Supplementary Tables

Table S1: Environmental variables in the studied samples.

Sample name	Soil temperature (°C)*	Air temperature (°C)	Soil pH	Moisture (%)	NO_3^--N (mg kg^{-1})	NH_4^+-N (mg kg^{-1})	TOC (%)	TN (g kg^{-1})	Released CH_4 (μg m^{-2} h^{-1})	Released CO_2 (mg m^{-2} h^{-1})	Released N_2O (μg m^{-2} h^{-1})	Plant biomass (g m^{-2})	Plant coverage (%)	Number of plant species
3200	12.91	8.87	7.88	22.4	0.928	3.698	6.84	5.35	-23.85	799	13.02	535.4	97	23
3200-3400	11.84	8.61	7.97	20.29	0.975	3.42	6.73	5.12	-30.82	797	-4	450.3	99	24
3200-3600	9.77	7.87	7.72	28.27	1.312	4.275	6.26	5.11				222.1	77	20
3200-3800	8.86	6.78	7.68	31.2	0.981	4.78	6.04	4.79	-14.32	545.9	2.07	323	97	25
3400-3200	12.91	8.87	7.74	23.44	0.938	1.287	6.59	5.62	-13.97	753.3	10.88	385.9	97	21
3400	11.84	8.61	7.77	21.94	0.838	2.078	6.3	5.54	-38.8	843.5	0.16	326.2	98	25
3400-3600	9.77	7.87	7.62	16.29	1.148	2.404	6.22	5.61				131.7	68	18
3400-3800	8.86	6.78	7.21	28.54	0.811	0.983	6.12	5.45	-32.65	502.1	-0.9	185.8	93	26
3600	9.77	7.87	7.59	25.63	1.585	1.984	5.99	5.12				139.9	72	17
3800-3200	12.91	8.87	7.17	24.1	1.202	1.383	5.66	4.98	-19.59	711.9	12.71	274.2	98	18
3800-3400	11.84	8.61	7.48	26.06	0.818	1.251	5.53	4.76	-34.12	748.5	2.27	248.6	98	19
3800-3600	9.77	7.87	7.68	33.58	1.752	1.329	5.48	4.85				176.9	80	15
3800	8.86	6.78	7.2	31.73	1.381	1.497	5.59	4.71	-12.98	408.6	1.38	199.5	77	14

*Soil samples were collected at the depth of 0-10 cm, and soil temperature was measured at 5 cm depth.

Table S2: PerMANOVA test of the differences in bacterial community structure based on Bray-Curtis distance measures (permutation: 9999).

T3400	**0.0117**		
T3600	**0.0001**	**0.0001**	
T3800	**0.0001**	**0.0006**	**0.0004**
	T3200	T3400	T3600

Values in bold means significant difference between two groups at $p<0.05$.

T3400 includes the samples transplanted to 3400 m and "home controls" at 3400 m.

Table S3: Bacterial diversity indices at 97% sequence similarity (per 2291 sequences).

Elevation (m)	Number of OTUs	Chao1 estimator of richness	Shannon’s diversity index	Shannon’s evenness
3200	1328±13	3233±165	6.893±0.005	0.959±0.001
3200-3400	1331±32	3412±186	6.888±0.032	0.958±0.002
3200-3600	1299±38	3264±50	6.854±0.054	0.956±0.004
3200-3800	1316±238	3308±280	6.882±0.027	0.958±0.002
3400-3200	1287±618	3278±299	6.831±0.066	0.954±0.003
3400	1373±2	3616±136	6.944±0.013	0.961±0.002
3400-3600	1317±22	3483±209	6.860±0.022	0.955±0.002*
3400-3800	1345±10	3442±176	6.919±0.010	0.960±0.001
3600	1292±8	3365±199	6.833±0.012	0.954±0.001
3800-3200	1279±28*	3225±178	6.787±0.033*	0.949±0.002*
3800-3400	1319±21	3203±58*	6.856±0.030*	0.954±0.002*
3800-3600	1296±26*	3356±216	6.856±0.034*	0.957±0.002*
3800	1461±75	4480±719	7.034±0.074	0.966±0.003

* Compared to their controls at “home” sites. The values of the transplanted samples were significantly decreased ($p<0.05$).

Table S4: Relative abundance (% of total reads) of abundant bacterial groups at the phylum (a), class (b), order (c) and genus (d) levels.

