



Figure S1. The scheme of BAGS incubation.

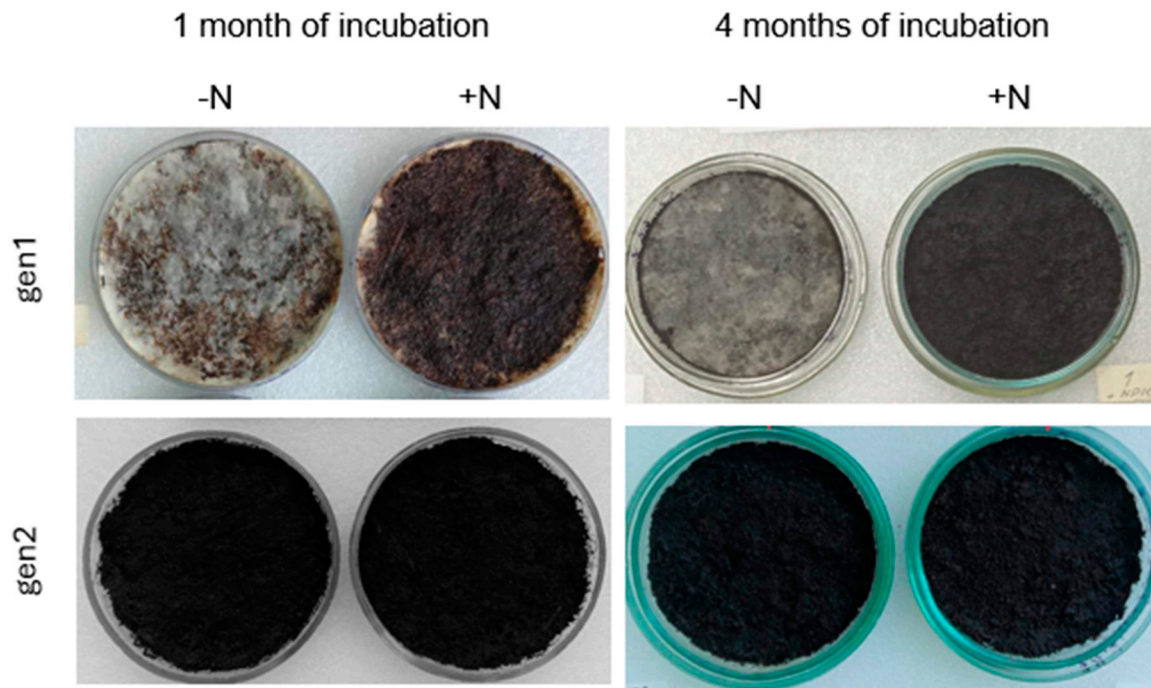


Figure S2. The cellulolytic activity of BAGS preparation. The activity is visualized by a degree of paper filter maceration. (-N) without stimulation by additional nitrogen, (+N) with stimulation by additional nitrogen. Upper row – gen1 BAGS from 2023, lower row – gen2 BAGS from 2024. Left column – preparation after 1 month of composting, right column – after 4 months of composting. Incubation with paper filter in all cases was for 2 months.

