Supplemental Materials

Text S1. Preparation of bacterial suspension

1. Preparation of soil extract

Weigh 2 g of background soil and place it in a 250 mL conical flask. Add 40 mL of ultrapure water along with 8 zeolite particles to the flask. Position the flask on a shaker at room temperature (20±1 ℃), shaking at a speed of 200 r/min for a duration of 2 hours. Finally, transfer the resulting soil suspension into a 100 mL centrifuge tube.

2. Impurity Removal and Concentration of Bacterial Suspension:

Insert the centrifuge tube into a centrifuge and spin at 1000 g for 12 minutes to obtain the supernatant. Subsequently, perform another centrifugation step at 3000 g for 30 minutes. From this process, extract 30 mL of the lower precipitate, which corresponds to obtaining approximately 15 mL of bacterial suspension from every gram of soil used. The resultant bacterial suspension should be mixed thoroughly and stored in a refrigerator at 4 °C for the following use.

Text S2. Alkali absorption method.

100 g of air-dried samples from each treatment were placed in separate beakers with an incubation at 60% of field capacity moisture level for seven days to restore soil biological activity. These samples were evenly spread over the bottom of 1 L wide-mouth glass bottle, respectively. A 50 mL beaker containing 30 mL 0.4 moL/L NaOH solution was hung in each of the bottles, which were sealed and cultivated in the dark at room temperature. A blank control group was also set up. Three replicates were set up for all the treatments. During cultivation process, water was added by weighing to keep the moisture content at 60%. The 50 mL beaker were replaced on days 3、6、9、12、15、21 and 30 after the start of the experiment. $BaCl_2$ solution (6 mL; 1 mol/L) along with 2 drops of 0.5 % (wt) phenolphthalein indicator were added to the 50 mL beaker. The solutions were titrated against a standard hydrochloric acid solution (0.2 mol/L). After each sample titration, a blower was used to blow air into the wide-mouth glass bottle for 1 min to circulate the gas in the bottle with the outside world.

Text S3. Bacterial community structure analysis

1. DNA extraction from soil and PCR amplification

16S rRNA amplicon sequencing was conducted by Genesky Biotechnologies Inc. (Shanghai, China). Total genomic DNA was extracted using the FastDNA® SPIN Kit for Soil (MP Biomedicals, Santa Ana, CA) in accordance with the manufacturer's instructions. Three replicates were performed for each sample. The integrity of the genomic DNA was assessed through agarose gel electrophoresis (wt % = 1.0 %). The concentration and purity of the genomic DNA were measured using a Nanodrop 2000 and Qubit 3.0 Spectrophotometer. The V4-V5 hypervariable regions of the 16S rRNA gene were amplified with primers 515F (5'-GTGCCAGCMGCCGCGG-3') and 907R (5'-CCGTCAATTCMTTTRAGTTT-3'), followed by sequencing on an Illumina NovaSeq 6000 sequencer.

2. Illumina read data processing and analysis

The raw read sequences were processed using QIIME2 software. Adaptor and primer sequences were trimmed utilizing the cutadapt plugin, while quality control and identification of amplicon sequence variants (ASVs) were performed with the DADA2 plugin. Taxonomic assignments for ASV representative sequences were carried out with a confidence

threshold of 0.7 using a pre-trained Naive Bayes classifier that had been trained on SILVA database (version 138.1).

3. Soil bacterial diversity analysis

OTU abundance and Alpha diversity analyses were conducted via the Genesky biological platform (http://cloud.geneskybiotech.com/#/tools/all). Chao1 index and Ace index served to characterize bacterial richness, whereas Shannon index and Simpson index provided insights into bacterial diversity; Coverage indicated whether sequencing depth was adequate to accurately reflect the compositional characteristics of microbial communities within samples.

Table S1. Physicochemical properties of the raw materials.

Raw materials	Moisture content (%)	pH	EC (ms/cm)	SOM (g/kg)	TN (g/kg)
Sewage sludge	8.46±1.57	6.58±0.02	3.08±0.78	190.04±5.17	13.10±0.46
Straw	3.10±0.25	7.10±0.02	1.35±0.02	582.06±2.64	7.57±0.00
Earthworm manure	7.12±1.21	6.28±0.12	5.12±0.03	115.39±9.56	4.94±0.05
Fly ash	-	9.04±0.02	0.70±0.02	-	-

Note: Each value represented on a air-dried weight base. "-" indicated below the detection limit.

Table S2. Soil water holding capacity (WHC) of 4 samples before cultivation.

Samples	Soil WHC before cultivation (g water/g soil)
1#	0.530±0.011
2#	0.570±0.014
3#	0.880±0.070
4#	0.680±0.019

Table S3. Alpha-diversity of bacterial communities in 4 samples.

Samples	Chao1	Simpson	Shannon	Good's coverage
1#	2213.01	0.992987	8.9276	0.9975
2#	2674.8	0.993799	9.45827	0.9971
3#	1741.53	0.983591	8.38793	0.9989
4#	1818.2	0.989298	8.38475	0.9993

Figure S1. Rarefaction curve for 4 technosols samples.