	3200	3200-3400	3200-3600	3200-3800	3400-3200	3400	3400-3600	3400-3800	3600	3800-3200	3800-3400	3800-3600	3800
a) phylum													
Proteobacteria	31.08±0.37ab	29.48±0.98bc	33.74±0.40ab	29.61±1.01bc	33.26±1.35ab	30.22±1.05bc	35.20±0.26a	32.79±1.69ab	31.63±1.03ab	32.90±1.16ab	26.22±1.43c	32.85±0.78ab	30.60±1.48abc
Actinobacteria	30.69±0.60a	30.93±1.13a	21.87±0.25d	27.16±1.11abc	27.79±1.13abc	30.99±1.51a	21.90±1.94d	28.28±1.57abc	23.44±0.64cd	31.05±0.41a	28.85±1.66ab	20.66±1.14d	24.33±1.15bcd
Acidobacteria	10.13±0.49cde	11.70±1.08abcde	13.07±0.26abcd	12.95±0.44abcd	9.98±0.94de	10.58±0.97bcde	13.46±1.33abc	10.45±0.60cde	13.91±0.05ab	9.05±0.76e	12.47±0.95abcd	14.97±0.77a	12.63±0.75abcd
Bacteroidetes	5.02±0.38bcd	4.87±0.25bcd	4.02±0.28d	5.35±0.38abc	4.98±0.49bcd	5.49±0.20abc	3.80±0.36d	4.98±0.37bcd	4.74±0.15cd	5.89±0.18abc	6.59±0.39a	5.49±0.20abc	6.20±0.34ab
Planctomycetes	3.54±0.11a	3.08±0.40abc	2.90±0.14abc	2.36±0.19c	2.55±0.12bc	2.72±0.17bc	2.40±0.21c	3.01±0.16abc	2.66±0.21bc	3.23±0.17ab	2.52±0.08bc	2.44±0.09bc	2.62±0.22bc
Verrucomicrobia	1.29±0.02cd	1.06±0.09d	3.03±0.20a	2.84±0.38a	1.28±0.33cd	1.29±0.21cd	3.27±0.09a	2.26±0.26abc	2.58±0.11ab	1.08±0.14d	1.60±0.19bcd	2.68±0.51a	2.85±0.32a
Thaumarchaeota	1.70±0.25abc	1.92±0.13abc	1.20±0.05c	1.95±0.25abc	2.59±0.65ab	1.44±0.19bc	1.75±0.21abc	1.56±0.17bc	1.02±0.32c	1.98±0.16abc	2.79±0.26a	1.13±0.08c	2.25±0.45abc
Chloroflexi	1.64±0.11ab	1.59±0.12ab	1.66±0.22ab	1.44±0.25ab	2.12±0.08a	1.72±0.24ab	1.72±0.35ab	1.75±0.21ab	1.56±0.08ab	1.64±0.17ab	1.98±0.09a	1.14±0.14b	1.44±0.19ab
Gemmatimonadetes	1.12±0.15cd	1.35±0.29bcd	1.11±0.08cd	1.25±0.15bcd	2.17±0.24a	1.59±0.12bc	0.92±0.04d	1.25±0.07bcd	0.86±0.15d	1.08±0.20cd	1.76±0.10ab	1.00±0.04cd	1.40±0.05bcd
Firmicutes	1.19±0.15abc	0.95±0.30bc	0.63±0.14c	0.77±0.08bc	2.14±0.65a	0.81±0.08bc	0.68±0.08c	1.02±0.31abc	1.93±0.20ab	1.53±0.14abc	1.12±0.01abc	1.40±0.41abc	1.08±0.35abc
Nitrospirae	0.12±0.04e	0.54±0.10de	2.14±0.28a	1.54±0.18abc	0.48±0.11de	0.58±0.27de	2.17±0.21a	0.97±0.10cd	1.89±0.16ab	0.13±0.04e	1.09±0.32cd	1.57±0.09abc	1.38±0.21bc
b) class													
Actinobacteria	27.21±0.83ab	27.75±0.87ab	19.08±0.37d	23.62±0.99bc	24.73±0.86abc	28.76±1.17a	18.48±1.72d	25.32±1.55abc	21.27±0.65cd	27.58±0.47ab	26.09±1.69ab	18.36±1.32d	21.37±0.81cd
Alphaproteobacteria	17.59±0.86abc	16.89±0.89abc	17.02±0.37abc	14.38±0.57cd	18.51±1.91ab	16.15±0.74abc	16.75±0.04abc	16.85±0.78abc	14.87±0.82bcd	18.77±0.72a	12.38±1.07d	13.79±0.52cd	14.55±1.01cd
Betaproteobacteria	5.46±0.16e	6.29±0.56de	7.38±0.09bcd	7.74±0.30abc	6.34±0.54de	6.65±0.19cde	8.98±0.16a	7.89±0.34abc	7.57±0.31bcd	5.53±0.23e	6.61±0.07cde	8.96±0.38a	8.51±0.45ab
Acidobacteria_Gp4	2.40±0.43d	2.46±0.29d	4.98±0.06ab	4.96±0.48ab	3.33±0.27bcd	3.08±0.55cd	5.75±0.64a	3.71±0.16bcd	4.26±0.55abc	2.28±0.18d	3.22±0.22cd	4.95±0.36ab	4.31±0.45abc
Deltaproteobacteria	2.50±0.48c	2.46±0.21c	4.93±0.19a	3.14±0.13c	2.91±0.66c	2.88±0.33c	5.05±0.39a	3.43±0.16bc	4.69±0.52ab	2.88±0.20c	3.22±0.03c	5.82±0.41a	3.01±0.43c
Sphingobacteriia	2.84±0.23de	3.29±0.09bcde	2.71±0.22e	3.68±0.24abcd	2.72±0.23e	3.46±0.14bcde	2.52±0.20e	3.38±0.17bcde	3.17±0.23cde	3.39±0.21bcde	4.41±0.29a	3.83±0.07abc	4.16±0.43ab
Gammaproteobacteria	4.36±0.38a	2.85±0.24b	2.88±0.22b	3.10±0.13ab	4.32±0.72a	3.10±0.36ab	2.76±0.32b	3.38±0.28ab	3.16±0.14ab	4.38±0.11a	2.88±0.26b	2.78±0.42b	2.88±0.34b
Acidobacteria_Gp6	3.84±0.30ab	4.38±0.37a	2.77±0.02cd	2.53±0.04d	2.31±0.31def	1.64±0.18efg	0.86±0.06g	1.47±0.20fg	2.42±0.23de	3.74±0.33ab	3.61±0.10abc	2.82±0.14cd	3.01±0.16bcd
Planctomycetia	3.27±0.13a	2.95±0.42abc	2.77±0.17abc	2.18±0.25c	2.42±0.10bc	2.59±0.19abc	2.20±0.23c	2.91±0.11abc	2.55±0.20abc	3.16±0.17ab	2.37±0.05bc	2.33±0.13bc	2.53±0.20abc
Spartobacteria	0.76±0.07c	0.55±0.05c	2.12±0.48a	2.11±0.30a	0.64±0.10c	0.68±0.16c	2.11±0.12a	1.37±0.20abc	1.73±0.13ab	0.63±0.15c	0.87±0.18bc	1.72±0.42ab	2.17±0.24a
Acidobacteria_Gp7	0.71±0.04bc	1.16±0.19abc	1.03±0.11abc	0.92±0.16abc	1.11±0.27abc	1.62±0.34a	1.50±0.18a	1.28±0.08ab	1.35±0.25ab	0.47±0.10c	1.30±0.17ab	1.47±0.15ab	0.89±0.04abc

