Supporting Information

Text S1 Details for 16S rRNA high-throughput sequencing test

In brief, according to the characteristics of the amplified region, based on the IonS5^{TM}XL sequencing platform (Meiji, Shanghai, China), single-end sequencing is used to construct a library by sorting, trimming and screening the raw data. The clean sequences were then clustered into operational taxonomic units (OTUs) by filtering, followed by species annotation and abundance analysis. Further alpha diversity analysis and beta diversity analysis were conducted, and rarefaction curves were constructed. Prior to library construction, samples were tested with final optical density (OD) value between 1.8 and 2.0. Sequencing libraries were generated using NEBNext® Ultra™ DNA Library Prep Kit for Illumina (NEB, USA) following manufacturer's recommendations and index codes were added to attribute sequences to each sample. The clustering of the index-coded samples was performed on a cBot Cluster Generation System according to the manufacturer's instructions. After cluster generation, the library preparations were sequenced on an Illumina HiSeq platform (Illumina Novaseq6000, PE150, USA) and paired-end reads were generated. The specific processing steps were as follows: 1) remove the reads which contain low quality bases (default quality threshold value ≤ 38) above a certain portion (default length of 40 bp); 2) remove the reads in which the N base has reached a certain percentage (default length of 10 bp); 3) remove reads which shared the overlap above a certain portion with Adapter (default length of 15 bp) (Handelsman et al., 1998). DIAMOND software (V0.9.9) was used for taxonomy prediction and common functional database annotations (Nielsen et al., 2014). Functional databases include KEGG database (Version 2018-01-01) (Kanehisa et al., 2006), eggNOG database (Version 4.5) (Powell et al., 2014), and Carbohydrate-Active EnZymes (CAZy) database (Version 201801) (Cantarel et al., 2009).

