Table S1 Topological properties of collinear network of soil bacterial communities

Network indicators	W0P0	W0P1	W1P0	W1P1
Nodes	59	51	60	80
Edges	100	100	100	100
average_degree	3.39	3.922	3.333	2.5
clustering_coefficient	0.095	0.176	0.113	0.053
betweenness_centralization	0.183	0.215	0.201	0.236
degree_centralization	0.442	0.422	0.469	0.462
Graph density（GD）	0.058	0.078	0.056	0.032
Modularity（MD）	0.49	0.403	0.394	0.633

Table S2 Topological properties of collinear network of soil fungal communities

Network indicators	W0P0	W0P1	W1P0	W1P1
Nodes	59	51	60	80
Edges	100	100	100	100
average_degree	2.597	3.03	2.5	3.509
clustering_coefficient	0.059	0.474	0.055	0.148
betweenness_centralization	0.116	0.141	0.095	0.299
degree_centralization	0.4	0.092	0.31	0.491
Graph density（GD）	0.034	0.047	0.032	0.063
Modularity（MD）	0.567	0.721	0.625	0.428

Table S3 Topological properties of collinear network of soil bacterial and fungal communities

Network indicators	W0P0	W0P1	W1P0	W1P1
Nodes	100	100	100	100
Edges	1609	1572	1572	1634
Positive correlation edge proportion	49.10%	48.92%	50.45%	53.06%

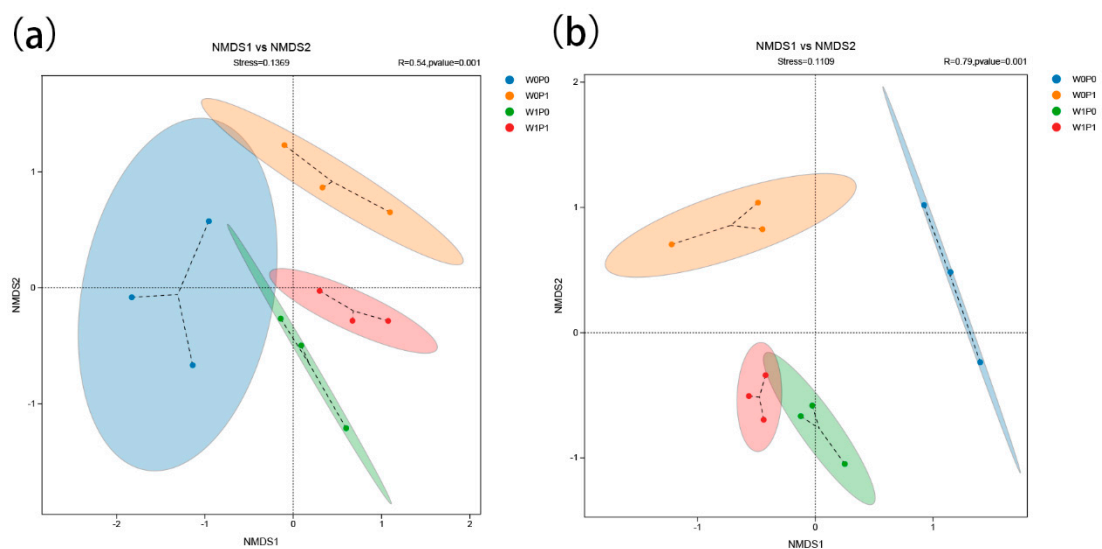|				
Negative correlation edge proportion	50.90%	51.08%	49.55%	46.94%
Graph density（GD）	0.325	0.318	0.318	0.33
Modularity（MD）	0.646	0.65	0.65	0.57

Figure S1 Non-metric multi-dimensional scaling (NMDS) plots of bacterial (a) and fungus (b) communities based on Bray-Curtis dissimilarities
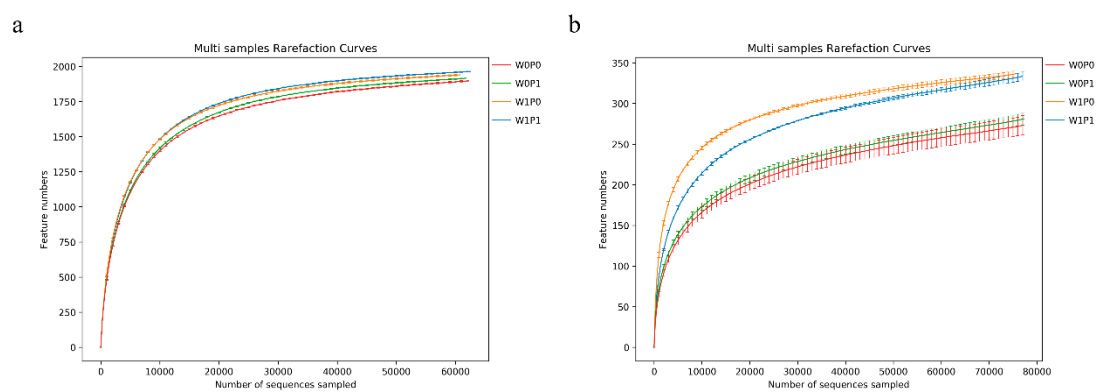