Acidobacteria_Gp3	0.67±0.02de	0.80±0.11bcde	1.53±0.15abcd	1.31±0.07bcde	0.71±0.29cde	0.92±0.02bcde	1.59±0.48abc	0.77±0.06cde	1.69±0.42ab	0.42±0.07e	0.99±0.17bcde	2.20±0.13a	1.09±0.07bcde
Nitrospira	0.09±0.04e	0.51±0.08de	2.14±0.28a	1.50±0.17abc	0.45±0.10de	0.58±0.27de	2.14±0.21a	0.96±0.11cd	1.88±0.14ab	0.12±0.04e	1.02±0.34cd	1.57±0.09abc	1.35±0.20bc
c) order													
Actinomycetales	13.25±0.54ab	13.97±1.11a	7.25±0.22d	9.89±0.85bcd	11.19±0.63abc	13.14±1.44ab	7.11±1.17d	10.10±1.13bcd	8.80±0.07cd	14.58±0.51a	12.19±1.40abc	7.23±0.65d	9.09±0.28cd
Rhizobiales	11.92±0.75ab	11.16±0.64abcd	11.68±0.51abc	9.44±0.21cde	12.49±1.09ab	10.39±0.53bcde	9.12±0.41de	10.19±0.22bcde	8.51±0.41e	13.43±0.45a	8.54±0.52e	8.69±0.50e	8.86±0.73de
Solirubrobacterales	6.36±0.22a	5.38±0.16abc	4.37±0.25cde	4.74±0.26cde	4.73±0.29cde	6.05±0.26ab	3.75±0.38e	5.44±0.09abc	4.79±0.40cde	6.33±0.28a	5.21±0.43abcd	4.04±0.20de	4.87±0.44bcde
Sphingobacteriales	2.84±0.23de	3.29±0.09bcde	2.71±0.22e	3.68±0.24abcd	2.72±0.23e	3.46±0.14bcde	2.52±0.20e	3.38±0.17bcde	3.17±0.23cde	3.39±0.21bcde	4.41±0.29a	3.83±0.07abc	4.16±0.43ab
Gaiellales	2.36±0.16c	3.65±0.53abc	3.01±0.12abc	3.91±0.11ab	3.86±0.53ab	4.09±0.40ab	3.10±0.32abc	4.29±0.38a	3.17±0.42abc	2.31±0.16c	3.70±0.23abc	2.74±0.25bc	3.17±0.44abc
Planctomycetales	3.16±0.11a	2.76±0.42abc	2.62±0.22abc	2.07±0.26c	2.30±0.08bc	2.50±0.21abc	2.01±0.16c	2.82±0.14abc	2.42±0.15abc	3.06±0.23ab	2.24±0.03bc	2.26±0.12bc	2.40±0.20abc
Acidimicrobiales	2.53±0.21abc	1.85±0.22bcd	1.88±0.34bcd	2.60±0.08a	1.96±0.14abcd	2.21±0.09abcd	2.01±0.06abcd	2.55±0.14ab	1.91±0.10bcd	1.83±0.26cd	2.23±0.11abcd	1.92±0.19abcd	1.80±0.13d
Myxococcales	1.63±0.32c	1.37±0.21c	3.30±0.20a	1.73±0.07bc	1.85±0.51bc	1.57±0.07c	2.58±0.16ab	1.89±0.10bc	2.25±0.15bc	1.95±0.16bc	1.91±0.16bc	3.20±0.07a	1.46±0.20c
Burkholderiales	2.01±0.13ab	1.86±0.25ab	1.62±0.22b	2.31±0.25ab	1.63±0.09b	1.47±0.12b	1.76±0.24b	2.07±0.25ab	1.79±0.32b	1.98±0.20ab	1.69±0.14b	2.34±0.23ab	2.69±0.16a
Nitrososphaerales	1.70±0.25abc	1.92±0.13abc	1.20±0.05c	1.95±0.25abc	2.59±0.65ab	1.44±0.19bc	1.75±0.21abc	1.56±0.17bc	1.02±0.32c	1.98±0.16abc	2.79±0.26a	1.13±0.08c	2.25±0.45abc
Rhodospirillales	1.19±0.08bc	1.47±0.17abc	1.22±0.09abc	1.44±0.23abc	1.31±0.21abc	1.48±0.14abc	1.96±0.18a	1.62±0.27abc	1.75±0.22ab	1.25±0.13abc	0.93±0.17c	1.59±0.04abc	1.50±0.22abc
Xanthomonadales	1.70±0.14ab	1.30±0.17ab	0.70±0.03b	0.89±0.05b	2.17±0.70a	1.41±0.26ab	0.73±0.17b	1.18±0.20ab	0.89±0.13b	2.14±0.22a	1.00±0.18b	0.64±0.12b	0.79±0.13b
Nitrospirales	0.09±0.04e	0.51±0.08de	2.14±0.28a	1.50±0.17abc	0.45±0.10de	0.58±0.27de	2.14±0.21a	0.96±0.11cd	1.88±0.14ab	0.12±0.04e	1.02±0.34cd	1.57±0.09abc	1.35±0.20bc
d) genus													
Gp4	2.37±0.40e	2.40±0.29e	4.98±0.06ab	4.82±0.45abc	3.32±0.26cde	3.06±0.55de	5.70±0.64a	3.70±0.16bcde	4.23±0.55abcd	2.26±0.16e	3.13±0.22de	4.93±0.37abc	4.13±0.49abcd
Gaiella	2.36±0.16c	3.65±0.53abc	3.01±0.12abc	3.91±0.11ab	3.86±0.53ab	4.09±0.40ab	3.10±0.32abc	4.29±0.38a	3.17±0.42abc	2.31±0.16c	3.70±0.23abc	2.74±0.25bc	3.17±0.44abc
Gp6	3.84±0.30ab	4.38±0.37a	2.77±0.02cd	2.53±0.04d	2.31±0.31def	1.64±0.18efg	0.86±0.06g	1.47±0.20fg	2.42±0.23de	3.74±0.33ab	3.61±0.10abc	2.82±0.14cd	3.01±0.16bcd
Solirubrobacter	3.03±0.05abc	2.94±0.04abcd	1.83±0.15e	2.50±0.04cd	2.88±0.20abcd	3.07±0.01abc	1.72±0.25e	3.27±0.09ab	2.28±0.17de	3.39±0.21a	3.10±0.26abc	1.85±0.12e	2.63±0.24bcd
Nitrososphaera	1.70±0.25abc	1.92±0.13abc	1.20±0.05c	1.95±0.25abc	2.59±0.65ab	1.44±0.19bc	1.75±0.21abc	1.56±0.17bc	1.02±0.32c	1.98±0.16abc	2.79±0.26a	1.13±0.08c	2.25±0.45abc
Pseudonocardia	2.72±0.33ab	1.61±0.36cd	1.81±0.08bcd	1.21±0.14cd	2.23±0.53abc	1.31±0.23cd	1.69±0.11cd	1.37±0.13cd	1.21±0.25cd	2.91±0.18a	1.29±0.21cd	2.05±0.18abc	0.96±0.02d
Bradyrhizobium	1.66±0.31a	1.43±0.23a	1.72±0.23a	1.24±0.21a	1.31±0.24a	1.53±0.05a	1.28±0.17a	1.27±0.13a	1.00±0.09a	1.50±0.12a	1.66±0.21a	1.06±0.05a	1.22±0.16a
Spartobacteria_genera_ incertae_sedis	0.76±0.07b	0.54±0.04b	2.12±0.48a	2.11±0.30a	0.64±0.10b	0.68±0.16b	2.11±0.12a	1.37±0.20ab	1.73±0.13a	0.61±0.14b	0.87±0.18b	1.70±0.41a	2.17±0.24a

