Supplementary Material

Table S1 Genera (relative abundance >1% in at least one samples)

Genus	Control	AH-SS	TA-SS	SA-SS
Levilinea	3.11	2.97	7.1	2.34
Ottowia	5.92	3.48	0.48	6.53
Clostridium sensu stricto	0.69	5.72	0.61	5.35
Acetoanaerobium	3.29	1.64	3.08	2.78
Saccharibacteria_genera_incertae_sedis	1.33	2.37	1.59	3.19
Papillibacter	0	3.53	1.78	2.32
Aquihabitans	0.86	0.54	4.17	1.35
Solibacillus	0	0.01	6.47	0
Rhodopseudomonas	0.53	2.03	1.17	2.8
Ilumatobacter	0.93	2.1	0.79	2.65
Comamonas	6.31	1	0.05	0.23
Acinetobacter	1.11	1.13	0.7	3.42
Clostridium XlVa	0.02	1.81	0.4	3.41
Thermomonas	1.17	1.58	1.1	1.15
Catabacter	0.16	2.28	1.19	0.91
Litorilinea	1.12	1.52	0.69	1.39
Arenimonas	1.85	1.53	0.01	1.37
Macellibacteroides	0.04	1.32	2.02	0.72
Rhodopirellula	1.34	0.28	0.81	1.98
Clostridium IV	0.02	2.32	0.15	1.24
Terrimonas	4.38	0.18	0.02	0.1
Novosphingobium	1.3	1.07	0.24	1.37
Anderseniella	0.24	0.33	2.55	0.4
Limnobacter	1.58	0.82	0.28	1.34
Oscillibacter	0.01	0.49	0.44	2.72
Telmatospirillum	1.31	1.53	0	0.99
Exiguobacterium	0.4	0.96	0.79	1.33
Proteiniclasticum	0.32	0.94	1.88	0.1
Thermogutta	0.83	0.11	1.53	0.95
Gemmobacter	1.25	0.35	0.39	1.44
Gp10	3.78	0.03	0.05	0.05
Cloacibacillus	0.23	0.56	1.2	0.83
Terrisporobacter	0.11	1.38	0.53	0.74
Petrimonas	0.04	0.38	1.99	0.16
Hyphomicrobium	0.4	0.32	1.16	0.82
Intestinimonas	0.02	0.68	0.03	1.9

Romboutsia	0.93	0.16	1.24	0.21
Aridibacter	1.26	0.49	0.44	0.46
Citrobacter	0.26	0.72	0.36	1.1
Anaerofilum	0.01	1.42	0.02	0.9
Methylocystis	0.29	0.26	1.18	0.61
Ferruginibacter	1.91	0.1	0.27	0.13
Ornatilinea	1.1	0.36	0.38	0.3
Thauera	1.9	0.08	0.09	0.08
Bacteroides	0.01	1.08	0.22	0.37
Povalibacter	1.09	0.3	0.22	0.29
Flavonifractor	0.02	0.34	0.01	1.28
Gemmiger	0.02	0.31	0.02	1.09
Parasegetibacter	1.58	0.09	0.01	0.02
Trichococcus	0.15	0.02	1.1	0
GpXIII	0	1.19	0	0
Mariniphaga	1.12	0.06	0.07	0.05
Ignavibacterium Ignavibacterium	1.1	0	0	0
unclassified	14.23	19.51	26.59	10.06

