Supporting Information:

Supporting Table Legends

Table S1 The relative abundance of the top 100 microorganisms in the microbial communities from FPs for the production of CSAB.

Table S2 The phylogenetic profile of the top 20 Eukaryotes in the FPs.

Table S1 The relative abundance of the top 100 microorganisms in the microbial communities from FPs for the production of CSAB.

No.	Genus	Relative abundance %	No.	Genus	Relative abundance %
1	***Lactobacillus***	5.2786 ± 0.3149	51	***Alkaliflexus***	0.3219 ± 0.0028
2	***Clostridium IV***	4.9691 ± 0.1620	52	***Ashbya***	0.3013 ± 0.0090
3	***Methanosarcina***	4.5661 ± 0.1770	53	***Anaerovorax***	0.2872 ± 0.0014
4	***Fervidicella***	3.4687 ± 0.2722	54	***Victivallis***	0.2824 ± 0.0027
5	***Methanobacterium***	3.4588 ± 0.1834	55	***Alistipes***	0.2779 ± 0.0004
6	***Methanoculleus***	3.3356 ± 0.1921	56	***Escherichia***	0.2768 ± 0.0009
7	***Galactomyces***	3.2678 ± 0.0690	57	***Clostridium XlVb***	0.3069 ± 0.0565
8	***Acinetobacter***	3.1072 ± 0.2021	58	***Streptomyces***	0.2686 ± 0.0019
9	***Syntrophomonas***	3.0227 ± 0.1715	59	***Lysinibacillus***	0.259 ± 0.00420
10	***Petrimonas***	2.8713 ± 0.0659	60	***Oscillibacter***	0.2357 ± 0.0079
11	***Proteiniphilum***	2.8602 ± 0.0605	61	***Pelotomaculum***	0.2269 ± 0.0011
12	***Sedimentibacter***	2.7047 ± 0.0717	62	***Lutispora***	0.2262 ± 0.0001
13	***Methanocorpusculum***	2.5556 ± 0.0914	63	***Clostridium XII***	0.2107 ± 0.0035
14	***Pseudomonas***	2.5351 ± 0.0486	64	***Haloplasma***	0.2061 ± 0.0015
15	***Ruminococcus***	2.5434 ± 0.0281	65	***Paludibacter***	0.2048 ± 0.0008
16	***Clostridium XlVa***	2.2947 ± 0.2343	66	***Klebsiella***	0.203 ± 0.00110
17	***Methanobrevibacter***	2.1137 ± 0.1850	67	***Tetrapisispora***	0.1982 ± 0.0016
18	***Acholeplasma***	1.9586 ± 0.0392	68	***Cloacibacillus***	0.1976 ± 0.0011
19	***Candida***	1.7114 ± 0.1301	69	***Brevundimonas***	0.1879 ± 0.0038
20	***Thermogymnomonas***	1.6644 ± 0.0399	70	***Gracilibacter***	0.1868 ± 0.0028
21	***Tissierella***	1.5643 ± 0.0561	71	***Salmonella***	0.1794 ± 0.0037
22	***Aminobacterium***	1.5205 ± 0.0120	72	***Penicillium***	0.1757 ± 0.0013
23	***Sphingobacterium***	1.4348 ± 0.0321	73	***Butyricicoccus***	0.1722 ± 0.0026
24	***Stenotrophomonas***	1.2439 ± 0.0086	74	***Wautersiella***	0.1639 ± 0.0038
25	***Olsenella***	1.2164 ± 0.0015	75	***Gluconacetobacter***	0.1594 ± 0.0007
26	***Flavobacterium***	1.0585 ± 0.0521	76	***Fusarium***	0.1576 ± 0.0003
27	***Sporanaerobacter***	0.9944 ± 0.0161	77	***Faecalibacterium***	0.1483 ± 0.0030
28	***Trichosporon***	0.9900 ± 0.0291	78	***Chryseobacterium***	0.1456 ± 0.0013
29	***Methanosaeta***	0.7319 ± 0.0052	79	***Microbacterium***	0.1372 ± 0.0057
30	***Asteroleplasma***	0.7007 ± 0.0018	80	***Aquabacterium***	0.1331 ± 0.0008
31	***Dysgonomonas***	0.6596 ± 0.0108	81	***Ogataea***	0.1295 ± 0.0011
32	***Treponema***	0.6204 ± 0.0156	82	***Achromobacter***	0.1283 ± 0.0003
33	***Bacteroides***	0.5944 ± 0.0058	83	***Eremothecium***	0.1273 ± 0.0005
34	***Clostridium III***	0.5883 ± 0.0015	84	***Cryptococcus***	0.1253 ± 0.0005
35	***Paenibacillus***	0.5581 ± 0.0107	85	***Pedobacter***	0.1165 ± 0.0021
36	***Parabacteroides***	0.5463 ± 0.0023	86	***Thermoanaerobacter***	0.1152 ± 0.0004
37	***Acetobacter***	0.5244 ± 0.0098	87	***Butyrivibrio***	0.1130 ± 0.0007
38	***Dipodascus***	0.4805 ± 0.0014	88	***Tepidanaerobacter***	0.1115 ± 0.0004
39	***Bacillus***	0.4795 ± 0.0013	89	***Corynebacterium***	0.1095 ± 0.0002
40	***Oxobacter***	0.4646 ± 0.0125	90	***Blautia***	0.1094 ± 0.0001
41	***Prevotella***	0.4361 ± 0.0064	91	***Methanogenium***	0.1089 ± 0.0006
42	***Syntrophaceticus***	0.4188 ± 0.0046	92	***Leuconostoc***	0.1078 ± 0.0004
43	***Serratia***	0.4098 ± 0.0052	93	***Rummeliibacillus***	0.1071 ± 0.0001
44	***Pichia***	0.4010 ± 0.0035	94	***Saccharofermentans***	0.1043 ± 0.0019
45	***Caloramator***	0.3866 ± 0.0010	95	***Aneurinibacillus***	0.0986 ± 0.0012
46	***Geotrichum***	0.3765 ± 0.0018	96	***Cellvibrio***	0.0946 ± 0.0003
47	***Arcobacter***	0.3704 ± 0.0021	97	***Methanosphaerula***	0.0934 ± 0.0009
48	***Alkalibaculum***	0.361 ± 0.00460	98	***Chitinophaga***	0.0885 ± 0.0015
49	***Acetivibrio***	0.3505 ± 0.0038	99	***Arthrobacter***	0.0864 ± 0.0004
50	***Advenella***	0.3397 ± 0.0078	100	***Pantoea***	0.0805 ± 0.0045