Gp7	0.71±0.04bc	1.16±0.19abc	1.03±0.11abc	0.92±0.16abc	1.11±0.27abc	1.62±0.34a	1.50±0.18a	1.28±0.08ab	1.35±0.25ab	0.47±0.10c	1.30±0.17ab	1.47±0.15ab	0.89±0.04abc
Nocardioides	1.08±0.12abcd	1.35±0.19abc	0.50±0.05cd	1.12±0.09abcd	1.18±0.09abcd	1.95±0.43a	0.55±0.18bcd	0.93±0.30bcd	0.87±0.16bcd	1.22±0.23abcd	1.46±0.35ab	0.42±0.08d	0.90±0.11bcd
Nitrospira	0.07±0.02f	0.38±0.07ef	1.92±0.25ab	1.35±0.14bcd	0.38±0.11ef	0.54±0.25ef	2.04±0.21a	0.90±0.09cde	1.78±0.12ab	0.10±0.03f	0.76±0.26de	1.44±0.10abc	1.28±0.21bcd
Gemmatimonas	0.83±0.15bc	0.93±0.15bc	0.89±0.05bc	0.97±0.15bc	1.53±0.23a	1.05±0.09abc	0.70±0.06c	1.05±0.09abc	0.65±0.14c	0.74±0.12bc	1.25±0.01ab	0.89±0.05bc	0.96±0.10bc
Blastococcus	1.29±0.48ab	1.86±0.16a	0.24±0.02c	0.99±0.19bc	1.09±0.13ab	1.41±0.06ab	0.31±0.14c	0.64±0.14bc	0.25±0.08c	1.11±0.17ab	1.28±0.25ab	0.19±0.03c	0.99±0.15bc

Duncan’s multiple comparison was used. Values labeled with red color were higher than those not labeled.

