

Table S2. Phylogenetic diversity (PD), net relatedness index (NRI), and nearest taxa index (NTI) results for the 16S rRNA gene (16S rDNA) and 18S rRNA gene (18S rDNA) sequences, respectively.

Mineral	Horizon	Community	16S rDNA				18S rDNA			
			PD	<i>N</i>	NRI	NTI	PD	<i>N</i>	NRI	NTI
Apatite	O	Ap_O_1	28.26	139	0.03	-2.01	67.44	135	-1.21	-1.29
		Ap_O_2	85.94	730	1.30	1.54	34.17	59	-1.38	-1.26
	E	Ap_E_1	114.81	1136	7.36	4.72	NA	NA	NA	NA
		Ap_E_2	92.61	992	6.54	5.18	89.40	110	3.60	-0.49
	B	Ap_B_1	59.31	413	0.13	0.23	103.16	183	-0.55	-1.00
		Ap_B_2	97.87	864	4.78	3.32	67.55	170	-1.71	-1.80
Biotite	O	Bio_O_1	55.24	377	-0.66	-0.05	NA	NA	NA	NA
		Bio_O_2	15.37	70	0.56	1.85	39.72	61	-1.37	-1.48
	E	Bio_E_1	23.18	118	-2.17	-3.74	51.15	97	-1.31	-1.68
		Bio_E_2	38.67	257	-3.09	-1.16	92.67	200	-1.40	-2.11
	B	Bio_B_1	50.84	361	-3.58	-4.05	277.68	973	-0.96	-1.22
		Bio_B_2	25.84	141	1.25	1.51	108.88	254	-1.27	-1.02
Oligoclase	O	Oli_O_1	9.61	43	0.03	0.73	292.99	848	-3.24	-3.38
	E	Oli_E_1	21.24	87	0.18	1.03	222.29	648	-1.02	-1.10
		Oli_E_2	17.49	90	1.80	2.59	344.81	1152	-2.29	-1.89
	B	Oli_B_1	9.15	47	1.11	2.06	384.33	1239	-2.07	-1.56
		Oli_B_2	19.08	96	1.39	1.73	500.43	1928	-1.67	-2.69

Patterns of relatedness (i.e., whether microbial communities are phylogenetically structured) were investigated by computing metrics of community phylogenetic structure (Webb et al., 2002 and Webb, 2000). Communities were compared in relation to the net relatedness index (NRI) and the nearest taxon index (NTI) both of which indicate whether members of a community co-occur with closely related taxa more often than expected by chance (i.e., clustering; high and positive values) or not (i.e., overdispersion; low and negative values).

Notes: 1000 randomisations were used to calculate NRI and NTI. Numbers in bold signify P significance at an alpha level of 0.05. *N* = number of operational taxonomic units (OTUs) observed in a community, NA = Data not available.