Supplementary Material

Table S1. Distribution of the number of tags across the soil samples

	Sample	Seq_num	Organelle _num	Out_target_num	Chimeras _num	Filtered_num
CK0-10	CK0-10-1	44040	61	102	6169	37708
CK0-10	CK0-10-2	72904	193	19	10010	62682
CK0-10	CK0-10-3	47928	84	250	6147	41447
CK10-20	CK10-20-1	38267	49	159	2126	35933
CK10-20	CK10-20-2	49968	107	226	7202	42433
CK10-20	CK10-20-3	51387	83	227	1335	49742
CK20-30	CK20-30-1	40649	36	151	3488	36974
CK20-30	CK20-30-2	43199	21	99	310	42769
CK20-30	CK20-30-3	49248	23	214	5286	43725
CK30-40	CK30-40-1	45271	28	94	4048	41101
CK30-40	CK30-40-2	40968	26	115	438	40389
CK30-40	CK30-40-3	46980	26	185	1128	45641
SR0-10	SR0-10-1	49253	70	134	3784	45265
SR0-10	SR0-10-2	39836	210	113	1674	37839
SR0-10	SR0-10-3	43962	89	190	2769	40914
SR10-20	SR10-20-1	45038	46	205	971	43816
SR10-20	SR10-20-2	47284	75	142	7193	39874
SR10-20	SR10-20-3	50311	20	191	4580	45520
SR20-30	SR20-30-1	42941	47	170	5682	37042
SR20-30	SR20-30-2	47012	43	166	2537	44266
SR20-30	SR20-30-3	51558	34	150	1171	50203
SR30-40	SR30-40-1	44716	38	220	5174	39284
SR30-40	SR30-40-2	45939	58	134	514	45233
SR30-40	SR30-40-3	44089	19	82	1312	42676

CK 0-10, CK 10-20, CK 20-30 and CK 30-40 represent soil samples derived from control treatment at 0-10, 10-20, 20-30 and 30-40 cm depths. SR 0-10, SR 10-20, SR 20-30 and SR 30-40 represent soil samples taken from the sugarcane straw retention treatment at depths of 0-10, 10-20, 20-30 and 30-40 cm.

Table S2. Alpha diversity index

Diversity index	Depth (cm)	Treatment	
		CK	**SR**
Shannon index	0-10	7.63±0.16A[a]a[b]	7.82±0.06Aa
	10-40	7.65±0.07Aa	7.82±0.03Aa
ACE index	0-10	13189.12±4448.97Aa	19143.06±339.26Aa
	10-40	17604.97±812.78Aa	19408.38±534.97Aa
Chao1 index	0-10	9811.45±2767.28Aa	13669.78±313.80Aa
	10-40	12570.96±618.48Aa	13871.86±255.07Aa

The values at depths of 10-40 cm are weighted means CK, control; SR, sugarcane straw retention. The values within the column are mean ± SE (stand error). a Depth means that within a column followed by the same capital letter (A, B, and C) are not significantly different (P> 0.05).b The means of treatment within a depth followed by the same lowercase letter (a, b and c) are not significantly different (P> 0.05).