Table S5: The number of OTUs significantly associated to each site ($p<0.05$) through indicator analysis.

	associated to 1 site				associated to 2 sites						associated to 3 sites				Total number
	G1000*	G0100	G0010	G0001	G1100	G0110	G0011	G1010	G0101	G1001	G1110	G1101	G0111	G1011	
Acidobacteria	14	7	31	7	18	3	22	1	7	2	0	11	8	2	133
Actinobacteria	46	31	26	8	42	4	38	1	11	8	2	36	20	2	275
Alphaproteobacteria	42	5	34	8	22	1	16	0	3	4	1	11	10	4	161
Betaproteobacteria	11	5	21	1	6	0	7	0	3	2	1	3	9	0	69
Deltaproteobacteria	5	2	23	4	4	0	6	0	0	0	0	0	2	1	47
Gammaproteobacteria	10	1	4	2	5	0	1	0	0	1	0	0	1	0	25
unclassified Proteobacteria	3	4	2	0	0	0	0	0	0	1	0	1	1	1	13
Armatimonadetes	0	1	1	0	1	0	0	0	0	0	0	0	0	0	3
Bacteroidetes	7	8	7	5	4	0	5	1	3	1	0	4	2	0	47
Chlamydiae	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Chloroflexi	1	1	4	0	3	0	3	0	1	0	0	1	0	1	15
Firmicutes	3	1	3	1	0	0	1	0	0	0	0	0	0	1	10
Gemmatimonadetes	4	0	2	3	4	0	0	0	1	0	0	0	0	0	14
Latescibacteria	1	0	1	1	0	0	0	0	0	0	0	0	0	0	3
Nitrospirae	0	1	2	0	2	0	4	0	0	0	0	0	3	0	12
Planctomycetes	9	4	4	1	1	0	0	0	1	1	0	0	0	0	21
Thaumarchaeota	4	1	0	1	6	0	2	0	1	1	0	3	3	0	22
Verrucomicrobia	0	2	6	1	0	1	11	0	0	1	0	1	0	1	24
candidate division WPS-2	1	0	0	0	1	0	0	0	0	0	0	0	0	0	2
unclassified bacteria	21	14	24	2	13	2	11	1	4	1	1	7	4	1	106
Total number	183	88	195	45	132	11	127	4	35	23	5	78	63	14	1003

* G=group. G is followed by site number, representing the objective elevations (3200, 3400, 3600 and 3800m sequentially), in which 1 indicates association and 0 indicates no association to a site. For example, G1101 represents the group of OTUs associated to 3200, 3400 and 3800m, but not associated to 3600m.

Table S6: OTUs with the highest p-value (p<0.001) associated to each site through indicator analysis.

Group*	OTU_ID	Phylum/Class	Family/Genus
(a) G1000			
	131	Alphaproteobacteria	*Geminicoccus*
	503	Actinobacteria	*Streptomyces*
	1110	Alphaproteobacteria	*Microvirga*
	731	Actinobacteria	*Pseudonocardia*
	120	Alphaproteobacteria	*Mesorhizobium*
	1501	Alphaproteobacteria	Hyphomicrobiaceae
	1258	Thaumarchaeota	*Nitrososphaera*
	3229	Alphaproteobacteria	*Microvirga*
	2705	Acidobacteria	Gp4
	1120	Alphaproteobacteria	*Pedomicrobium*
(b) G0100			
	1449	Actinobacteria	Intrasporangiaceae
	3884	Bacteroidetes	Chitinophagaceae
(c) G0010			
	5420	Acidobacteria	Gp7
	1003	Acidobacteria	Gp4
	5675	Acidobacteria	Gp2
	5331	Alphaproteobacteria	*Rhodomicrobium*
	5352	Acidobacteria	Gp1
	3967	Alphaproteobacteria	Rhodospirillaceae
	6042	Alphaproteobacteria	Hyphomicrobiaceae
	5851	Deltaproteobacteria	*Anaeromyxobacter*

	5255 Deltaproteobacteria	*Cystobacter*
	5587 Acidobacteria	Gp4
(d) G1100		
	414 Actinobacteria	*Pseudonocardia*
	38 Thaumarchaeota	*Nitrososphaera*
	212 Actinobacteria	*Solirubrobacter*
	460 Actinobacteria	*Rubrobacter*
	761 Actinobacteria	*Agromyces*
	553 Acidobacteria	Gp6
	289 Gammaproteobacteria	*Steroidobacter*
	1853 Acidobacteria	Gp6
	602 Thaumarchaeota	*Nitrososphaera*
	181 Actinobacteria	*Microlunatus*
(e) G0011		
	1759 Nitrospirae	*Nitrospira*
	814 Actinobacteria	*Pseudonocardia*
	3935 Actinobacteria	*Gaiella*
	3901 Verrucomicrobia	Spartobacteria_genera_incertae_sedis
	4973 Thaumarchaeota	*Nitrososphaera*
	2183 Alphaproteobacteria	Rhodospirillaceae
	4635 Nitrospirae	*Nitrospira*
	4149 Nitrospirae	*Nitrospira*
	601 Betaproteobacteria	Oxalobacteraceae
	5207 Acidobacteria	Gp1
(f) G0101		
	3797 Actinobacteria	*Gaiella*