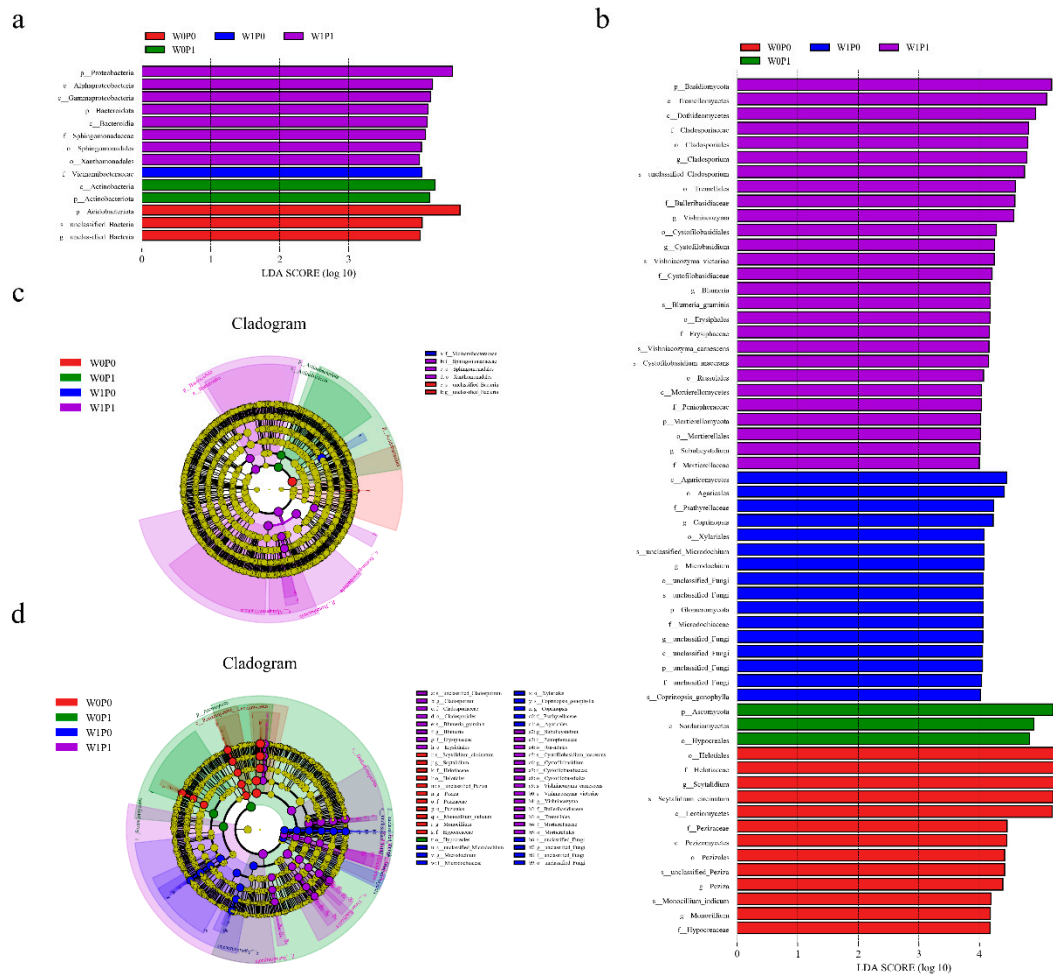Figure S2 Rarefaction curves of (a) 16S rRNA genes and (b) ITS genes.

Figure S3 LEfSe analysis results showed that there were significant differences in soil bacterial groups (a) and fungal communities (b) under the four treatments; Cladogram plotted from LEfSe analysis showing significant differences (P < 0.05) in relative abundance of ITS gene-based bacterial taxa (c) and fungal taxa (d) across the five treatments.