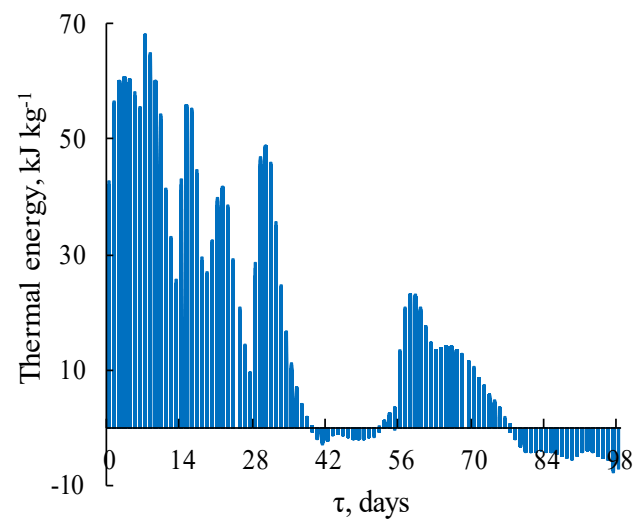


**Table S1.** Morphological composition of ms-OFMSW (fraction <70 mm) and the heat capacity of its components

No	Components	Content*, % (m/m)	Heat capacity kJ kg <sup>-1</sup> °C <sup>-1</sup> [19]	Weighted average heat capacity, kJ kg <sup>-1</sup> °C <sup>-1</sup>
1.	Food waste	55.87 ± 2.43	1.99	1.11
2.	Waste paper	8.56 ± 0.37	1.40	0.12
3.	Plastic	8.27 ± 0.79	1.73	0.14
4.	Stone, sand, ceramics	7.77 ± 0.21	1.03	0.08
5.	Combined materials (Tetra Pak, etc.)	6.85 ± 0.31	1.36	0.09
6.	Glass	6.16 ± 0.24	0.66	0.04
7.	Wood	4.48 ± 0.22	1.61	0.07
8.	Metal	0.69 ± 0.03	0.93	0.01
9.	Textile	0.56 ± 0.02	1.29	0.01
10.	Other (fraction less than 15 mm)	0.79 ± 0.03	1.33	0.01
Total:		100.00		1.68