	3196	Actinobacteria	*Modestobacter*
(g) G1001			
	1063	Actinobacteria	*Solirubrobacter*
	17	Bacteroidetes	*Ohtaekwangia*
	1112	Actinobacteria	*Solirubrobacter*
(h) G1101			
	117	Acidobacteria	Gp4
	3	Actinobacteria	*Blastococcus*
	104	Actinobacteria	*Blastococcus*
	1210	Actinobacteria	*Gaiella*
	239	Actinobacteria	Intrasporangiaceae
	1359	Thaumarchaeota	*Nitrososphaera*
	567	Acidobacteria	Gp7
	144	Alphaproteobacteria	*Microvirga*
	726	Actinobacteria	*Solirubrobacter*
	1082	Actinobacteria	*Blastococcus*
(i) G0111			
	3538	Thaumarchaeota	Nitrososphaera
	1586	Betaproteobacteria	Rhodocyclaceae
	2856	Actinobacteria	*Gaiella*
	5093	Nitrospirae	*Nitrospira*
	1813	Bacteroidetes	*Terrimonas*
	3721	Actinobacteria	*Ilumatobacter*
(j) G1011			
	1309	Chloroflexi	Anaerolineaceae

*Top 10 OTUs are shown here if more than 10 OTUs were with $p<0.001$ in a group. G=group.

Table S7: Spearman’s correlation coefficients between environmental variables.

Objective elevation	.034													
Soil temperature	-.034	-1.000^{**}												
NO_3^--N	$.346^{*}$	.236	-.236											
NH_4^+-N	$-.661^{**}$	-.008	.008	-.162										
TOC	$-.833^{**}$	$-.414^{**}$	$.414^{**}$	$-.398^{*}$	$.474^{**}$									
TN	$-.414^{**}$	$-.328^{*}$	$.328^{*}$	$-.322^{*}$	.045	$.696^{**}$								
Moisture	.245	$.442^{**}$	$-.442^{**}$	$.341^{*}$	-.140	$-.493^{**}$	$-.542^{**}$							
Soil pH	$-.673^{**}$	$-.328^{*}$	$.328^{*}$	-.040	$.549^{**}$	$.658^{**}$	.274	-.205						
Plant biomass	$-.465^{**}$	$-.577^{**}$	$.577^{**}$	$-.447^{**}$	$.339^{*}$	$.538^{**}$	.091	-.151	$.437^{**}$					
Plant coverage	-.169	$-.571^{**}$	$.571^{**}$	$-.487^{**}$	.129	.271	-.017	-.194	.168	$.797^{**}$				
Number of plant species	$-.562^{**}$	-.122	.122	$-.599^{**}$	.215	$.504^{**}$	$.321^{*}$	-.068	.270	$.430^{**}$	$.489^{**}$			
Released CH_4	.006	-.070	.070	$.400^{*}$	.256	-.062	-.183	.332	-.035	.100	-.164	-.188		
Released CO_2	-.227	$-.664^{**}$	$.664^{**}$	-.253	.146	$.520^{**}$	$.427^{*}$	$-.594^{**}$	$.547^{**}$	$.635^{**}$	$.606^{**}$	.077	-.203	
Released N_2O	.105	$-.594^{**}$	$.594^{**}$	.162	-.026	.140	.124	-.270	-.088	.236	.109	-.333	.227	.186
	Initial elevation	Objective elevation	Soil temperature	NO_3^--N	NH_4^+-N	TOC	TN	Moisture	Soil pH	Plant biomass	Plant coverage	Number of plant species	Released CH_4	Released CO_2

** Correlation is significant at $p < 0.01$ level. * Significant at $p < 0.05$ level.

Table S8: Spearman's correlation between the relative abundance of important genera (relative abundance > 0.01%) and environmental variables.

