

## Supplementary Material

Table S1 Different biochar properties

Properties	Unit	WB	DMB	PWB
pH	-	8.31 ± 0.12	8.65 ± 0.23	9.21 ± 0.36
EC	mS/cm	2.11 ± 0.52	3.50 ± 0.38	1.31 ± 0.15
OM	g/kg	719.1 ± 5.2	470.1 ± 6.1	568.2 ± 4.6
N		60.4 ± 1.8	109.1 ± 3.9	49.6 ± 2.1
P	mg/kg	934.0 ± 8.6	9301.8 ± 29.3	1136 ± 6.5
K		1193.0 ± 36.5	11690.0 ± 87.2	4369.3 ± 58.2

Note: Value are mean ± standard deviation of three replicates. EC represents electrical conductivity. OM represents organic matter. N represents total available nitrogen. P represents total available phosphorus. K represents available potassium. WB represents wood biochar, DMB represents dairy manure biochar, PWB represents perishable waste biochar.

Table S2 The parameters of canonical correlation analysis of soil properties with bacterial community structure.

Parameters	CCA1	CCA2	r <sup>2</sup>	p value
pH	-0.962	-0.273	0.699	0.000
EC	-0.733	0.680	0.361	0.022
OM	-0.644	0.765	0.685	0.000
AN	0.984	-0.180	0.902	0.000
AP	-0.942	0.337	0.074	0.442
AK	-0.836	0.548	0.283	0.045
Dehydrogenase	-0.371	-0.929	0.058	0.557
Urease	0.995	-0.103	0.918	0.000
Phosphatase	0.995	0.103	0.941	0.000

Table S3 Spearman rank correlation and *p*-value of spearman correlation

Properties	<i>Proteobacteria</i>	<i>Bacteroidota</i>	<i>Acidobacteriota</i>	<i>Chloroflexi</i>	<i>Actinobacteriota</i>	<i>Patescibacteria</i>	<i>Verrucomicrobiota</i>
pH	0.452 (0.027)	0.700 <b>(0.000<sup>***</sup>)</b>	-0.487 <b>(0.016<sup>*</sup>)</b>	-0.485 <b>(0.016<sup>*</sup>)</b>	0.265 (0.211)	-0.101 (0.639)	0.108 (0.616)
EC	0.300 (0.154)	0.574 <b>(0.003<sup>**</sup>)</b>	-0.786 <b>(0.000<sup>***</sup>)</b>	-0.390 (0.060)	0.462 <b>(0.023<sup>*</sup>)</b>	0.300 (0.154)	-0.134 (0.531)
OM	-0.105 (0.625)	-0.005 (0.981)	-0.390 (0.059)	0.171 (0.424)	0.419 <b>(0.041<sup>*</sup>)</b>	0.558 <b>(0.005<sup>**</sup>)</b>	-0.010 (0.965)
AN	-0.337 (0.107)	-0.262 (0.217)	0.610 <b>(0.002<sup>**</sup>)</b>	0.238 (0.262)	-0.527 <b>(0.008<sup>**</sup>)</b>	-0.178 (0.405)	0.018 (0.932)
AP	0.226 (0.288)	0.274 (0.195)	-0.450 <b>(0.027<sup>*</sup>)</b>	-0.210 (0.324)	0.377 (0.069)	0.613 <b>(0.001<sup>**</sup>)</b>	0.152 (0.478)
AK	-0.007 (0.974)	0.114 (0.596)	-0.456 <b>(0.025<sup>*</sup>)</b>	-0.045 (0.834)	0.418 <b>(0.042<sup>*</sup>)</b>	0.751 <b>(0.000<sup>***</sup>)</b>	0.105 (0.625)
Dehydrogenase	0.054 (0.802)	0.058 (0.787)	-0.221 (0.300)	0.037 (0.862)	0.187 (0.382)	-0.063 (0.768)	-0.119 (0.579)
Urease	-0.382 (0.066)	-0.608 <b>(0.002<sup>**</sup>)</b>	0.687 <b>(0.000<sup>***</sup>)</b>	0.459 <b>(0.024<sup>*</sup>)</b>	-0.399 (0.053)	0.073 (0.734)	-0.053 (0.806)
Phosphatase	-0.457 <b>(0.025<sup>*</sup>)</b>	-0.365 (0.079)	0.578 <b>(0.003<sup>**</sup>)</b>	0.103 (0.630)	-0.417 <b>(0.042<sup>*</sup>)</b>	-0.090 (0.677)	0.140 (0.514)

Table S4 Properties of co-occurrence networks obtained under different test conditions

Topological properties	Average degree	Eigenvector centrality	Network density	Modularity
WB5	21.167	0.0121	0.450	0.498
WB10	20.383	0.0038	0.443	0.341
DMB5	18.298	0.0002	0.398	0.522
DMB10	15.875	0.0129	0.338	0.590
PWB5	21.000	0.0058	0.447	0.381
PWB10	16.130	0.0120	0.358	0.562
CDG	15.592	0.0196	0.325	0.644
RCA	16.000	0.0142	0.333	0.605

Table S5 Key species in soil bacterial networks across percentage.

