Table S1 Basic information of metagenomic sequencing data

Sample	Clean reads	Percent in raw reads (%)[a]	Contigs	ORFs[b]	Average length (bp)	N50[c]	N90[d]
CK-1	83,461,856	98.66	1,219,959	1,628,985	457.65	713	360
CK-2	83,043,850	98.71	1,214,327	1,593,029	456.61	711	358
CK-3	90,945,580	98.66	1,306,924	1,745,114	457.45	713	358
CK-4	83,463,278	98.64	1,238,622	1,665,009	462.79	739	363
T1-1	83,670,884	98.61	1,214,359	1,618,094	457.08	715	359
T1-2	91,354,726	98.62	1,353,256	1,775,242	450.44	689	356
T1-3	89,001,330	98.64	1,268,055	1,678,969	455.94	711	357
T1-4	83,443,590	98.66	1,269,206	1,604,492	442.63	660	352
T2-1	82,776,170	98.65	1,275,876	1,646,943	450.32	694	357
T2-2	82,812,812	98.58	1,299,189	1,727,870	456.51	725	360
T2-3	83,726,608	98.62	1,173,200	1,567,220	464.1	746	361
T2-4	83,816,852	98.68	1,286,783	1,694,022	451.41	702	358
T3-1	83,473,752	98.61	1,249,942	1,666,927	456.84	725	359
T3-2	83,758,994	98.63	1,239,958	1,634,289	454.31	706	358
T3-3	83,849,648	98.71	1,250,604	1,675,619	461.33	737	362
T3-4	83,37,340	98.71	1,233,541	1,639,444	456.94	723	359

T1, T2, and T3: 0.1%, 1%, and 5% PBAT, respectively.

a: The percentage of clean reads in raw reads; b: The number of sequences of open reading frames; c: Scan the length values of each sequence one by one from the largest to the smallest and accumulate them. When the accumulated value exceeds 50% of the total length of all sequences, the length value of the sequence is the N50; d: When the accumulated value exceeds 90%, the length value of the sequence is the N90.

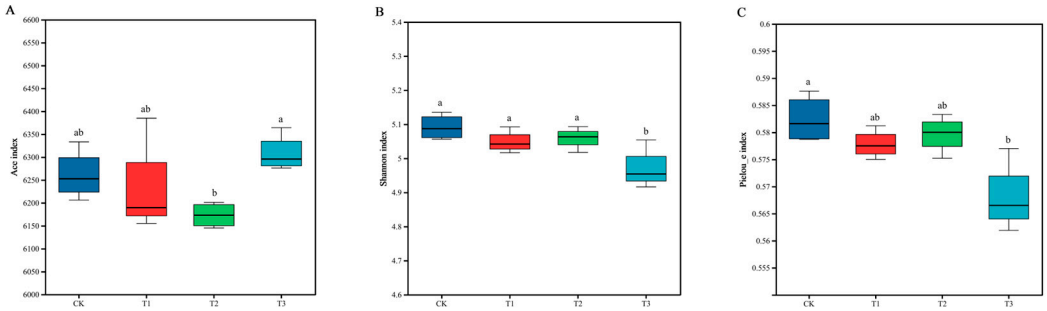


Figure S1. Comparison of the a-diversity indices under different treatments at the genus level. T1, T2, and T3: 0.1%, 1%, and 5% PBAT, respectively.

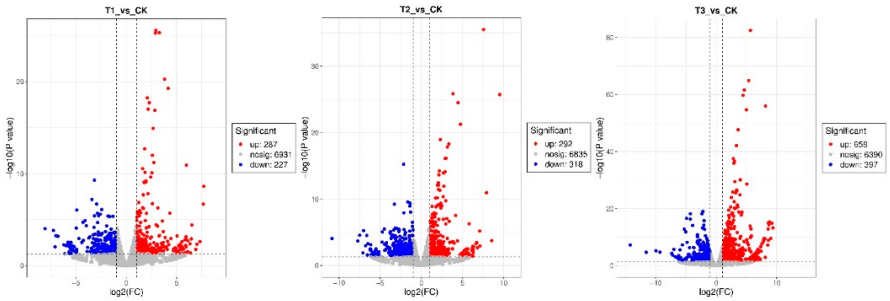


Figure S2. Volcano diagram of significantly enriched and depleted microbial genera in the soils treated with different dosages of PBAT MPs. T1, T2, and T3: 0.1%, 1%, and 5% PBAT, respectively.