	Soil temperature	Plant biomass	TOC	TN	NO_3^--N	NH_4^+-N	Moisture	Soil pH	Released CH_4^a	Released CO_2^a	Released N_2O^a
Gp4	-.634**	-.614**	-.264	-.068	.314	.116	.061	-.018	.030	-.501**	-.144
Gp6	.432**	.459**	-.059	-.532**	.072	.059	.071	.110	.044	.290	.143
Solirubrobacter	.380*	.438**	.127	.090	-.471**	-.351*	-.092	-.233	-.378	.284	.142
Pseudonocardia	.550**	.198	.229	.286	.030	.111	-.062	.200	.333	.416*	.399*
Spartobacteria_genera_incertae_sedis	-.749**	-.620**	-.372*	-.239	.287	.168	.287	-.278	.077	-.776**	-.248
Nocardioides	.368*	.538**	.235	.020	-.336*	-.106	-.272	.048	-.334	.504**	.108
Nitrospira	-.697**	-.714**	-.329*	-.105	.375*	.133	.137	-.102	.060	-.549**	-.379
Blastococcus	.409*	.683**	.300	-.016	-.458**	.076	-.296	.144	-.281	.323	.008
Terrimonas	-.242	.057	-.432**	-.688**	-.037	-.019	.357*	-.158	-.005	-.263	-.145
Gp17	.084	.040	.364*	.487**	-.144	-.089	-.350*	.077	-.178	.105	.044
Pedomicrobium	.665**	.514**	.499**	.275	-.066	.181	-.269	.328*	.140	.508**	.571**
Mesorhizobium	.553**	.518**	.424**	.350*	-.470**	-.054	-.331*	.016	-.080	.281	.304
Ferruginibacter	-.278	-.380*	-.586**	-.401*	.257	-.287	.392*	-.334*	-.343	-.159	-.097
Ohtaekwangia	.564**	.654**	.277	.060	-.478**	.013	-.254	-.016	.055	.534**	.338
Subdivision3_genera_incertae_sedis	-.415**	-.469**	-.060	.237	.107	-.048	.017	-.076	-.473*	-.209	-.286
Sphingomonas	.364*	.417**	.500**	.331*	-.454**	.077	-.276	.132	.071	.166	-.033
WPS_2_genera_incertae_sedis	.071	.469**	.171	-.041	-.274	.110	.131	.105	.012	-.018	.056
Microvirga	.555**	.660**	.339*	.095	-.450**	-.012	-.166	.049	-.059	.322	.390*
Steroidobacter	.579**	.474**	.363*	.231	-.417**	.151	-.329*	.247	-.037	.534**	.453*
Pirellula	.433**	.251	.194	.120	-.084	-.188	-.186	.064	-.312	.395*	.271
Geminicoccus	.035	.072	.035	.109	-.414**	-.197	-.084	-.195	-.546**	-.020	-.292

Gp1	-.569**	-.618**	-.297	-.092	.297	.227	.190	.007	-.151	-.310	-.546**
Amaricoccus	.545**	.644**	.478**	.279	-.391*	-.024	-.145	.102	-.035	.453*	.249
Hyphomicrobium	-.110	-.268	.030	.183	.418**	-.051	.039	-.120	.549**	-.067	.256
Devosia	.169	.117	.380*	.450**	-.225	-.017	-.371*	-.098	-.087	.169	.137
Gemmata	-.412*	-.454**	-.222	-.111	.283	.059	-.123	-.191	-.122	-.257	-.189
Phyllobacterium	.651**	.492**	.359*	.288	-.339*	-.059	-.217	.118	.182	.542**	.311
Lysobacter	.616**	.359*	.298	.241	-.265	-.172	-.304	-.004	-.064	.357	.451*
Phenylobacterium	.244	.079	.177	.361*	-.482**	-.158	-.295	-.132	-.337	.007	.024
Streptomyces	.505**	.391*	.351*	.357*	-.126	.055	-.282	.063	.217	.307	.304
Gp2	-.518**	-.666**	-.302	-.079	.420**	-.008	.260	-.040	-.234	-.390*	-.323
Geobacter	-.653**	-.635**	-.437**	-.140	.227	-.076	.246	-.202	-.140	-.553**	-.294
Aciditerrimonas	-.211	.063	-.230	-.338*	-.122	-.157	.288	-.230	.072	-.522**	.090
Microbacterium	.517**	.353*	.220	.027	-.040	-.167	-.213	.096	-.177	.426*	.212
Microlunatus	.526**	.571**	.272	-.023	-.110	.046	-.154	.417**	.068	.411*	.297
Rubrobacter	.723**	.603**	.411*	.323*	-.444**	-.144	-.398*	.098	-.057	.675**	.518**
Modestobacter	.076	.304	.158	.039	-.439**	-.084	-.144	.038	-.408*	.197	-.419*
Skermanella	.275	.491**	.223	.078	-.333*	-.068	-.029	.041	-.013	.025	-.006
Chelatococcus	.604**	.608**	.236	.199	-.319	-.011	-.112	.191	-.025	.441*	.267
Agromyces	.695**	.470**	.344*	.326*	-.295	-.211	-.381*	.047	-.156	.488**	.484*
Gp5	.202	.246	-.152	-.434**	.289	.166	.270	.254	.169	.150	.153
Cystobacter	-.494**	-.408*	-.166	-.167	.444**	.283	.240	.198	-.079	-.324	-.303
Luteimonas	.468**	.355*	.275	.336*	-.203	.068	-.131	.188	.278	.344	.316
Pseudoxanthomonas	.631**	.408*	.526**	.509**	-.286	-.026	-.446**	.210	-.089	.622**	.249
Anaeromyxobacter	-.287	-.527**	-.495**	-.256	.430**	-.069	.178	-.139	.086	-.393*	.016
Clostridium_sensu_stricto	-.435**	-.590**	-.524**	-.365*	.378*	-.135	.445**	-.277	.273	-.591**	-.063
Micromonospora	.166	.136	.146	.283	-.429**	-.257	-.306	-.076	-.350	.132	-.007