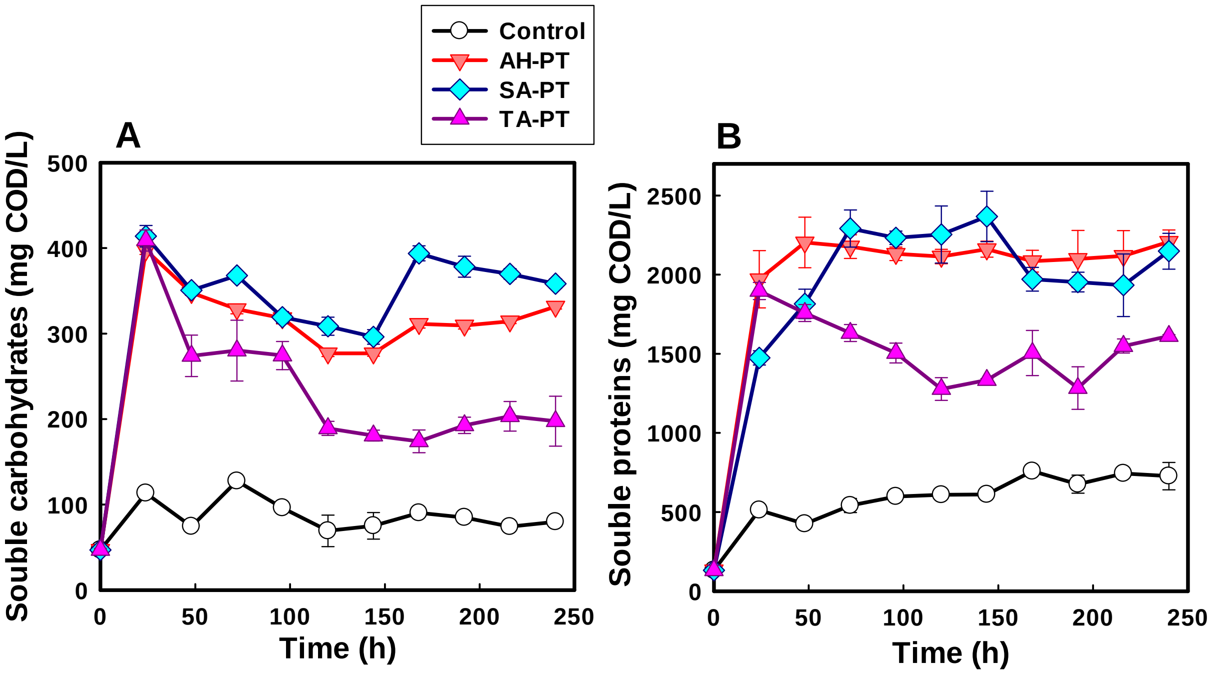

Fig. S1 Time-course profiles of soluble carbohydrates A and proteins B (Note: error bars represent standard deviation).

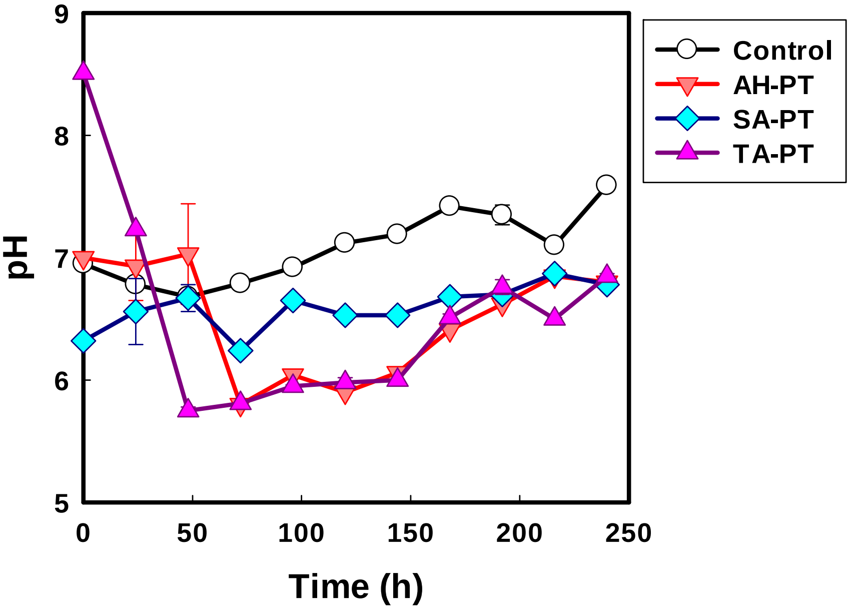

Fig. S2 Time-course profiles of pH evolution during WAS and SSR co-fermentation (Note: error bars represent standard deviation).