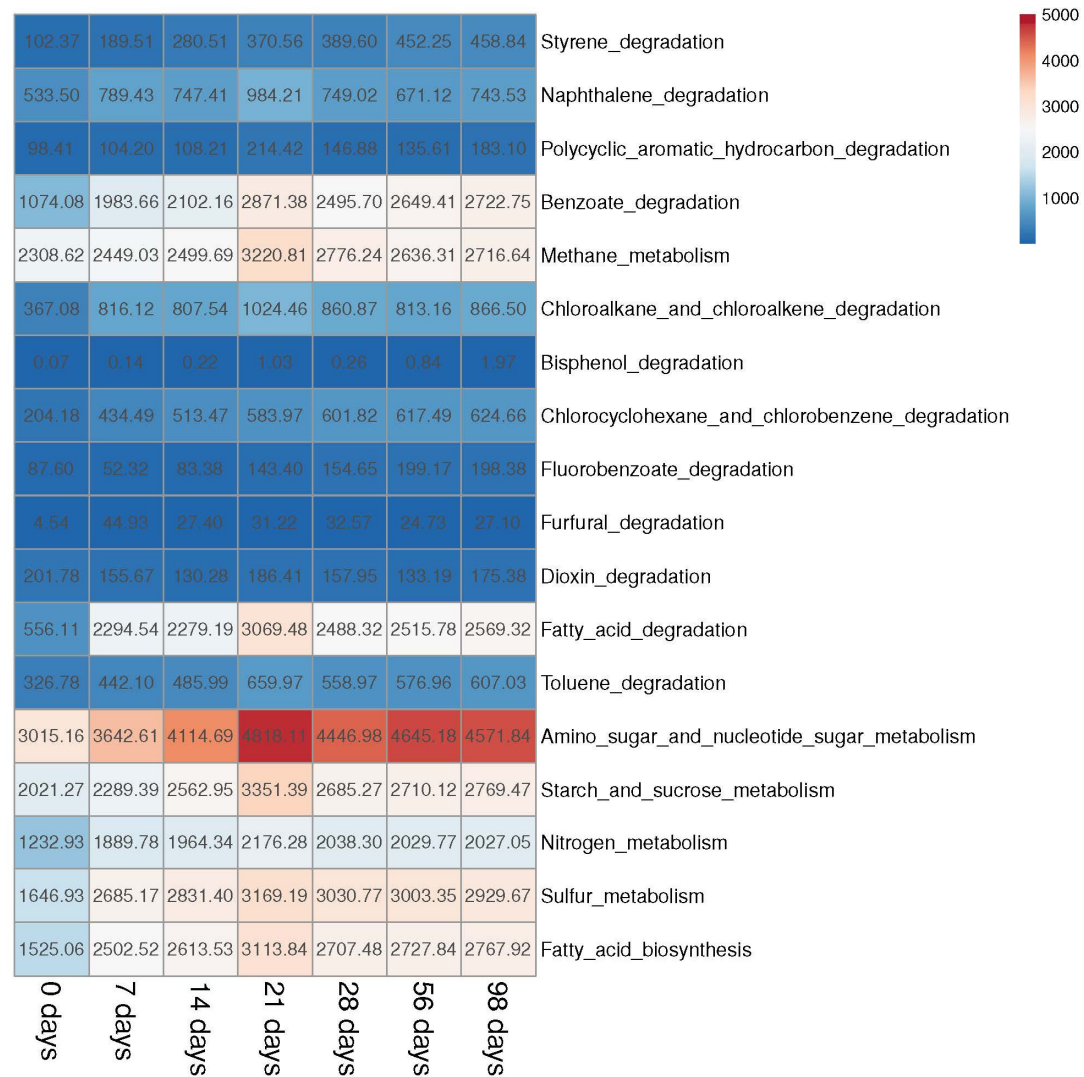
\* - average value ± standard deviation of three replicates



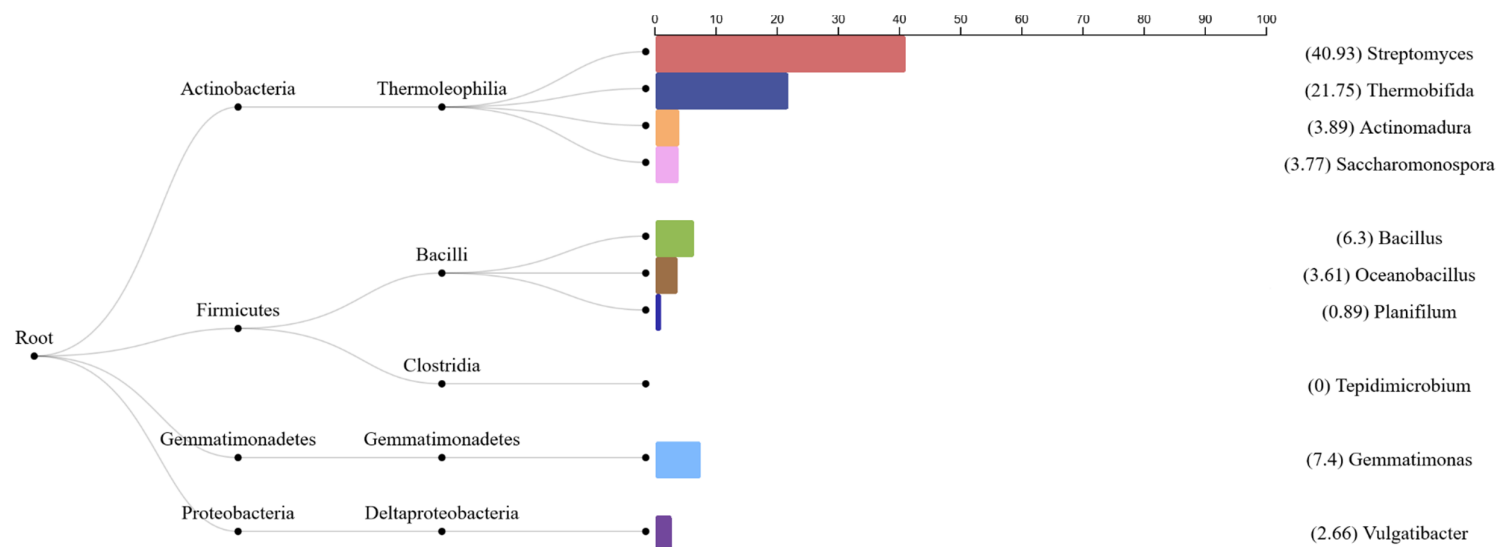
**Figure S1.** Heat release during composting

