Supplementary Text S1. DNA Extraction, metagenomic sequencing, data processing, and analysis

An extraction kit for soil DNA (MP Biomedical, Santa Ana CA, USA) was used to extract DNA from 0.5 g of soil samples. A Qubit 3.0 gel electrophoresis apparatus (Thermo Fisher Scientific, Waltham, USA) was used to determine the DNA purity. The DNA concentration was quantified using a Nanodrop 2000 (Thermo Fisher Scientific, Waltham, USA) to ensure A260/A280 = 1.8-2.0, and the DNA samples were stored at -80 ℃ for further analysis. To construct a library, the obtained DNA was randomly interrupted using a fragmentation buffer. Trimmomactic software was used to control DNA quality. The well-constructed library was sequenced using PE150 on the Illumina HiSeq 2500 high-throughput sequencing platform. Raw data files obtained from the sequencing were transformed into raw reads. MEGAHIT was used for de novo splicing to identify species with low abundance in the samples, and scaffolds with more than 500 bp obtained by reassembly were used for subsequent analysis. The MetaGeneMark was used to predict the open reading frames (ORFs). The prediction results for each sample and the assembled ORFs were combined, and the Linclust software was used for gene clustering and redundancy removal. The longest sequence in each cluster was selected as the representative sequence to obtain the gene catalogue (Unigenes). Clean data from quality control and the gene catalogue were used to calculate the abundance of each gene in each sample. The Unigenes sequence was compared with the NCBI-NR gene database for species annotation, and the gene abundance table was assembled to obtain species composition and abundance information at each taxonomic level. In addition, the software Metaphlan3 was used to classify clean reads into species quickly. Meanwhile, the predicted gene protein sequences were compared with KEGG, eggNOG, CAZyme and other databases to obtain functional annotation information. VFDB, ARGs, and MGEs databases were used to annotate these genes.