

**Table S1** Shannon and Faith's PD indices before and after transplanting in different microhabitats. All values were an average from all replicates  $\pm$  standard deviations. Black asterisks represent significant differences based on the ANOVA test. Values with the same letters within a column did not significantly differ based on the Tukey's multiple comparisons test.

Alpha diversity index	IS	IG	TS	TG
<b>Bacteria (Mean<math>\pm</math>SD)</b>				
Shannon*	7.28 $\pm$ 0.35a	7.27 $\pm$ 0.23a	5.84 $\pm$ 0.63b	6.74 $\pm$ 0.24a
Faith's PD*	250.44 $\pm$ 8.28a	258.93 $\pm$ 15.15a	222.14 $\pm$ 16.77b	244.66 $\pm$ 11.35a
<b>Fungi (Mean<math>\pm</math>SD)</b>				
Shannon	4.54 $\pm$ 0.18a	4.32 $\pm$ 0.66a	4.41 $\pm$ 0.42a	4.53 $\pm$ 0.35a
Faith's PD	172.97 $\pm$ 11.9a	186.5 $\pm$ 29.51a	172.64 $\pm$ 39.73a	175.08 $\pm$ 14.97a

**Table S2** The relative abundance of top 10 class level before and after transplanting in different microhabitats. All values were an average from all replicates  $\pm$  standard deviations. Black asterisks represent significant differences based on the ANOVA test. Values with the same letters within a column did not significantly differ based on the Tukey's multiple comparisons test.

	IS	IG	TS	TG
Class level of Bacteria (Mean $\pm$ SD)				
Alphaproteobacteria	16.66 $\pm$ 4.35a	18.19 $\pm$ 2.88a	17.68 $\pm$ 3.52a	22.06 $\pm$ 3.06a
<b>Gammaproteobacteria *</b>	12.07 $\pm$ 6.05b	6.39 $\pm$ 1.31b	30.71 $\pm$ 9.36a	10.47 $\pm$ 3.88b
Actinobacteria	14.75 $\pm$ 7.14a	15.58 $\pm$ 4.53a	13.71 $\pm$ 4.88a	10.09 $\pm$ 1.71a
<b>Unassigned *</b>	9.04 $\pm$ 3.52ab	11.11 $\pm$ 3.78ab	6.86 $\pm$ 1.89b	13.41 $\pm$ 3.36a
<b>Gemmatimonadetes *</b>	4.25 $\pm$ 0.75b	10.58 $\pm$ 2.14a	5.52 $\pm$ 2.74b	11.32 $\pm$ 2.89a
<b>Betaproteobacteria *</b>	6.97 $\pm$ 2.41a	7.22 $\pm$ 0.87a	3.96 $\pm$ 0.96b	7.37 $\pm$ 0.44a
Acidobacteria_Gp1	1.87 $\pm$ 1.72a	4.19 $\pm$ 1.86a	3.01 $\pm$ 0.81a	4.64 $\pm$ 1.7a
<b>Sphingobacteriia *</b>	1.96 $\pm$ 0.44b	1.47 $\pm$ 0.34b	4.06 $\pm$ 0.53a	2.29 $\pm$ 1.14b
<b>Acidobacteria_Gp6 *</b>	5.37 $\pm$ 3.03a	2.83 $\pm$ 0.95b	0.47 $\pm$ 0.17b	1.09 $\pm$ 0.37ab
<b>Deltaproteobacteria *</b>	4.63 $\pm$ 2.18a	2.64 $\pm$ 0.98ab	0.72 $\pm$ 0.37b	1.36 $\pm$ 0.49b
<b>LowAbundance *</b>	22.43 $\pm$ 3.57a	19.79 $\pm$ 1.93ab	13.31 $\pm$ 2.32c	15.89 $\pm$ 4.56bc
Class level of Fungi (Mean $\pm$ SD)				
<b>Sordariomycetes *</b>	48.24 $\pm$ 11.61a	23.62 $\pm$ 14.12b	44.8 $\pm$ 4.91b	42.99 $\pm$ 8.8b
<b>Unassigned *</b>	16.61 $\pm$ 10.31ab	23.42 $\pm$ 5.53a	13.17 $\pm$ 1.14ab	9.2 $\pm$ 2.55b
Agaricomycetes	4.26 $\pm$ 2.55a	17.6 $\pm$ 15.36a	8.3 $\pm$ 7.48a	11.57 $\pm$ 13.06a
<b>Mortierellomycetes *</b>	7.13 $\pm$ 6.34ab	15.21 $\pm$ 5.49a	3.1 $\pm$ 2.17b	8.84 $\pm$ 5.41ab
Leotiomycetes	7.08 $\pm$ 1.74a	7.94 $\pm$ 4.01a	6.47 $\pm$ 3.12a	5.67 $\pm$ 4.27a
Eurotiomycetes	6.84 $\pm$ 5.57a	2.72 $\pm$ 0.92a	10.05 $\pm$ 5.75a	5.05 $\pm$ 3.78a

Dothideomycetes	4.31±1.26a	3.01±2.04a	6.01±3.03a	5.48±2.07a
Tremellomycetes	2.46±1.11a	2.67±0.82a	4.91±2.5a	5.1±4.73a
Pezizomycetes	0.96±0.53a	1.08±0.7a	1.32±1.71a	2.2±1.85a
Spizellomycetes	1.02±2.03a	0.03±0.03a	0.98±1.48a	2.86±3.37a
LowAbundance	1.08±0.26a	2.71±2.55a	0.89±0.87a	1.04±0.73a

**Table S3** Properties of the microbiota association networks before and after transplanting in different microhabitats.