**Table S2.** Pearson correlations between microbiological and environmental variables:  $r_{crit}$  ( $f=4$ ,  $\alpha=0.05$ ) = 0.81 (Strode, Brokaw, 2015)

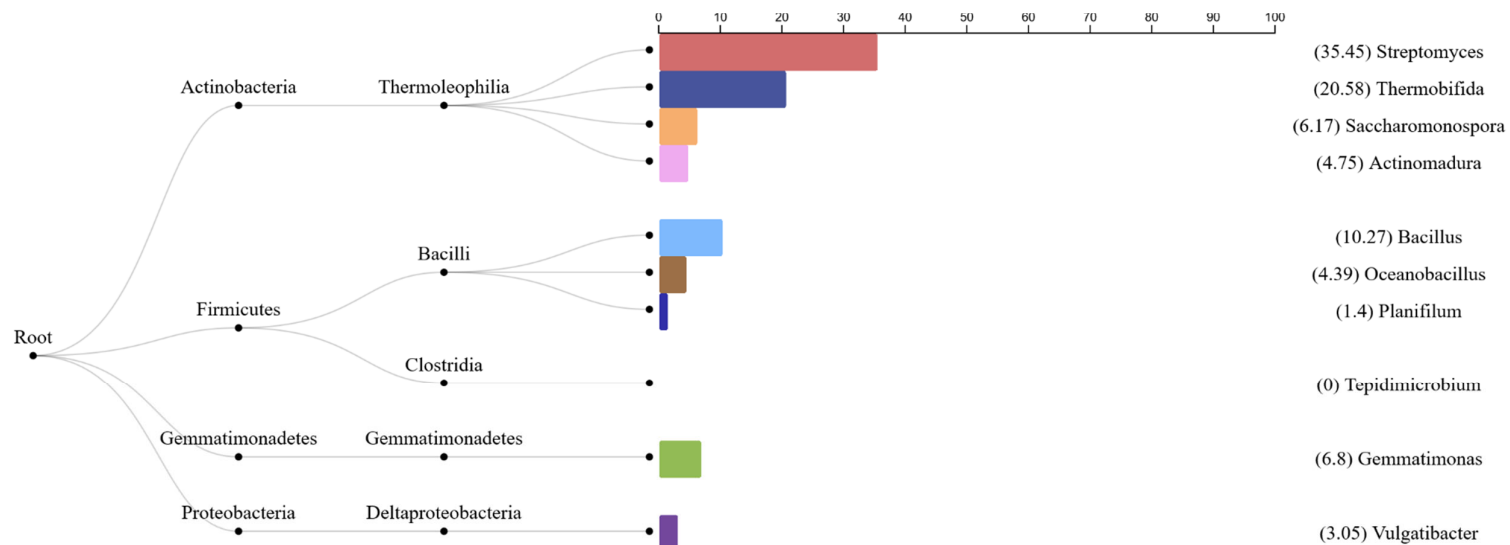
	CO <sub>2</sub> , g kg <sup>-1</sup> day <sup>-1</sup>	T, °C	NH <sub>3</sub> , mg kg <sup>-1</sup> day <sup>-1</sup>	EC, μS cm <sup>-1</sup>	pH	OM, %	C, %	N, %	C/N	GI, %	NI	Water content, %	Heat release, kJ kg <sup>-1</sup>
<i>Bacillus</i>	0.73	0.70	0.92	-0.37	0.67	-0.24	-0.24	-0.54	-0.32	0.06	-0.13	-0.89	0.87
<i>uncultured Bacillaceae</i>	-0.21	0.64	0.11	-0.80	0.04	0.97	0.97	-0.20	0.82	-0.79	-0.47	-0.46	0.38
<i>Ureibacillus</i>	-0.30	-0.91	0.98	-0.22	1.00	n.d.	n.d.	n.d.	n.d.	-0.64	-0.26	0.67	0.71
<i>Aeribacillus</i>	0.95	-0.96	0.81	0.85	0.92	n.d.	n.d.	n.d.	n.d.	0.75	-0.56	0.01	0.98
<i>Novibacillus</i>	-0.19	0.56	0.04	-0.50	0.01	0.76	0.76	-0.67	1.00	-0.59	0.11	-0.55	-0.17
<i>Streptomyces</i>	0.42	0.23	-0.54	0.11	-0.62	0.47	0.47	0.95	-0.91	0.33	-0.12	0.07	-0.18
<i>Tepidimicrobium</i>	0.96	0.47	0.79	-0.26	0.45	0.09	0.09	n.d.	n.d.	0.09	0.09	-0.74	0.93
<i>Thermobifida</i>	0.28	0.62	0.11	-0.69	0.15	0.92	0.92	-0.72	1.00	-0.79	0.02	-0.80	0.23
<i>Geobacillus</i>	-0.47	-0.82	1.00	-0.40	0.99	n.d.	n.d.	n.d.	n.d.	-0.77	-0.07	0.52	0.56