Phylum	WB5	WB10	DMB5	DMB10	PWB5	PWB10	CDG	RCA
<i>Proteobacteria</i>	45.83%	40.43%	38.30%	37.5%	35.42%	52.17%	30.61%	59.18%
<i>Bacteroidota</i>	16.67%	14.89%	14.89%	18.75%	18.75%	2.17%	4.08%	20.41%
<i>Acidobacteriota</i>	6.25%	6.38%	8.51%	6.25%	6.25%	10.87%	36.73%	6.12%
<i>Actinobacteriota</i>	6.25%	4.26%	6.38%	2.08%	6.25%	4.35%	-	-
<i>Planctomycetota</i>	4.17%	-	2.13%	2.08%	2.08%	-	2.04%	-
<i>Chloroflexi</i>	4.17%	4.26%	6.38%	6.25%	6.25%	13.04%	6.12%	4.08%
<i>Verrucomicrobiota</i>	4.17%	10.64%	4.26%	2.08%	6.25%	-	-	-
<i>Deinococcota</i>	4.17%	4.26%	2.13%	2.08%	2.08%	-	-	2.04%
<i>Nitrospirota</i>	2.08%	2.13%	2.13%	2.08%	2.08%	-	8.16%	2.04%
<i>Spirochaetota</i>	2.08%	2.13%	2.13%	-	2.08%	-	-	-
<i>Gemmatimonadota</i>	2.08%	4.26%	4.26%	2.08%	2.08%	2.17%	-	2.04%
<i>Patescibacteria</i>	2.08%	2.13%	6.38%	8.33%	6.25%	13.04%	-	2.04%
<i>Firmicutes</i>	-	4.26%	-	2.08%	-	-	-	-
<i>Bdellovibrionota</i>	-	-	2.13%	-	2.08%	-	-	-
<i>Myxococcota</i>	-	-	-	6.25%	-	2.17%	4.08%	-
<i>Dependentiae</i>	-	-	-	2.08%	2.08%	-	-	2.04%
<i>Latescibacterota</i>	-	-	-	-	-	-	4.08%	-
<i>Methylomirabilota</i>	-	-	-	-	-	-	2.04%	-
<i>Dadabacteria</i>	-	-	-	-	-	-	2.04%	-

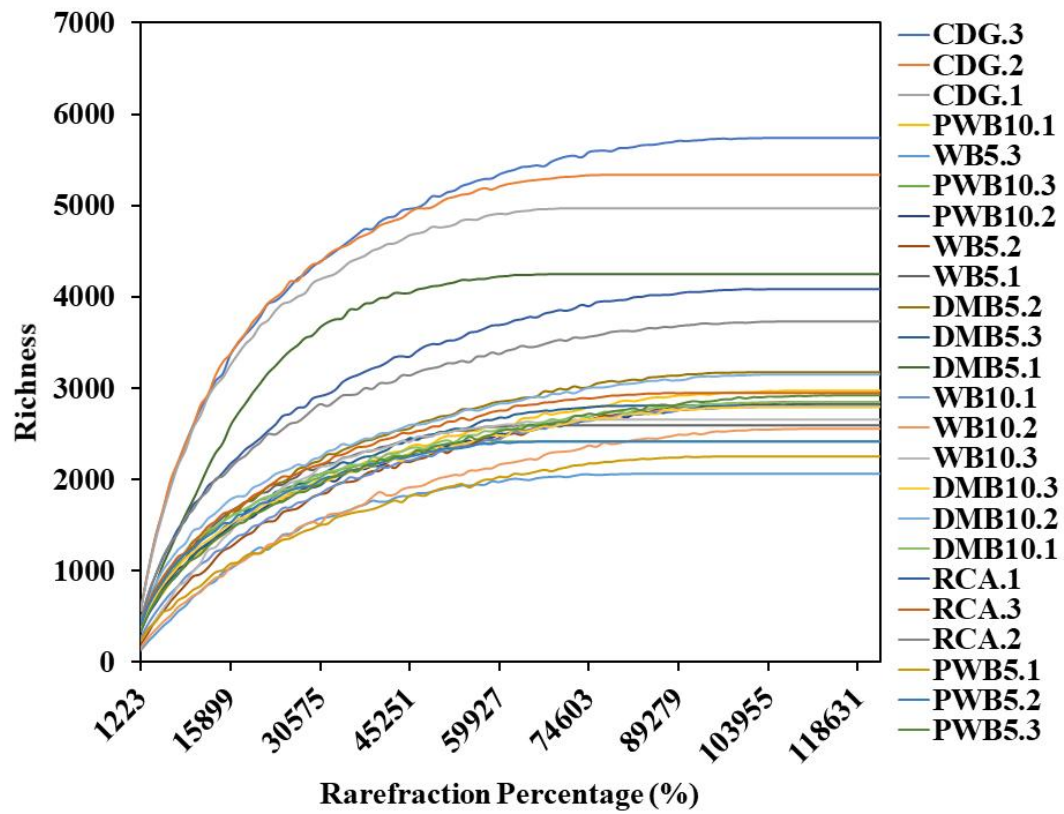


Fig. S1 Dilution Curve Analysis of Soil Sample Sequencing Depth in different test treatments. For each test treatment, three replicates were presented.