Properties of the networks	IS	IG	TS	TG
<b>Bacterial community</b>				
Nodes <sup>a</sup>	211	360	285	361
Edges <sup>b</sup>	1565	1268	1359	1624
Average degree distribution <sup>c</sup>	14.83	7.04	9.54	8.99
Average clustering coefficient <sup>d</sup>	0.33	0.51	0.39	0.47
Average path length <sup>e</sup>	4.85	12.25	5.68	8.26
Modularity <sup>f</sup>	0.67	0.84	0.69	0.81
Modules	14	23	24	19
<b>Fungal community</b>				
Nodes <sup>a</sup>	163	140	179	171
Edges <sup>b</sup>	762	560	421	490
Average degree distribution <sup>c</sup>	9.35	8.00	4.70	5.73
Average clustering coefficient <sup>d</sup>	0.37	0.34	0.31	0.34
Average path length <sup>e</sup>	4.01	4.02	3.80	2.18
Modularity <sup>f</sup>	0.61	0.73	0.84	0.77
Modules	20	14	24	19

<sup>a</sup> Number of AVSs with the Spearman correlation  $|r| > 0.8$  and P-value  $< 0.05$ . <sup>b</sup> Number of significant (P-value  $< 0.05$ ) correlations between nodes. <sup>c</sup> The larger the average distribution, the more complex the network distribution. <sup>d</sup> How nodes were embedded in their neighborhood, and the degree to which nodes tend to cluster together. <sup>e</sup> The capability of the nodes to form highly connected communities. <sup>f</sup> Modularity  $> 0.4$  suggested that the network has a modular structure.

**Table S4** Different types of ASVs, species classification, and average relative abundance in different groups. The bold numbers represented the relative abundance of ASV within the top 30 of the group.

No.	Name	Contribution rate (%) <sup>a</sup>	MeanDecrease Accuracy <sup>b</sup>	Type	Species classification		Average relative abundance			
					Class	Genus	IS	IG	TS	TG
Bacteria										
1	bASV_57	-	2.519	Important ASVs	Gammaproteobacteria	<i>Rhodanobacter</i>	0.000	0.014	<b>0.449</b>	0.054
2	bASV_75	-	2.438		Gemmatimonadetes	<i>Gemmatimonas</i>	0.015	<b>0.302</b>	0.003	0.007
3	bASV_16	-	2.110		Gammaproteobacteria	<i>Mizugakiibacter</i>	0.001	0.086	<b>1.172</b>	<b>0.370</b>
4	bASV_2	1.88	-		Gammaproteobacteria	<i>Mizugakiibacter</i>	0.023	<b>0.661</b>	<b>7.222</b>	<b>1.399</b>
5	bASV_9	0.33	-	Functional ASVs	Alphaproteobacteria	Unassigned	<b>0.350</b>	0.141	<b>0.789</b>	<b>0.776</b>
6	bASV_40	0.20	-		Gemmatimonadetes	<i>Gemmatimonas</i>	0.001	0.105	0.087	<b>0.773</b>
7	bASV_44	0.20	-		Alphaproteobacteria	Unassigned	<b>0.160</b>	0.074	<b>0.708</b>	0.134
8	bASV_22	0.18	-		Ktedonobacteria	Unassigned	0.002	<b>0.422</b>	<b>0.557</b>	<b>0.444</b>
9	bASV_90	0.16	-		Sphingobacteriia	<i>Chitinophaga</i>	0.000	0.013	0.128	<b>0.548</b>
10	bASV_46	0.14	-		Sphingobacteriia	Unassigned	0.003	0.075	<b>0.473</b>	0.151
11	bASV_87	0.11	-		Alphaproteobacteria	<i>Devosia</i>	0.087	0.148	0.221	<b>0.409</b>
12	bASV_230	0.09	-		Alphaproteobacteria	<i>Lacibacterium</i>	<b>0.304</b>	0.067	0.041	0.016
13	bASV_672	0.07	-		Acidobacteria_Gp16	<i>Gp16</i>	<b>0.224</b>	0.229	0.064	0.091
14	bASV_123	0.07	-		Alphaproteobacteria	<i>Pseudolabrys</i>	<b>0.231</b>	0.113	0.039	0.065
15	bASV_200	0.05	-		Betaproteobacteria	<i>Nitrosospira</i>	<b>0.201</b>	0.018	0.002	0.002
16	bASV_159	0.05	-		Acidobacteria_Gp1	<i>Gp1</i>	<b>0.175</b>	0.028	0.005	0.001
17	bASV_11	0.36	1.449		Gammaproteobacteria	<i>Rhodanobacter</i>	0.009	0.044	<b>1.114</b>	<b>0.403</b>
18	bASV_10	0.29	2.354		Acidobacteria_Gp1	<i>Acidobacterium</i>	0.004	0.069	<b>0.952</b>	<b>0.363</b>