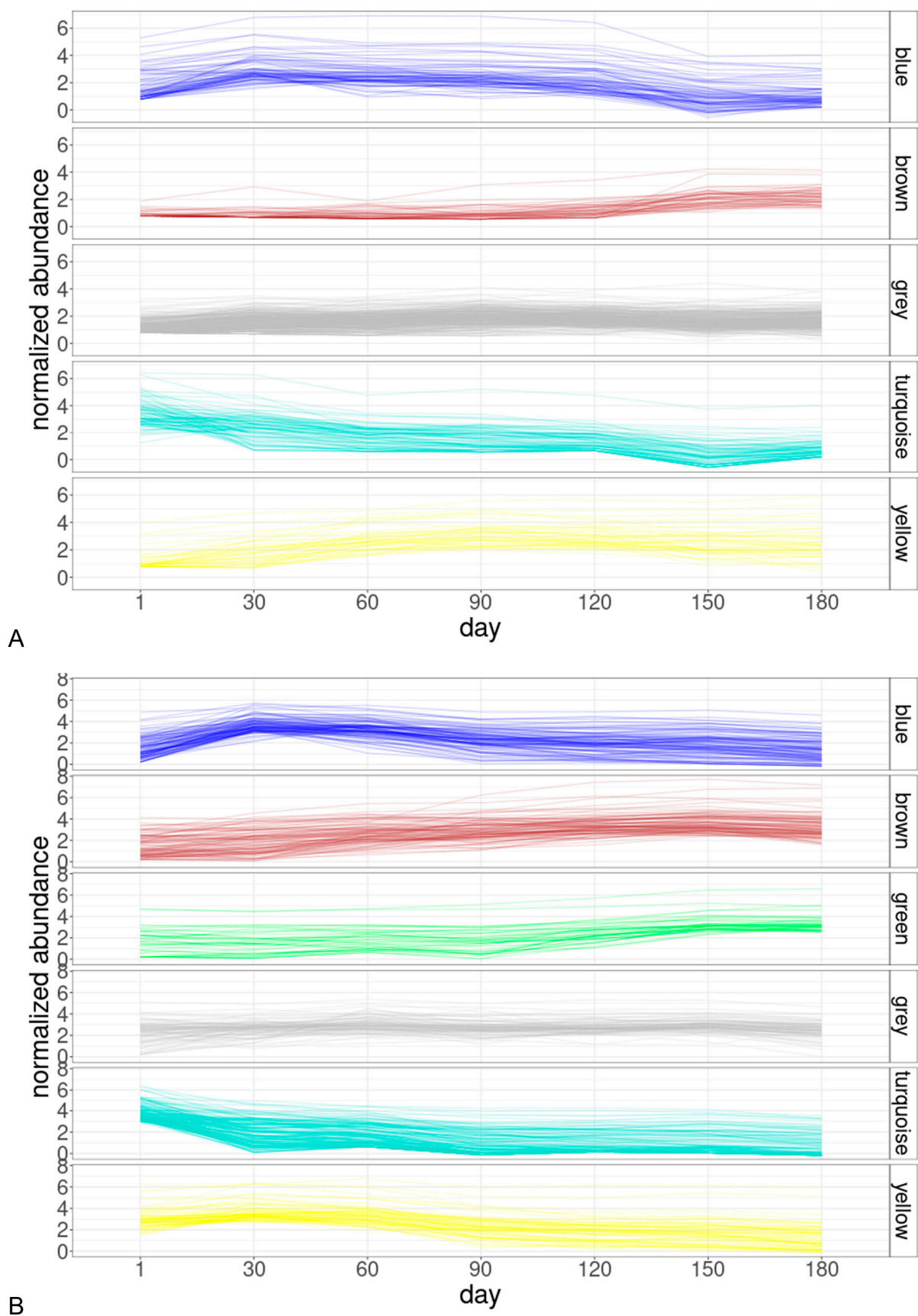


Figure S3. The network analysis (WGCNA) of ASVs coexpression in BAGS composting process. The normalized abundance of ASV clusters in gen1 BAGS (A) and gen2 BAGS (B).

