

Table S4. Spearman's rank correlation coefficients between relative abundance of OTUs and depth of serpentine minerals.

Taxonomy	Spearman's rank correlation coefficient	p-value*
k__Bacteria; p__Acidobacteria; c__Acidobacteria-6; o__iii1-15; f__ ; g__ ; s__	-0.7698168	0.0138233
k__Bacteria; p__Actinobacteria; c__Acidimicrobiia; o__Acidimicrobiales; f__ ; g__ ; s__	-0.81075183	0.00425812
k__Bacteria; p__Actinobacteria; c__Acidimicrobiia; o__Acidimicrobiales; f__ ; g__ ; s__	-0.77387235	0.01349225
k__Bacteria; p__Actinobacteria; c__Acidimicrobiia; o__Acidimicrobiales; f__ ; g__ ; s__	-0.7698168	0.0138233
k__Bacteria; p__Actinobacteria; c__Acidimicrobiia; o__Acidimicrobiales; f__ ; g__ ; s__	-0.76385923	0.0138233
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Actinosynnemataceae; g__ ; s__	0.73764792	0.02773051
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Nocardioidaceae; g__ ; s__	-0.7757131	0.0131689
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Pseudonocardiaceae; g__Amycolatopsis; s__	0.76431618	0.0138233
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Streptomycetaceae; g__Streptomyces; s__	0.73537608	0.02932494
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Streptomycetaceae; g__Streptomyces; s__	0.80667195	0.00478713
k__Bacteria; p__Actinobacteria; c__MB-A2-108; o__0319-7L14; f__ ; g__ ; s__	0.72063347	0.04441844
k__Bacteria; p__Actinobacteria; c__Thermoleophilia; o__Gaiellales; f__Gaiellaceae; g__ ; s__	-0.78609424	0.00854366
k__Bacteria; p__Actinobacteria; c__Thermoleophilia; o__Gaiellales; f__Gaiellaceae; g__ ; s__	-0.74966213	0.02017219
k__Bacteria; p__Actinobacteria; c__Thermoleophilia; o__Gaiellales; f__Gaiellaceae; g__ ; s__	-0.720236	0.04441844
k__Bacteria; p__Actinobacteria; c__Thermoleophilia; o__Gaiellales; f__Gaiellaceae; g__ ; s__	0.75973718	0.01472673
k__Bacteria; p__Actinobacteria; c__Thermoleophilia; o__Solirubrobacterales; f__ ; g__ ; s__	-0.71579186	0.04931098
k__Bacteria; p__Actinobacteria; c__Thermoleophilia; o__Solirubrobacterales; f__Conexibacteraceae; g__ ; s__	0.82413459	0.00299772

k__Bacteria; p__Actinobacteria; c__Thermoleophilia; o__Solirubrobacterales; f__Solirubrobacteraceae; g__ ; s__	0.75985048	0.01472673
k__Bacteria; p__Chloroflexi; c__Ellin6529; o__ ; f__ ; g__ ; s__	-0.72190739	0.04399233
k__Bacteria; p__Chloroflexi; c__P2-11E; o__ ; f__ ; g__ ; s__	0.73471789	0.02932494
k__Bacteria; p__Chloroflexi; c__P2-11E; o__ ; f__ ; g__ ; s__	0.74567669	0.0222152
k__Bacteria; p__Chloroflexi; c__P2-11E; o__ ; f__ ; g__ ; s__	0.75027611	0.02017219
k__Bacteria; p__Chloroflexi; c__TK10; o__B07_WMSP1; f__ ; g__ ; s__	-0.79882273	0.0055392
k__Bacteria; p__GAL15; c__ ; o__ ; f__ ; g__ ; s__	0.7561646	0.01652607
k__Bacteria; p__GAL15; c__ ; o__ ; f__ ; g__ ; s__	0.75985048	0.01472673
k__Bacteria; p__Gemmatimonadetes; c__Gemmatimonadetes; o__ ; f__ ; g__ ; s__	-0.83956694	0.00130184
k__Bacteria; p__Planctomycetes; c__Phycisphaerae; o__WD2101; f__ ; g__ ; s__	-0.88922654	5.27E-05
k__Bacteria; p__Planctomycetes; c__Phycisphaerae; o__WD2101; f__ ; g__ ; s__	-0.81089351	0.00425812
k__Bacteria; p__Proteobacteria; c__ ; o__ ; f__ ; g__ ; s__	-0.76722679	0.0138233
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Methylobacteriaceae; g__Methylobacterium; s__	0.84975305	0.00119961
k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__ ; f__ ; g__ ; s__	0.80045081	0.0055392
k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Comamonadaceae	0.74372798	0.0232746
k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Comamonadaceae; g__ ; s__	0.74102212	0.0250986
k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Comamonadaceae; g__ ; s__	0.74639294	0.0222152
k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Comamonadaceae; g__Delftia; s__	0.76377902	0.0138233
k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Oxalobacteraceae; g__ ; s__	0.71636767	0.04931098
k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Oxalobacteraceae; g__ ; s__	0.76464189	0.0138233
k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Oxalobacteraceae; g__ ; s__	0.78802707	0.00831419

k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Oxalobacteraceae; g__ ; s__	0.84139357	0.00130184
k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__MND1; f__ ; g__ ; s__	-0.81784035	0.00371264
k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__MND1; f__ ; g__ ; s__	-0.76848635	0.0138233
Unassigned	-0.7990866	0.0055392
Unassigned	-0.79150895	0.00750589
Unassigned	-0.76889889	0.0138233
Unassigned	-0.72782432	0.03667223

* p-value corrected by the Benjamini-Hochberg FDR procedure for multiple comparisons.