

Supplementary materials

Effects of vegetation restoration on soil bacterial communities, enzyme activities, and nutrients of reconstructed soil in a mining area on the Loess Plateau, China

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Table S1 Basic description of the sampling sites.

Vegetation restoration modes	Abbreviation	Altitude (m)	Main species
Brushland	BL1	1257	<i>C. mirophylla; H.rhamnoides</i>
	BL2	1206	<i>A. fruticosa; C. mirophylla</i>
	BL3	1225	<i>H. rhamnoides; P.humilis</i>
Forestland	FL1	1262	<i>P. tabulaeformis; P. beijingensis; P. sylvestris</i>
	FL2	1263	<i>P. beijingensis</i>
	FL3	1201	<i>P. sibirica</i>
Grassland	GL1	1245	<i>P. sphondyloides; A. cristatum; S. bungeana</i>
	GL2	1249	<i>H. altaicus; M. sativa</i>
	GL3	1262	<i>A. adsurgens; S. bungeana; M. sativa; A. cristatum</i>
Unreclaimed land	UL1	1255	None
	UL2	1253	None

Table S2 Adonis analysis between different sampling sites

Group	Df	Sum of Sq	F	R ²	Pr (>F)
BL~FL	1	0.004	0.244	0.058	0.7
BL~GL	1	0.008	0.799	0.167	0.6
BL~UL	1	0.092	11.03	0.786	0.1
FL~UL	1	0.124	5.067	0.628	0.1
GL~FL	1	0.022	1.033	0.205	0.5
GL~UL	1	0.066	3.951	0.568	0.2

Note: The results of Adonis analysis indicate that bacterial communities have no significant difference with four sampling sites ($P < 0.01$). BL: Brushland, FL: Forestland, GL: Grassland, UL: Unreclaimed land

Table S3 Pearson's correlation coefficients relating soil biochemical properties to relative abundance of the dominant bacterial groups at the phylum level

	Moisture	pH	SOM	AN	AP	CAT	ALP	URE	SUC	MBC	MBN
<i>Acidobacteria</i>	0.58	-0.34	0.48	0.78**	-0.09	0.66*	0.06	0.56	0.45	0.50	0.46
<i>Actinobacteria</i>	0.03	-0.31	-0.45	-0.69*	0.80**	-0.57	-0.52	-0.62	-0.81**	-0.52	-0.79**
<i>Bacteroidetes</i>	0.20	0.58	-0.09	-0.18	0.19	-0.38	0.48	-0.23	-0.02	-0.03	0.31
<i>Chloroflexi</i>	0.66*	-0.56	0.48	0.54	-0.19	0.55	-0.18	0.50	0.26	0.42	0.14
<i>Cyanobacteria</i>	-0.32	0.31	-0.27	-0.72*	0.27	-0.84**	-0.10	-0.60	-0.41	-0.44	-0.50
<i>Gemmatimonadetes</i>	0.65*	-0.90**	0.05	0.70*	-0.01	0.69*	-0.14	0.58	0.19	0.42	0.25
<i>Nitrospirae</i>	0.68*	-0.45	0.86**	0.80**	0.15	0.14	0.18	0.54	0.55	0.79**	0.53
<i>Proteobacteria</i>	0.49	0.46	0.77**	0.29	-0.78**	0.11	0.63*	0.24	0.41	0.24	0.66*
<i>Saccharibacteria</i>	-0.44	0.62*	-0.50	-0.82**	0.01	-0.68*	-0.26	-0.65*	-0.51	-0.73*	-0.58
<i>Verrucomicrobia</i>	0.52	-0.36	-0.19	-0.27	0.06	-0.32	-0.52	-0.09	-0.26	-0.08	-0.42

Note: *Correlation is significant at $P < 0.05$ (two-tailed); **Correlation is significant at $P < 0.01$ (two-tailed)