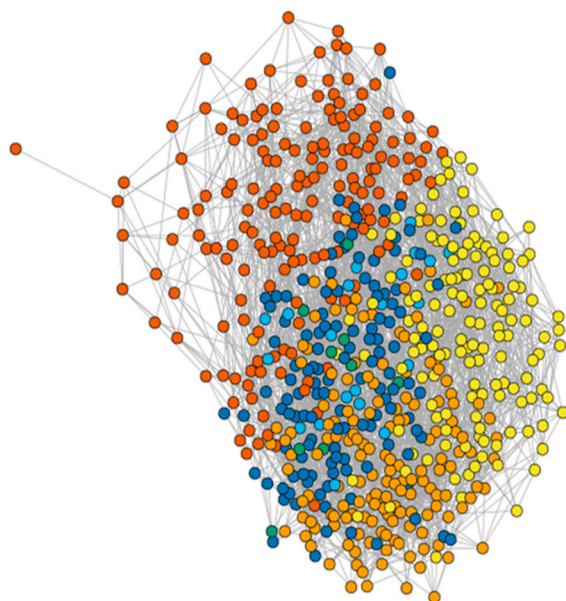
	oat_straw						
Bacteroidota; Terrimonas-	0.1	0.2	0.1	0.2	0.5	1.4	1.2
Pseudomonadota; IS-44-	0	0	0.1	0.1	0.2	0.7	0.6
Nanoarchaeota; AR15-	0	0	0	0	0	0.8	0.8
Myxococcota; f__Haliangiaceae_Seq316-	0	0	0	0	0	0.3	0.3
Nanoarchaeota; GW2011_GWC1_47_15-	0	0	0.1	0	0.1	0.1	0.4
Acidobacteriota; Bryobacter-	0	0	0.1	0.1	0.1	0.2	0.2
Myxococcota; f__Haliangiaceae_Seq447-	0	0	0	0	0.1	0.2	0.3
Patescibacteria; o__Candidatus Magasanikbacteria_Seq714-	0	0	0	0	0	0.2	0.3
Pseudomonadota; c__Alphaproteobacteria_Seq554-	0	0	0	0	0	0.2	0.2
Bacteroidota; Chryseotalea-	0	0	0	0	0	0.2	0.2
Spirochaetota; Salinispira-	0	0	0	0	0	0.2	0.2
Gemmatimonadota; f__Gemmatimonadaceae_Seq336-	0	0	0	0	0	0.2	0.3
Myxococcota; f__Blri41_Seq462-	0	0	0	0	0	0.2	0.2
Patescibacteria; c__Parcubacteria_Seq1266-	0	0	0	0	0	0.1	0.2
Chloroflexota; o__Aggregatilineales_Seq480-	0	0	0	0	0	0.1	0.2
Patescibacteria; o__Candidatus Magasanikbacteria_Seq862-	0	0	0	0	0	0.2	0.1
Methylomirabilota; o__Rokubacteriales_Seq703-	0	0	0	0	0	0.1	0.1
Verrucomicrobiota; f__Puniceicoccaceae_Seq1201-	0	0	0	0	0	0.2	0.1
Myxococcota; f__Blri41_Seq738-	0	0	0	0	0	0.2	0.1
Myxococcota; f__Blri41_Seq995-	0	0	0	0	0	0.1	0.2
Pseudomonadota; MND1-	0	0	0	0	0	0.2	0.1
Chloroflexota; f__Anaerolineaceae_Seq306-	0	0	0	0	0	0.1	0.2
Pseudomonadota; Aquicella-	0	0	0	0	0	0.2	0.1
Pseudomonadota; o__Rhodospirillales_Seq943-	0	0	0	0	0	0.2	0.1
Pseudomonadota; Reyranella-	0	0	0	0	0	0.1	0.1
Bacteroidota; Chryseolinea-	0	0	0	0	0	0.1	0.1
Elusimicrobiota; o__MVP-88_Seq1236-	0	0	0	0	0	0.2	0.1
Elusimicrobiota; c__Lineage IIa_Seq1038-	0	0	0	0	0	0.1	0.1
Planctomycetota; c__OM190_Seq1052-	0	0	0	0	0	0.1	0.1
Nanoarchaeota; o__Woesearchaeales_Seq1411-	0	0	0	0	0	0.1	0.1
Patescibacteria; c__ABY1_Seq2454-	0	0	0	0	0	0.1	0.2
Myxococcota; f__Blri41_Seq894-	0	0	0	0	0	0.1	0.1
Verrucomicrobiota; f__Pedosphaeraceae_Seq677-	0	0	0	0	0	0.1	0.1
Patescibacteria; o__Candidatus Buchananbacteria_Seq547-	0	0	0	0	0	0.1	0.1
Pseudomonadota; o__Micavibrionales_Seq1410-	0	0	0	0	0	0	0.1
Bdellovibrionota; OM27 clade-	0	0	0	0	0	0.1	0.1
Planctomycetota; c__vadinHA49_Seq1575-	0	0	0	0	0	0.1	0.1
Myxococcota; f__Haliangiaceae_Seq2012-	0	0	0	0	0	0.1	0.1
Patescibacteria; c__Parcubacteria_Seq3064-	0	0	0	0	0	0.1	0.1
Spirochaetota; Spirochaeta 2-	0	0	0	0	0	0.1	0.1
Remaining taxa (8)-	0	0	0	0	0.1	0.5	0.5
	os_1-	os_30-	os_60-	os_90-	os_120-	os_150-	os_180-