<i>Paenibacillus</i>	-0.94	0.84	0.41	-0.59	-0.85	0.28	0.28	0.75	-0.09	-0.22	-1.00	0.23	-0.29
<i>Planifilum</i>	0.37	0.24	0.96	-0.52	0.41	0.62	0.62	-1.00	0.78	-0.62	-0.09	-0.69	0.78
<i>Saccharomonospora</i>	-0.77	-0.27	-0.64	0.19	0.35	-0.10	-0.11	-0.79	1.00	-0.05	0.45	0.29	-0.71
<i>Oceanobacillus</i>	-0.20	-0.28	-0.46	-0.04	0.74	0.33	0.33	-0.87	0.97	-0.31	0.39	-0.08	-0.14
<i>Vulgatibacter</i>	-0.90	-0.83	-0.58	0.85	0.43	-0.98	-0.98	n.d.	n.d.	0.67	0.50	0.78	-0.96
SO134	-0.59	-0.84	-0.72	0.62	0.76	-0.54	-0.54	-0.88	0.33	0.33	0.69	0.52	-0.70
<i>Thermomyces</i>	0.31	0.21	-0.37	0.31	0.53	-0.48	-0.48	-0.70	-0.30	0.50	0.31	-0.28	-0.09
<i>Penicillium</i>	0.15	-0.10	0.75	-0.27	-0.04	0.82	0.82	0.92	0.78	-0.28	-0.37	-0.02	0.69
<i>Microascus</i>	-0.17	0.41	0.29	-0.08	0.15	-0.70	-0.70	0.64	-0.91	0.08	0.02	-0.26	-0.13
<i>Aspergillus</i>	0.37	-0.05	0.76	-0.17	0.23	0.06	0.06	-0.44	0.23	-0.11	-0.15	-0.25	0.77
Chao1 prokaryotes	-0.06	-0.11	-0.25	0.79	0.24	-0.81	-0.81	0.36	-0.96	0.88	0.20	0.23	-0.37
Shannon prokaryotes	-0.53	-0.41	-0.72	0.78	-0.06	-0.77	-0.77	0.50	-0.96	0.67	0.16	0.64	-0.79
Chao1 fungi	0.27	-0.10	0.72	-0.36	-0.21	0.66	0.66	0.55	0.39	-0.39	-0.34	-0.05	0.68
Shannon fungi	-0.01	-0.28	0.58	-0.21	-0.27	0.39	0.39	0.70	0.21	-0.34	-0.32	0.17	0.46