Virgisporangium	.279	.491**	.276	.039	-.232	-.148	-.027	.049	-.079	.389*	.050
Asanoa	.542**	.352*	.296	.012	-.049	.102	-.154	.135	.314	.217	.415*
Caulobacter	-.030	-.135	-.143	.177	-.105	-.294	-.126	-.523**	.218	-.071	.074
Rhodopseudomonas	.242	.331*	.462**	.245	-.209	.258	-.001	.331*	.111	.108	.082
Kribbella	.425**	.577**	.540**	.371*	-.452**	.121	-.291	.288	-.394*	.613**	-.006
Chitinophaga	-.440**	-.303	-.261	-.175	-.089	.072	.021	-.239	-.027	-.438*	-.431*
Sphaerobacter	.425**	.301	.276	.254	-.262	-.053	-.144	.063	.110	.398*	.104
Paenibacillus	.373*	-.075	.157	.446**	-.214	-.056	-.440**	.133	-.196	.538**	.037
Defluviicoccus	-.150	-.479**	-.232	.081	.342*	-.016	-.104	-.306	.028	-.273	.226
Craurococcus	.424**	.428**	.461**	.318	-.294	.138	-.169	.148	.172	.098	.347
Lentzea	.264	.258	.515**	.315	-.648**	.199	-.444**	.333*	-.286	.195	-.112
Sphingorhabdus	.570**	.344*	.390*	.204	-.177	.196	-.415**	.198	.059	.523**	.349
Adhaeribacter	.208	.614**	.381*	.041	-.547**	.329*	-.324*	.319	.015	.213	.104
Rhodomicrobium	-.217	-.538**	-.217	-.033	.426**	.007	.220	.127	0	0	0
Afipia	-.059	.068	.203	.429**	-.261	-.052	.020	-.015	-.164	-.011	-.155
Pelosinus	-.144	-.494**	-.228	-.055	.381*	-.046	.035	.034	-.327	.025	-.025
The number of genera ($p<0.05$)	49	61	32	27	36	5	18	11	11	33	16
The number of genera ($p<0.01$)	34	35	14	8	20	0	5	2	2	17	3

a) Release of N_2O, CO_2 and CH_4, values of samples transplanted to 3600 m were not measured.

** Correlation is significant at $p<0.01$ level (orange color), * Significant at $p<0.05$ level (yellow color).

Supplementary Figures

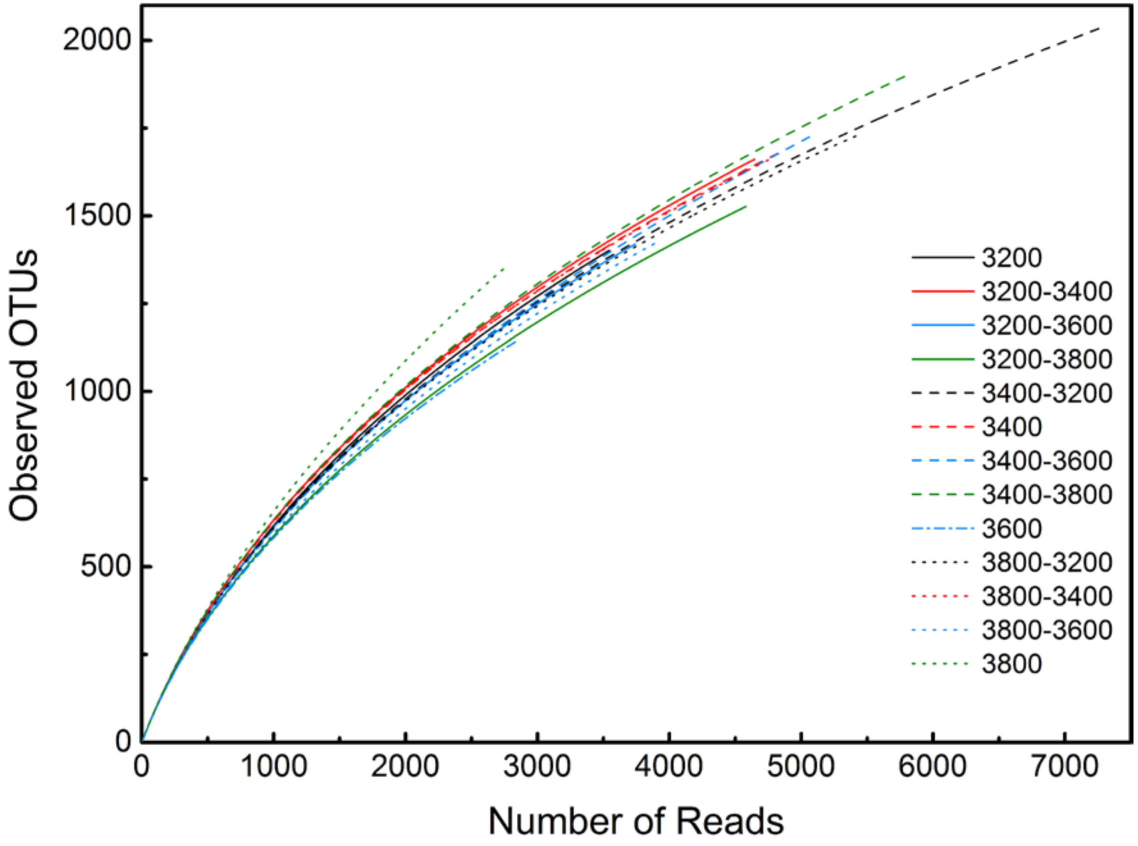

Fig. S1: Rarefaction curve of observed OTUs before re-sampling. Average value of triplicate or duplicate samples in each treatment was used.