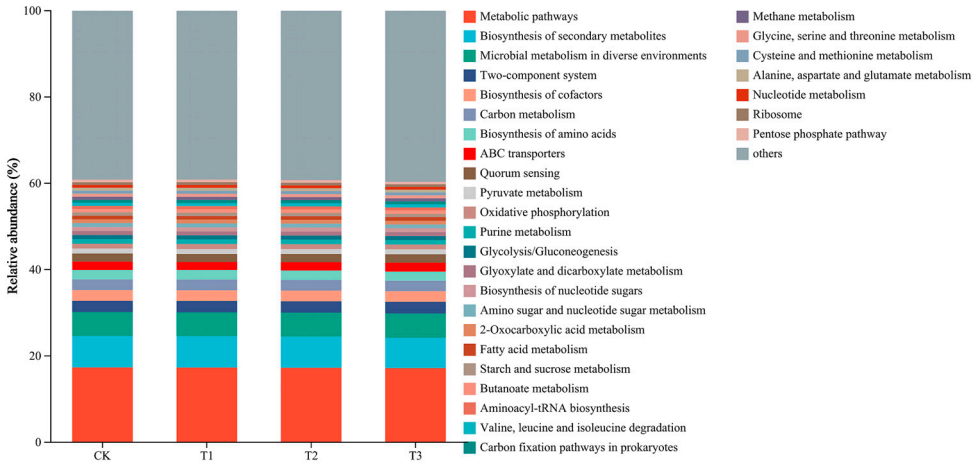


Figure S3. Relative abundances of the 30 most abundant KEGG pathways at level 3 in different treatments. T1, T2, and T3: 0.1%, 1%, and 5% PBAT, respectively.

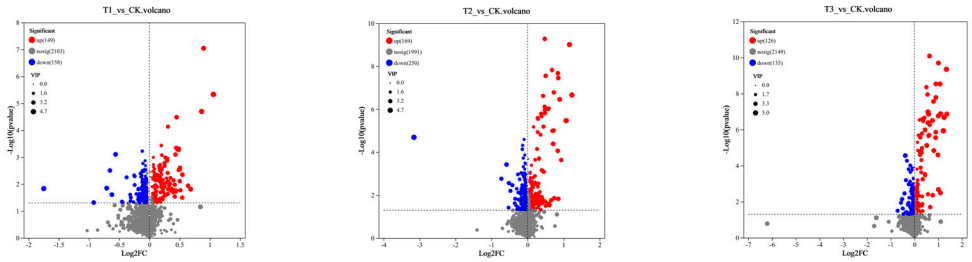
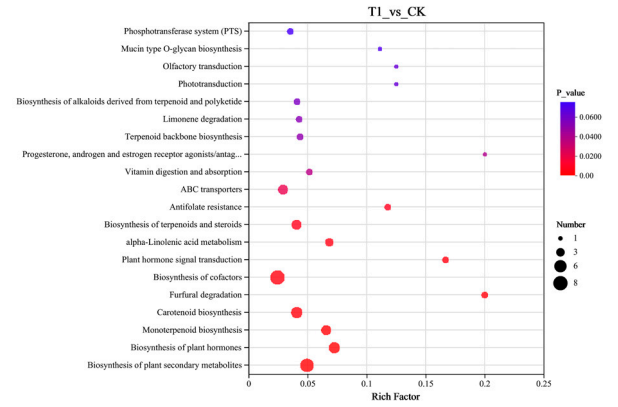
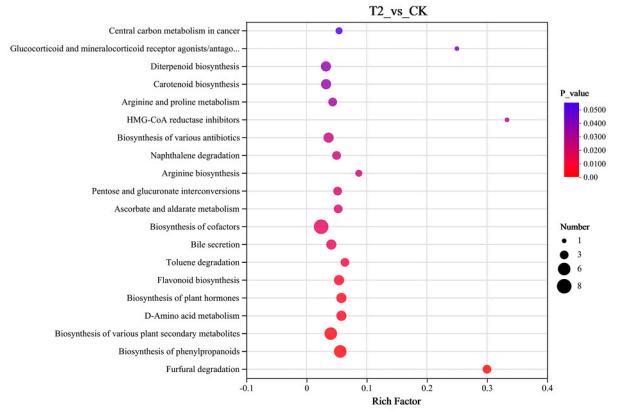


Figure S4. Volcano plots of the identical biomarkers shared between the CK and PBAT treatments. The red, blue and grey dots indicate upregulated, downregulated, and no differential metabolites, respectively. T1, T2, and T3: 0.1%, 1%, and 5% PBAT, respectively.





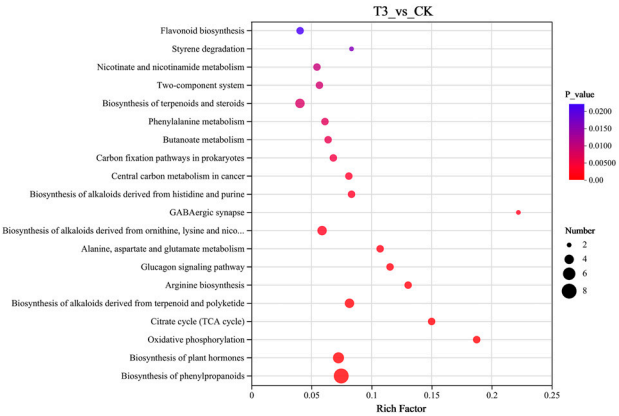


Figure S5. KEGG enrichment metabolic pathways shared between CK and PBAT groups. T1, T2, and T3: 0.1%, 1%, and 5% PBAT, respectively.