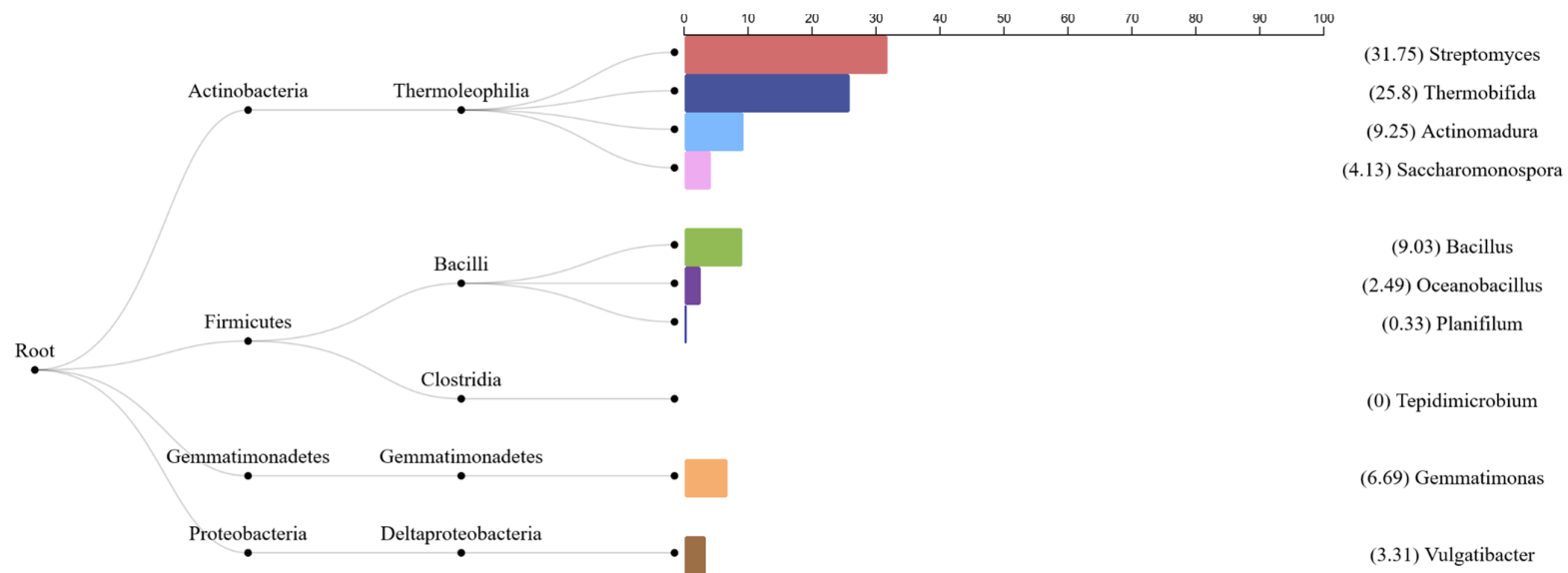
**Figure S2.** The heat map of prokaryotic microbiota functional profiles on day 0, 7, 14, 21, 28, 56, and 98 of composting. The number of genes related to particular metabolic pathway is shown by color.



(a)



(b)



(c)

**Figure S3.** Dendrograms showing key microorganisms and their phylogenetic lines involved in metabolism of: (a) starch and sucrose, (b) methane, (c) fatty acid degradation.