species accumulation curves
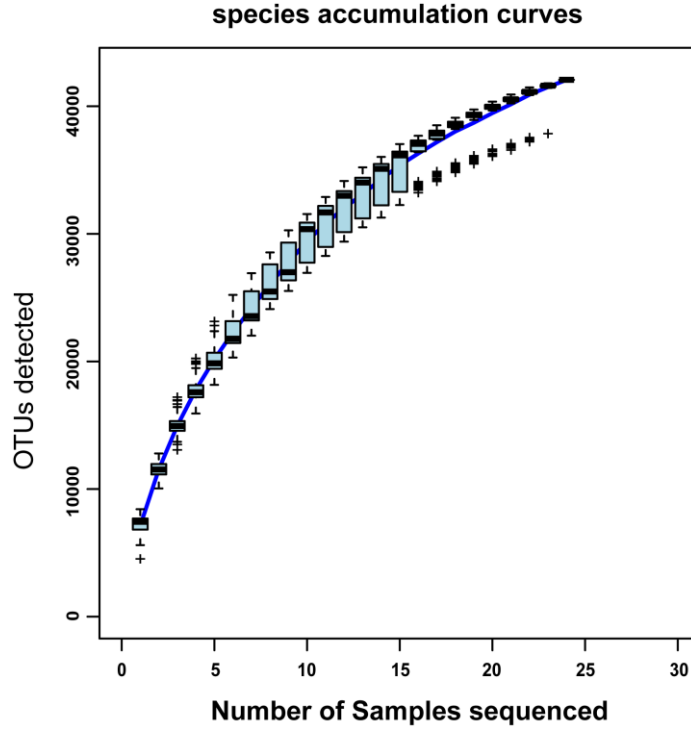
Figure S1. The species accumulation curves presenting the adequacy for sample size. With increasing sample size, the interquartile range became smaller and the detected OTUs approached 30000. After the sample size reached 15, the curve began to plateau, suggesting that the sample size selected for sequencing was sufficient for further analysis.

Table S3. The relative abundance (%) of selected genera in high-abundance phyla at 0-10 and 10-40 cm depths in the sugarcane straw retention (SR) and the control (CK) treatments

Bacterial	Soil depth(cm)	Treatments	
Genus		CK	SR
Geobacter	0-10	1.23±0.06aaAb	0.82±0.13bB
	10-40	1.72±0.19aA	1.76±0.21aA
Latescibacteria_genera_incertaesedis	0-10	1.84±0.09aA	1.57±0.04aB
	10-40	1.45±0.04bA	1.38±0.09aA
Gp6	0-10	3.85±0.43aA	3.12±0.19aA
	10-40	2.30±0.04bB	3.06±0.22aA
Subdivision3_genera_incertaesedis	0-10	4.33±0.93aA	2.89±0.33aA

	10-40	2.38±0.09aB	2.78±0.07aA
Sphingomonas	0-10	1.26±0.24aA	3.39±0.95aA
	10-40	0.73±0.10aB	1.05±0.05aA
Gp2	0-10	3.12±0.29bA	3.18±0.11bA
	10-40	5.22±0.35aA	3.77±0.14aB
Gemmatimonas	0-10	3.10±0.11aA	3.29±0.09aA
	10-40	2.43±0.20bA	2.72±0.10bA
Nitrospira	0-10	1.44±0.24bA	1.24±0.04bA
	10-40	2.31±0.18aA	1.91±0.10aA
Gp4	0-10	2.11±0.33aA	1.71±0.08aA
	10-40	1.03±0.09bA	1.48±0.15aA
Anaeromyxobacter	0-10	1.05±0.09bA	0.98±0.10bA
	10-40	1.53±0.08aA	1.54±0.17aA
Kofleria	0-10	1.59±0.21aA	1.92±0.05aA
	10-40	1.17±0.10aA	1.25±0.06bA
Gp1	0-10	5.51±0.39aA	6.11±0.53aA
	10-40	7.06±0.52aA	6.63±0.74aA
Gp3	0-10	4.62±0.47aA	4.22±0.28aA
	10-40	4.79±0.19aA	4.48±0.24aA
Gp7	0-10	1.17±0.06aA	1.20±0.11aA
	10-40	1.33±0.09aA	1.36±0.08aA
Gp5	0-10	0.99±0.15aA	1.01±0.06aA
	10-40	1.07±0.08aA	1.04±0.02aA
Gaiella	0-10	0.95±0.09aA	1.07±0.09aA
	10-40	1.02±0.08aA	0.93±0.05aA

Values at 10–40 cm depths are weighted means. CK, control; SR, sugarcane straw retention. Values in the column are means ± SE (Standard Error). a Treatment means within a depth followed by the same lower case letter (a, b, and c) are not significantly different at P = 0.05. b Depth means within a treatment followed by the same upper case letter (A, B, and C) are not significantly different at P = 0.05.