Figure S4. The heatmap of brown cluster of ASVs in gen1 BAGS.

	oat_straw						
Patescibacteria; c__Gracilbacteria_Seq106-	0.1	0.2	0.2	3.7	10.5	10.8	8.4
Bacteroidota; Chryseolinea-	0	0.1	0.3	0.8	2.4	4.3	6.4
Bacteroidota; Terrimonas-	0.1	0.5	1.2	2.2	3.3	2.2	1.4
Pseudomonadota; f__TRA3-20_Seq919-	0	0.1	0.3	0.7	1.2	1.7	2.2
Planctomycetota; f__WD2101 soil group_Seq1825-	0	0	0	0.3	0.7	1.2	1.8
Pseudomonadota; IS-44-	0.1	0.1	0.2	0.5	0.8	1	1.1
Pseudomonadota; f__Xanthobacteraceae_Seq91-	0.2	0.2	0.5	0.9	0.8	0.6	0.4
Myxococcota; f__Haliangiaceae_Seq447-	0.1	0.1	0.2	0.7	0.9	0.8	0.5
Pseudomonadota; MND1-	0	0.1	0.2	0.4	0.7	0.9	1.1
Pseudomonadota; SWB02-	0.1	0.1	0.4	0.4	0.6	0.7	0.6
Bacteroidota; Chryseotalea-	0	0.3	0.4	0.4	0.5	0.5	0.4
Myxococcota; f__Haliangiaceae_Seq19673-	0	0	0.1	0.8	0.6	0.4	0.4
Chloroflexota; f__Roseiflexaceae_Seq88-	0.1	0.1	0.3	0.5	0.4	0.4	0.3
Gemmatimonadota; f__Gemmatimonadaceae_Seq336-	0	0.2	0.3	0.2	0.3	0.4	0.5
Chlamydiota; f__cvE6_Seq592-	0	0	0.1	0.6	0.5	0.4	0.2
Hydrogenedentes; f__Hydrogenedensaceae_Seq140-	0.1	0.2	0.3	0.4	0.3	0.3	0.3
Pseudomonadota; o__CCD24_Seq232-	0	0.2	0.3	0.4	0.3	0.3	0.3
Planctomycetota; f__Pirellulaceae_Seq4472-	0	0	0	0.1	0.4	0.5	0.7
Bacteroidota; Edaphobaculum-	0	0.2	0.3	0.4	0.3	0.3	0.2
Chloroflexota; c__JG30-KF-CM66_Seq83-	0.1	0.1	0.2	0.3	0.3	0.3	0.4
Pseudomonadota; Amphiplicatus-	0	0	0.1	0.2	0.4	0.5	0.4
Pseudomonadota; Bradyrhizobium-	0.1	0.1	0.2	0.3	0.3	0.3	0.3
Pseudomonadota; Dongia-	0.1	0.1	0.1	0.2	0.3	0.3	0.4
Bacteroidota; f__Chitinophagaceae_Seq1471-	0	0	0.1	0.2	0.3	0.4	0.4
Acidobacteriota; o__Vicinamibacterales_Seq3464-	0	0	0.1	0.2	0.3	0.4	0.3
Pseudomonadota; Acidibacter-	0	0	0.1	0.1	0.3	0.3	0.3
Planctomycetota; f__WD2101 soil group_Seq820-	0	0	0.1	0.2	0.3	0.3	0.3
Verrucomicrobiota; f__Pedosphaeraceae_Seq791-	0	0	0.1	0.1	0.3	0.3	0.3
Patescibacteria; c__Gracilbacteria_Seq7867-	0	0	0	0.4	0.2	0.3	0.2
Gemmatimonadota; f__Gemmatimonadaceae_Seq1103-	0.1	0.1	0.2	0.2	0.2	0.2	0.2
Planctomycetota; f__Phycisphaeraceae_Seq787-	0	0	0	0.1	0.2	0.3	0.4
Acidobacteriota; o__Vicinamibacterales_Seq804-	0	0.1	0.1	0.2	0.3	0.2	0.1
Chlamydiota; f__Simkaniaceae_Seq436-	0	0	0.1	0.2	0.1	0.2	0.2
Planctomycetota; f__CPla-3 termite group_Seq501-	0	0.1	0.1	0.1	0.2	0.2	0.1
Pseudomonadota; o__Rhodospirillales_Seq668-	0	0.1	0.1	0.2	0.2	0.2	0.1
Myxococcota; f__Haliangiaceae_Seq794-	0	0	0.1	0.3	0.2	0.1	0.1
Acidobacteriota; Bryobacter-	0	0	0.1	0.2	0.2	0.2	0.1
Bacteroidota; Hassallia-	0	0	0	0.1	0.2	0.2	0.3
Chlamydiota; o__Chlamydiales_Seq3055-	0.1	0	0.1	0.2	0.2	0.1	0.1
Thermodesulfobacteriota; p__Thermodesulfobacteriota_Seq6124-	0	0	0.1	0.1	0.1	0.1	0.3
Remaining taxa (45)-	0.4	0.6	1.5	4.2	4.9	4.8	4.4
	gen2_1-	gen2_30-	gen2_60-	gen2_90-	gen2_120-	gen2_150-	gen2_180-