The genus of sequences was assigned using whole affiliated SSU rRNA sequences from metagenomic databases against the RDP database. All data are presented as means ± standard deviations. This microbial data had been reported in the authors' previous work https://doi.org/10.1111/jam.14279.

Table S2 The phylogenetic profile of the top 20 Eukaryotes in the FPs.

No.	Genus	Class	Kingdom	Relative abundance in Eukaryotes (%)
1	***Galactomyces***	Saccharomycetales	Fungi	40.3234 ± 3.2124
2	***Candida***	Saccharomycetales	Fungi	11.0386 ± 1.2313
3	***Trichosporon***	Tremellomycetes	Fungi	5.1845 ± 0.3356
4	***Dipodascus***	Saccharomycetales	Fungi	3.5005 ± 0.0076
5	***Pichia***	Saccharomycetales	Fungi	2.8116 ± 0.1792
6	***Geotrichum***	Saccharomycetales	Fungi	2.5520 ± 0.0987
7	***Ashbya***	Saccharomycetales	Fungi	2.1048 ± 0.0077
8	***Tetrapisispora***	Saccharomycetales	Fungi	1.3355 ± 0.0324
9	***Penicillium***	Eurotiomycetes	Fungi	1.1492 ± 0.0549
10	***Fusarium***	Sordariomycetes	Fungi	0.9821 ± 0.0093
11	***Ogataea***	Saccharomycetales	Fungi	0.8763 ± 0.0761
12	***Eremothecium***	Saccharomycetales	Fungi	0.8354 ± 0.0025
13	***Cryptococcus***	Tremellomycetes	Fungi	0.8234 ± 0.0136
14	***Clavispora***	Saccharomycetales	Fungi	0.5638 ± 0.0074
15	***Isaria***	Sordariomycetes	Fungi	0.5578 ± 0.0053
16	***Pilobolus***	Mucoromycotina_X	Fungi	0.5013 ± 0.0017
17	***Aspergillus***	Eurotiomycetes	Fungi	0.4375 ± 0.0082
18	***Bullera***	Tremellomycetes	Fungi	0.4267 ± 0.0033
19	***Derxomyces***	Tremellomycetes	Fungi	0.4171 ± 0.0102
20	***Mucor***	Mucoromycotina_X	Fungi	0.3630 ± 0.0019

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