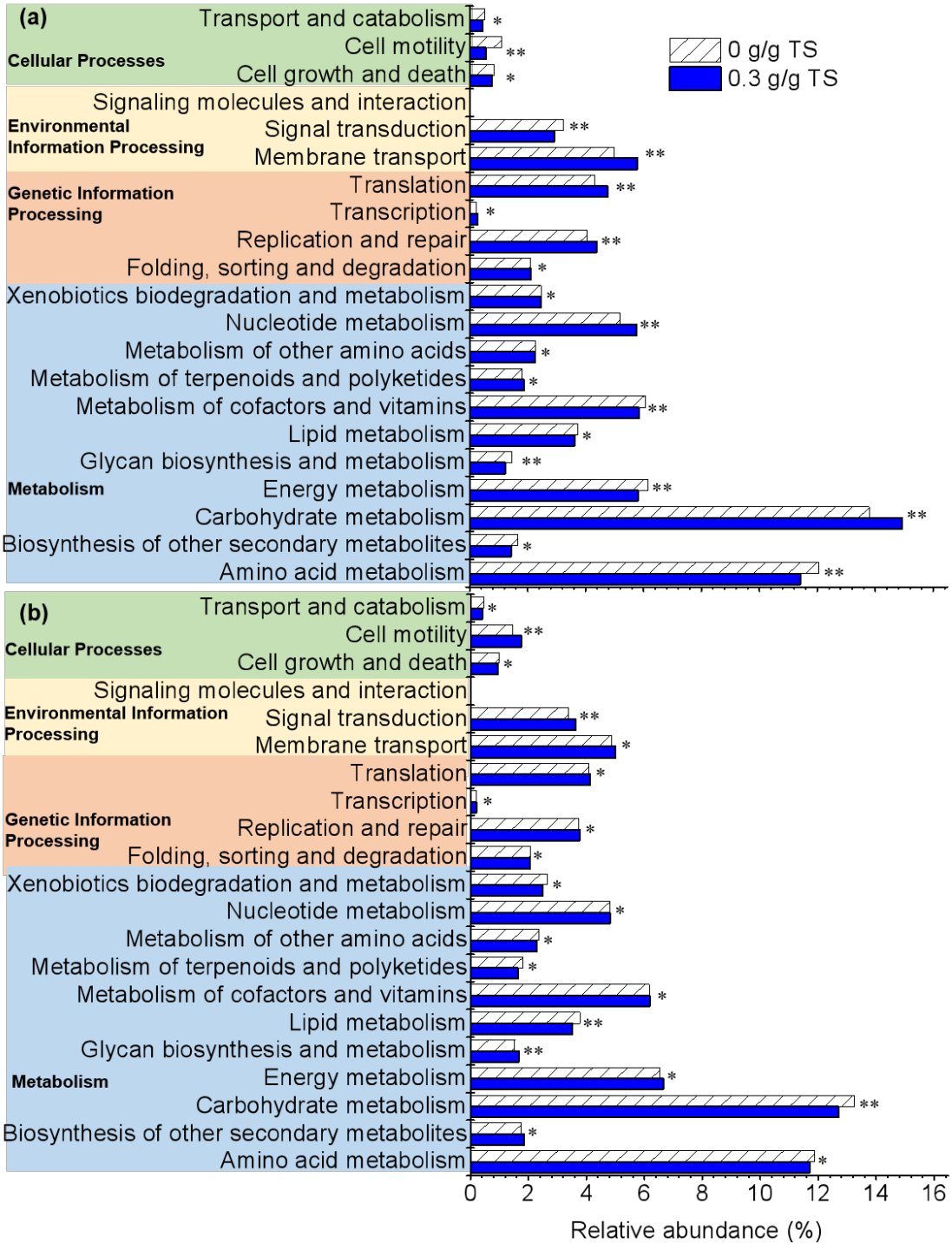

Fig. S1 The bacterial function profiles according to different composting sampling dates: (a) day 1, Level 2 function categories; (b) day 35, Level 2 function categories. * denotes the process difference between 0 g/g total solids (TS) and 0.3 g/g TS was not significant ($p > 0.05$), while ** denotes the process difference between 0 g/g TS and 0.3 g/g TS was significant ($p < 0.05$).

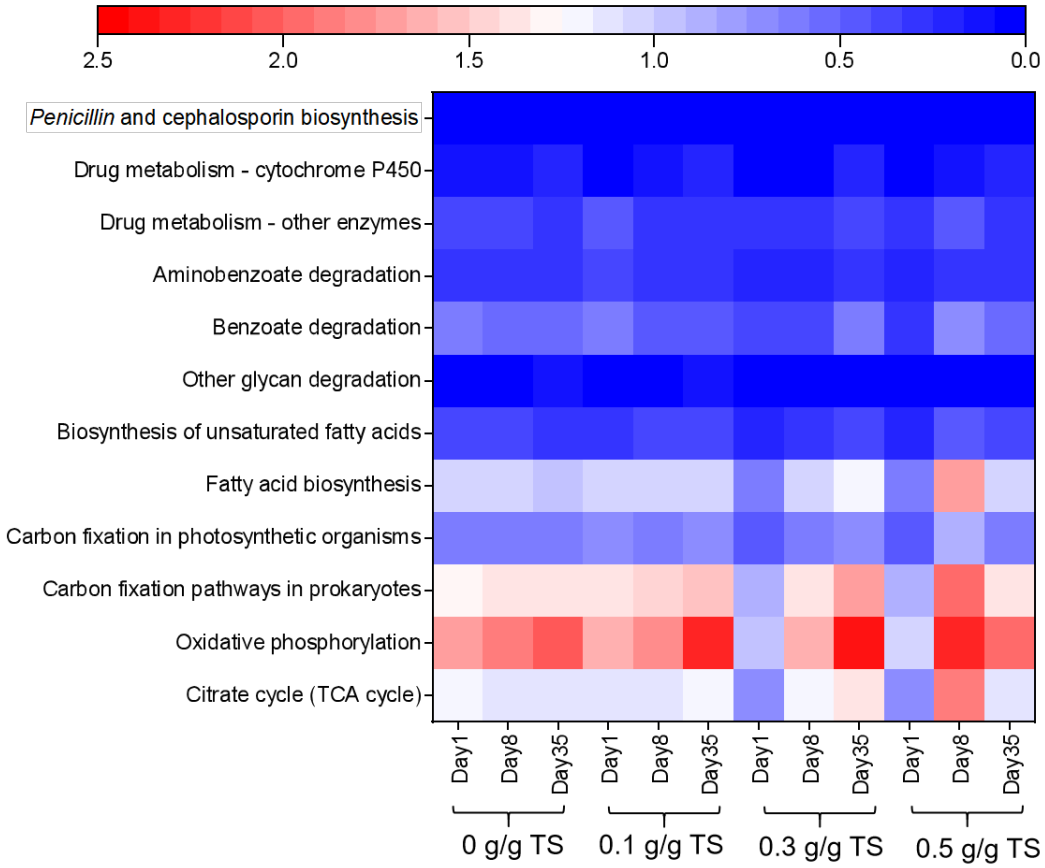

Fig. S2 The Level 3 KEGG ortholog function predictions about the abundance of metabolic functions.

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