Figure S5. The heatmap of brown cluster of ASVs in gen2 BAGS.

BAGS2023 (gen1)



BAGS2024 (gen2)

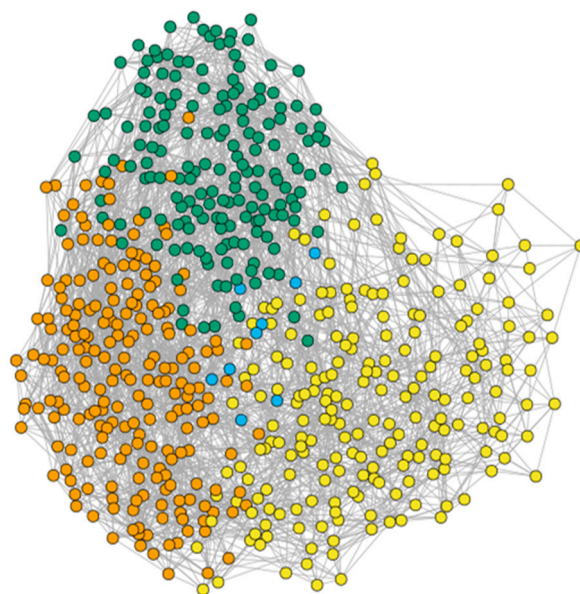


Figure S6. The cooccurrence network for gen1 BAGS (left) and gen2 BAGS (right).

