

Table S1 The dominant bacterial genera and their relative abundance in the soil of three plots

Samples	Genus	The relative abundance
PA	<i>Subgroup_6</i>	4.34%
	<i>Candidatus_Udaeobacter</i>	3.57%
	<i>Thiobacillus</i>	2.86%
	<i>KD4-96</i>	2.27%
	<i>Bradyrhizobium</i>	2.11%
	<i>Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium</i>	1.63%
	<i>Subgroup_2</i>	1.60%
	<i>Mycobacterium</i>	1.15%
	<i>Sphingomonas</i>	1.15%
	<i>RB41</i>	1.04%
PB	<i>Burkholderia-Caballeronia-Paraburkholderia</i>	12.62%
	<i>Subgroup_2</i>	5.25%
	<i>Bradyrhizobium</i>	3.26%
	<i>Acidothermus</i>	2.50%
	<i>Bryobacter</i>	2.48%
	<i>Mycobacterium</i>	1.91%
	<i>Candidatus_Solibacter</i>	1.78%
	<i>Candidatus_Udaeobacter</i>	1.75%
	<i>Roseiarcus</i>	1.70%
	<i>AD3</i>	1.60%
	<i>Granulicella</i>	1.48%
	<i>Candidatus_Xiphinematobacter</i>	1.34%
	<i>Subgroup_6</i>	1.30%
	<i>Conexibacter</i>	1.22%
PC	<i>Subgroup_2</i>	4.99%

<i>Bradyrhizobium</i>	3.96%
<i>Subgroup_6</i>	3.53%
<i>Burkholderia-Caballeronia-Paraburkholderia</i>	3.18%
<i>Candidatus_Udaeobacter</i>	2.63%
<i>Mycobacterium</i>	2.54%
<i>Bryobacter</i>	2.28%
<i>Acidothermus</i>	1.62%
<i>Candidatus_Solibacter</i>	1.45%
<i>AD3</i>	1.38%
<i>KD4-96</i>	1.38%
<i>Sphingomonas</i>	1.38%
<i>RB41</i>	1.18%
<i>IMCC26256</i>	1.10%
<i>Conexibacter</i>	1.03%
<i>Roseiarcus</i>	1.01%

Note: PA, the soil sample from the plot A (132°3'2.35"E, 46°7'20.19"N, 230m asl); PB, soil sample from the plot B (132°3'2.35"E, 46°7'20.19"N, 230m asl); PC, soil sample from the plot C (129°39'52.70"E, 42°33'31.75"N, 380 m asl).