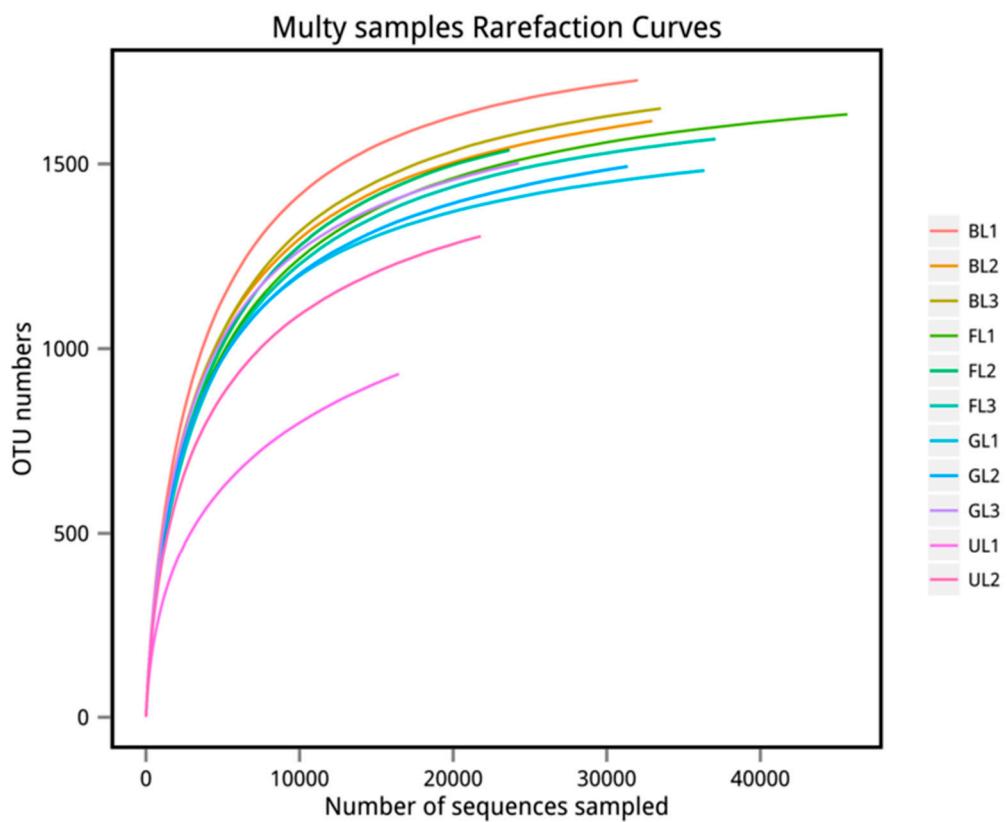


Figure S1 Rarefaction curve analysis for four sampling sites.

Note: at a similarity level of 97%, BL: Brushland, FL: Forestland, GL: Grassland, UL: Unreclaimed land.

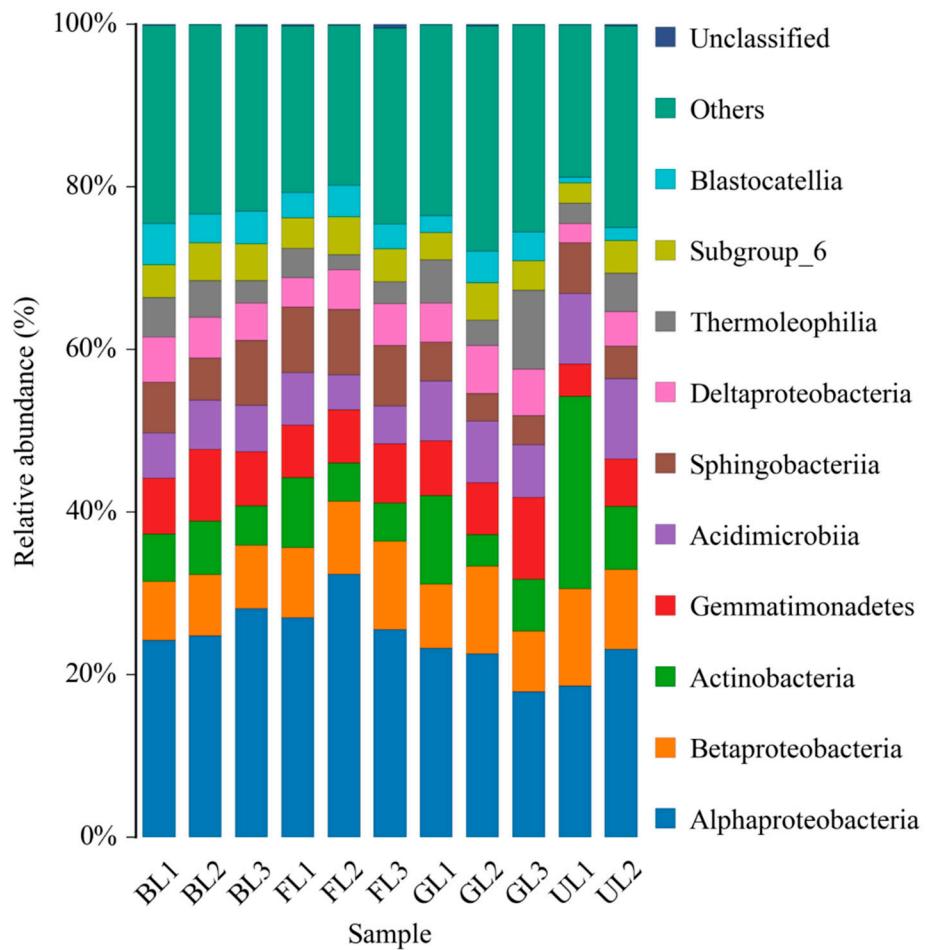


Figure S2 Relative abundance of bacteria at class level.