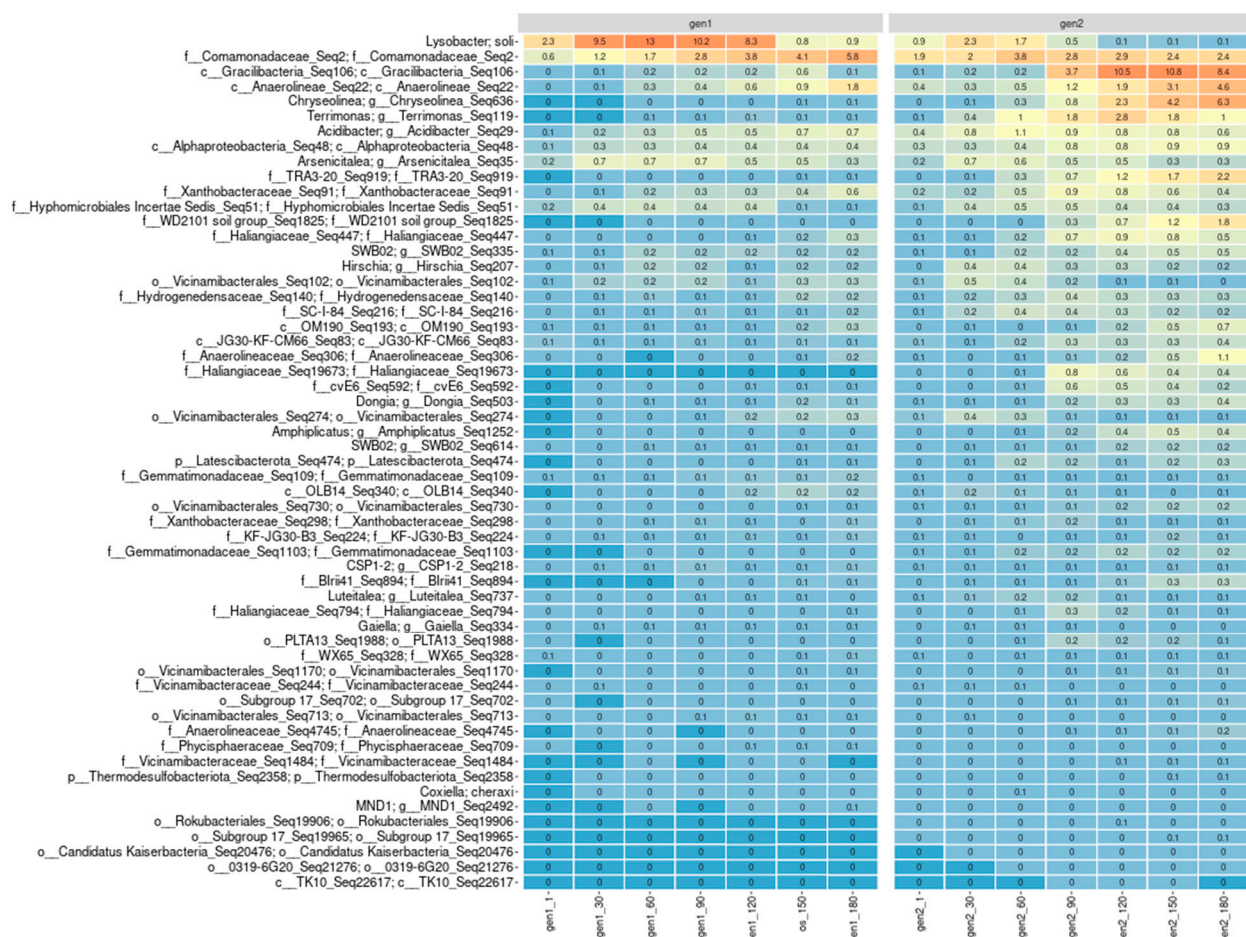


Figure S7. The heatmap of ASVs, correlating with MAGs, isolated from the metagenome of the mature phase of the effective BAGS.