19	bASV_35	0.15	1.175	Important functional ASVs	Alphaproteobacteria	Unassigned	0.109	0.037	<b>0.611</b>	0.121
20	bASV_31	0.15	1.401		Alphaproteobacteria	<i>Bradyrhizobium</i>	<b>0.414</b>	<b>0.270</b>	0.056	0.040
<b>Fungi</b>										
1	fASV_1	-	3.354	Important ASVs	Sordariomycetes	<i>Fusarium</i>	<b>7.308</b>	0.432	<b>8.566</b>	<b>3.489</b>
2	fASV_6	-	2.188		Sordariomycetes	Unassigned	0.128	0.158	<b>6.608</b>	0.157
3	fASV_32	-	2.405		Unassigned	Unassigned	0.005	0.011	0.101	<b>2.218</b>
4	fASV_45	-	2.273		Unassigned	Unassigned	0.310	<b>1.828</b>	0.055	0.007
5	fASV_28	-	3.166		Sordariomycetes	<i>Staphylotrichum</i>	<b>1.189</b>	0.208	<b>0.677</b>	0.098
6	fASV_65	-	2.173		Eurotiomycetes	Unassigned	<b>0.977</b>	0.011	0.000	0.003
7	fASV_70	-	3.275		Mortierellomycetes	<i>Mortierella</i>	0.000	<b>0.874</b>	0.000	0.003
8	fASV_121	-	2.147		Mortierellomycetes	<i>Mortierella</i>	0.057	0.005	0.030	<b>0.758</b>
9	fASV_78	-	3.004		Sordariomycetes	Unassigned	0.018	0.000	0.004	<b>0.738</b>
10	fASV_111	-	2.294		Unassigned	Unassigned	0.023	0.003	<b>0.620</b>	0.016
11	fASV_98	-	2.237	Leotiomycetes	<i>Pseudogymnoascus</i>	0.000	0.002	0.000	0.657	
12	fASV_13	1.02	-	Tremellomycetes	<i>Guehomyces</i>	0.541	<b>0.634</b>	<b>1.987</b>	<b>2.846</b>	
13	fASV_14	0.91	-	Mortierellomycetes	<i>Mortierella</i>	<b>2.143</b>	<b>1.747</b>	0.229	0.054	
14	fASV_20	0.68	-	Sordariomycetes	Unassigned	<b>1.289</b>	0.011	<b>1.345</b>	<b>1.394</b>	
15	fASV_10	0.90	-	Unassigned	Unassigned	<b>3.421</b>	0.377	0.103	0.044	
16	fASV_39	0.69	-	functional ASVs	Sordariomycetes	<i>Gibberella</i>	0.036	0.075	<b>0.871</b>	<b>1.919</b>
17	fASV_42	0.64	-		Dothideomycetes	<i>Alternaria</i>	0.097	0.025	<b>1.416</b>	<b>1.220</b>
18	fASV_34	0.41	-		Mortierellomycetes	<i>Mortierella</i>	<b>0.941</b>	<b>1.063</b>	0.413	0.331
19	fASV_84	0.33	-		Tremellomycetes	<i>Solicoccozyma</i>	0.292	0.084	<b>1.110</b>	0.502
20	fASV_69	0.27	-		Tremellomycetes	<i>Solicoccozyma</i>	0.496	<b>0.847</b>	0.304	0.181
21	fASV_40	0.38	-		Sordariomycetes	<i>Cephalotrichum</i>	0.278	<b>1.240</b>	0.035	0.023

22	fASV_85	0.24	-		Sordariomycetes	<i>Dactylonectria</i>	0.043	<b>0.908</b>	0.009	0.004
23	fASV_2	2.37	2.982		Unassigned	Unassigned	<b>4.150</b>	<b>8.774</b>	<b>4.187</b>	<b>0.798</b>
24	fASV_31	0.49	2.301	Important Functional ASVs	Sordariomycetes	<i>Fusarium</i>	<b>0.804</b>	0.208	<b>1.510</b>	<b>1.070</b>
25	fASV_18	0.40	1.412		Unassigned	<i>Unassigned</i>	0.055	0.031	<b>1.109</b>	0.580
26	fASV_52	0.36	2.383		Leotiomycetes	<i>Geomyces</i>	0.208	0.074	<b>1.055</b>	0.596
27	fASV_113	0.31	2.522		Mortierellomycetes	<i>Mortierella</i>	0.091	<b>1.174</b>	0.031	0.046
28	fASV_44	0.31	2.288		Sordariomycetes	<i>Unassigned</i>	<b>0.841</b>	0.023	0.360	0.577

<sup>a</sup> Contribution rate of ASVs that significantly contribute to community differences using SIMPER's algorithm. <sup>b</sup> The mean decrease accuracy of feature importance ASVs obtained through the random forest algorithm.