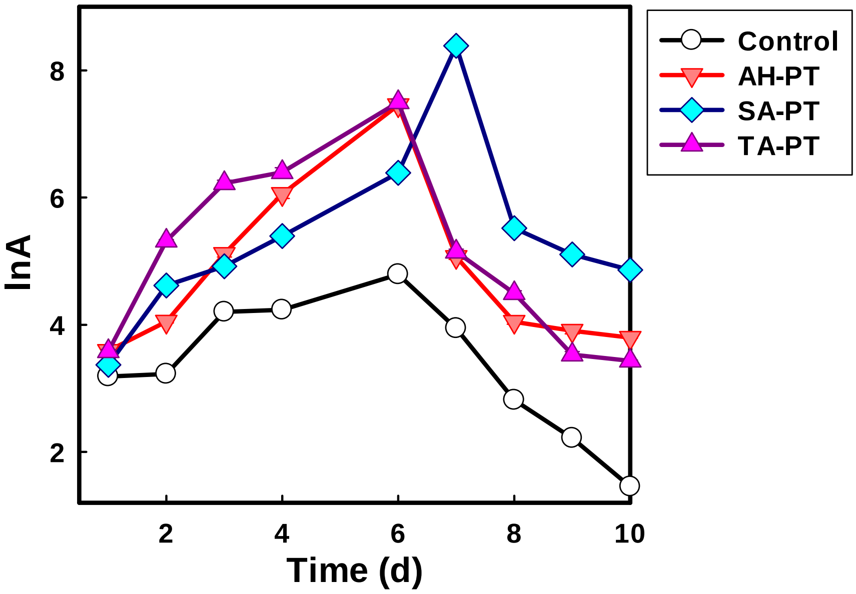

Fig. S3 Calculation results of apparent acidification rate constant k_{VFA} (Note: A reprsent $[C_{max}/C_{VFAs}-1]/[\ C_{max}/C_{VFAs,0}-1]$).

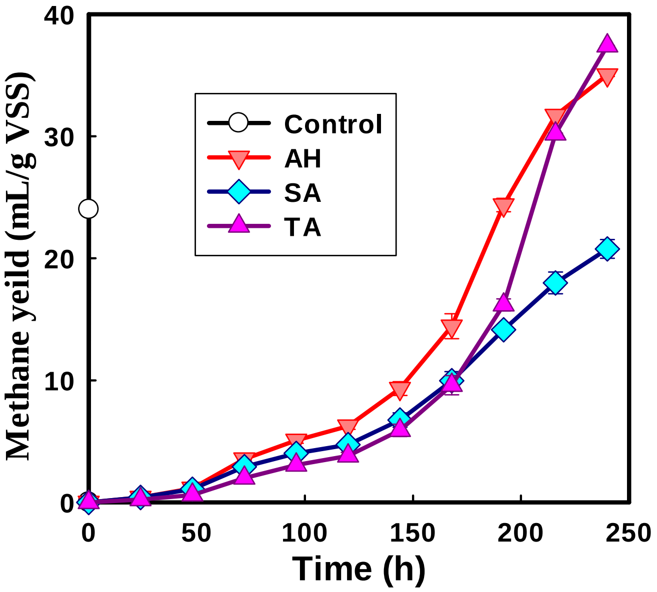

Fig. S4 Time-course profile of methane yield during WAS and SSR co-fermentation.

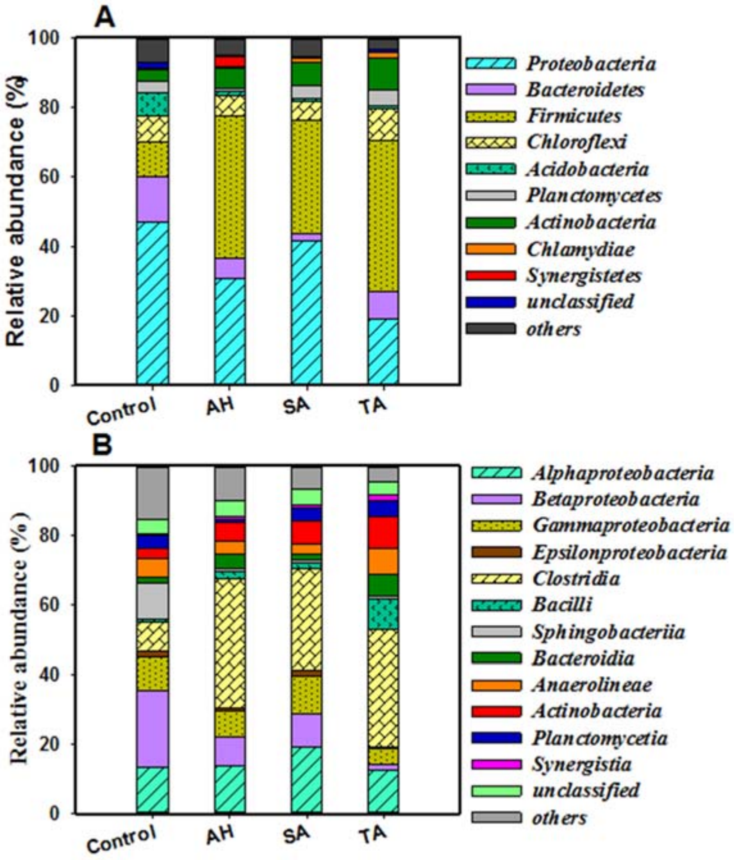

Fig. S5 Taxonomic classification of pyrosequences from bacterial communities of five samples at the phyla A and class B levels.