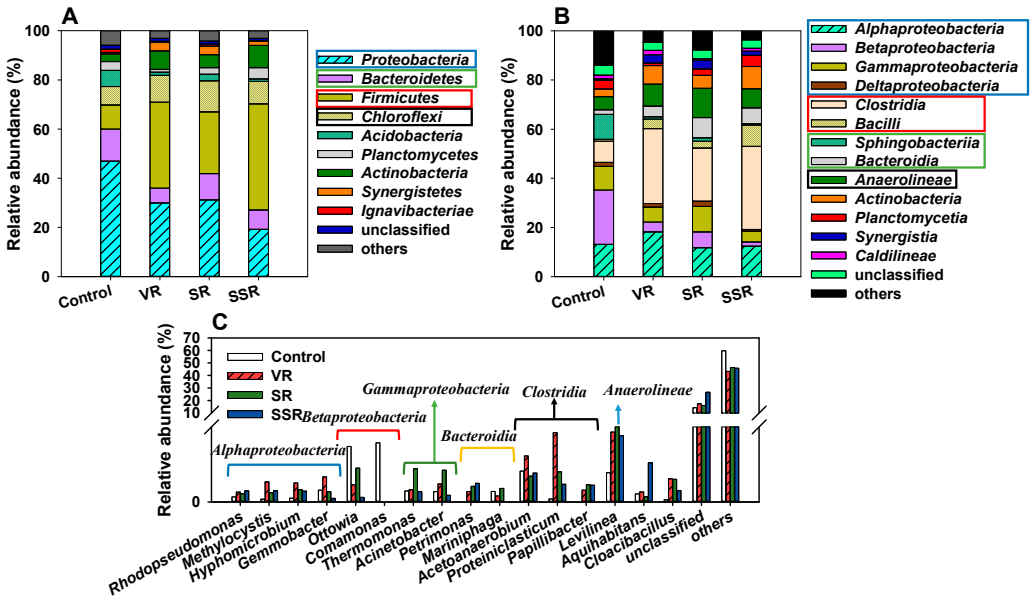

Figure S3. Taxonomic classification of pyrosequences from bacterial communities of five samples, A is bacterial communities at the phylum level, B is bacterial communities at the class level, C is bacterial communities at the genus level.

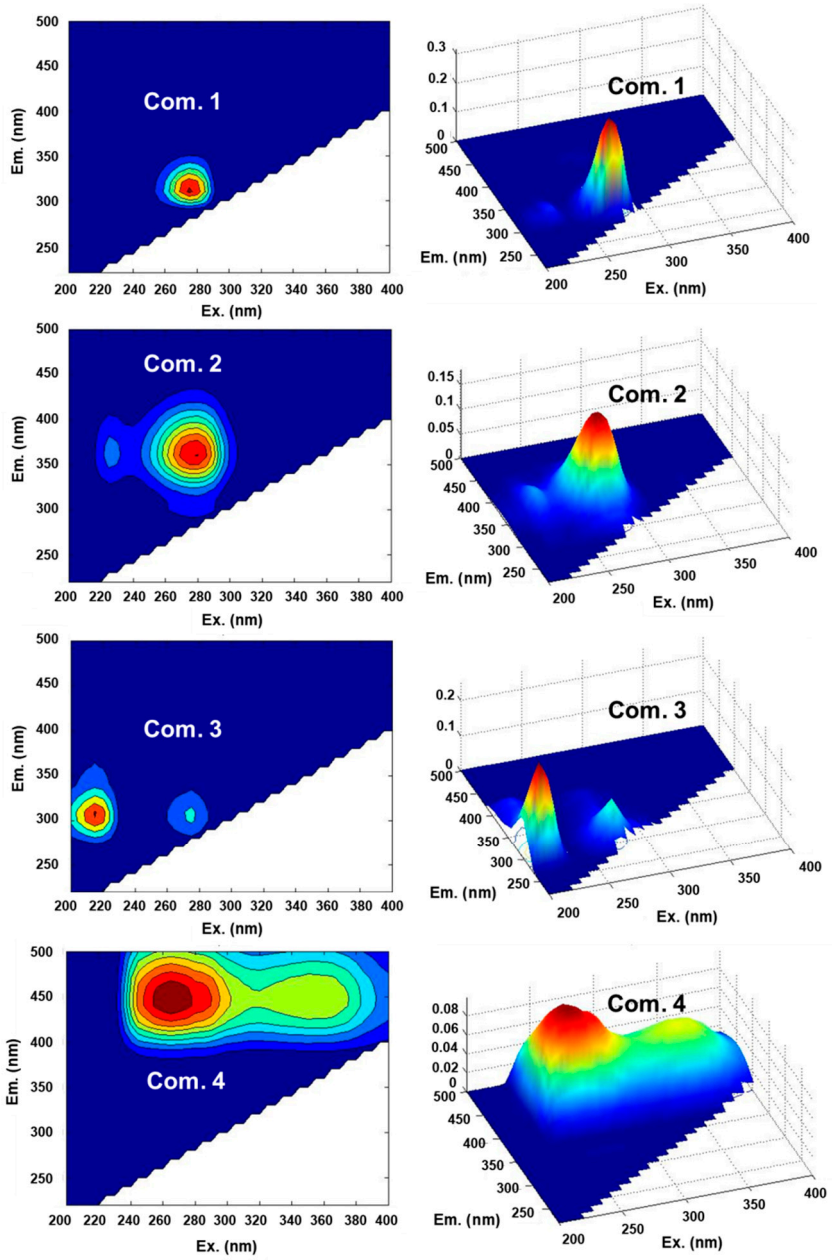

Figure S4. Four components of DOM decomposed by the PARAFAC approach: (Com. 1) tryptophan-like substances, Ex/Em (270/350); (Com. 2) tyrosine-like substances, Ex/Em (270/300); (Com. 3) protein-like substances, Ex/Em (225/300); (Com. 4) fulvic-like substrates, Ex/Em (300/440). DOM was obtained from the co-digesting WAS and three PWs.

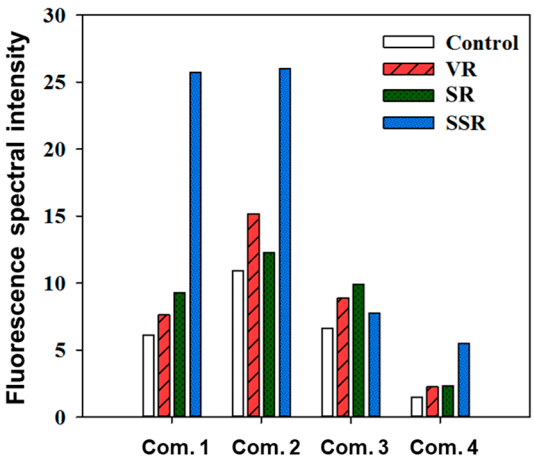

Figure S5. Fluorescence spectral intensity of components in the DOM samples obtained from the co-digesting WAS and three PWs.