SUPPLEMENTAL MATERIAL

Table S1. PERMANOVA results for the UniFrac pairwise dissimilarity of the relative abundance of bacterial sequences, based on 16S gene, and the Bray-Curtis distance of the relative abundance of fungal sequences, based on ITS gene Illumina MiSeq sequencing, using a non-parametric permutational approach. The explanatory variables are activity, precipitation pattern, depth and their interaction. The analysis is nested by mesocosm.

Source of variation	Degrees of freedom	Sum of squares	Mean squares	F value	R2	P value
Bacteria						
Mesocosm level						
Activity	1	0.754	0.754	92.33	0.611	<0.001
Precip. pattern	1	0.014	0.014	1.667	0.011	0.176
Activity × Precip. pattern	1	0.003	0.003	0.39	0.003	0.745
Residuals	22	0.180	0.008		0.146	
Depth level						
Depth	2	0.049	0.024	3.185	0.040	0.021
Depth × Activity	2	0.021	0.011	1.389	0.017	0.225
Depth × Precip. pattern	2	0.023	0.012	1.531	0.019	0.186
Depth × Activity × Precip. pattern	2	0.014	0.007	0.915	0.011	0.413
Residuals	36	0.275	0.008		0.223	
Fungi						
Mesocosm level						
Activity	1	0.813	0.813	11.956	0.093	<0.001
Precip. pattern	1	0.323	0.323	4.748	0.037	<0.001
Activity × Precip. pattern	1	0.071	0.071	1.047	0.008	0.347
Residuals	22	1.495	0.068		0.171	
Depth level						
Depth	2	1.246	0.623	5.622	0.143	<0.001
Depth × Activity	1	0.071	0.071	0.643	0.008	0.929
Depth × Precip. pattern	2	0.517	0.258	2.333	0.059	0.001
Depth × Activity × Precip. pattern	2	0.148	0.074	0.668	0.017	0.974
Residuals	36	3.988	0.111		0.457	

Table S2. PERMANOVA results for the UniFrac pairwise dissimilarity and the Bray-Curtis distance of the relative abundance of bacterial and fungal sequences, based on 16S and ITS gene Illumina MiSeq sequencing, respectively, both in the active and the inactive communities, using a non-parametric permutational approach. The explanatory variables are precipitation pattern, depth and their interaction. The analysis is nested by mesocosm.

Source of variation	Degrees of freedom	Sum of squares	Mean squares	F value	R2	P value
Active bacterial community						
Precip. pattern	1	0.010	0.010	0.998	0.032	0.096
Depth	2	0.038	0.019	1.837	0.119	0.038
Mesocosm	8	0.103	0.013	1.243	0.322	0.163
Precip. Pattern × Depth	2	0.024	0.012	1.133	0.073	0.324
Residuals	14	0.146	0.010		0.453	
Inactive bacterial community						
Precip. pattern	1	0.006	0.006	1.880	0.041	0.106
Depth	2	0.032	0.016	4.632	0.200	<0.001
Mesocosm	8	0.062	0.008	2.272	0.393	<0.001
Precip. Pattern × Depth	2	0.010	0.005	1.447	0.063	0.089
Residuals	14	0.048	0.003		0.303	
Active fungal community						
Precip. pattern	1	0.250	0.250	1.515	0.050	0.002
Depth	2	0.853	0.427	2.585	0.170	0.001
Mesocosm	8	1.222	0.153	0.926	0.243	0.002
Precip. Pattern × Depth	2	0.395	0.197	1.196	0.078	0.176
Residuals	14	2.311	0.165		0.459	
Inactive fungal community						
Precip. pattern	1	0.144	0.144	1.704	0.050	0.017
Depth	2	0.588	0.294	3.485	0.204	0.001
Mesocosm	8	0.708	0.088	1.048	0.245	0.393
Precip. Pattern × Depth	2	0.268	0.134	1.589	0.093	0.009
Residuals	14	1.182	0.084		0.409	

Fig. S1. Photograph of one of the mesocosms used in the study.

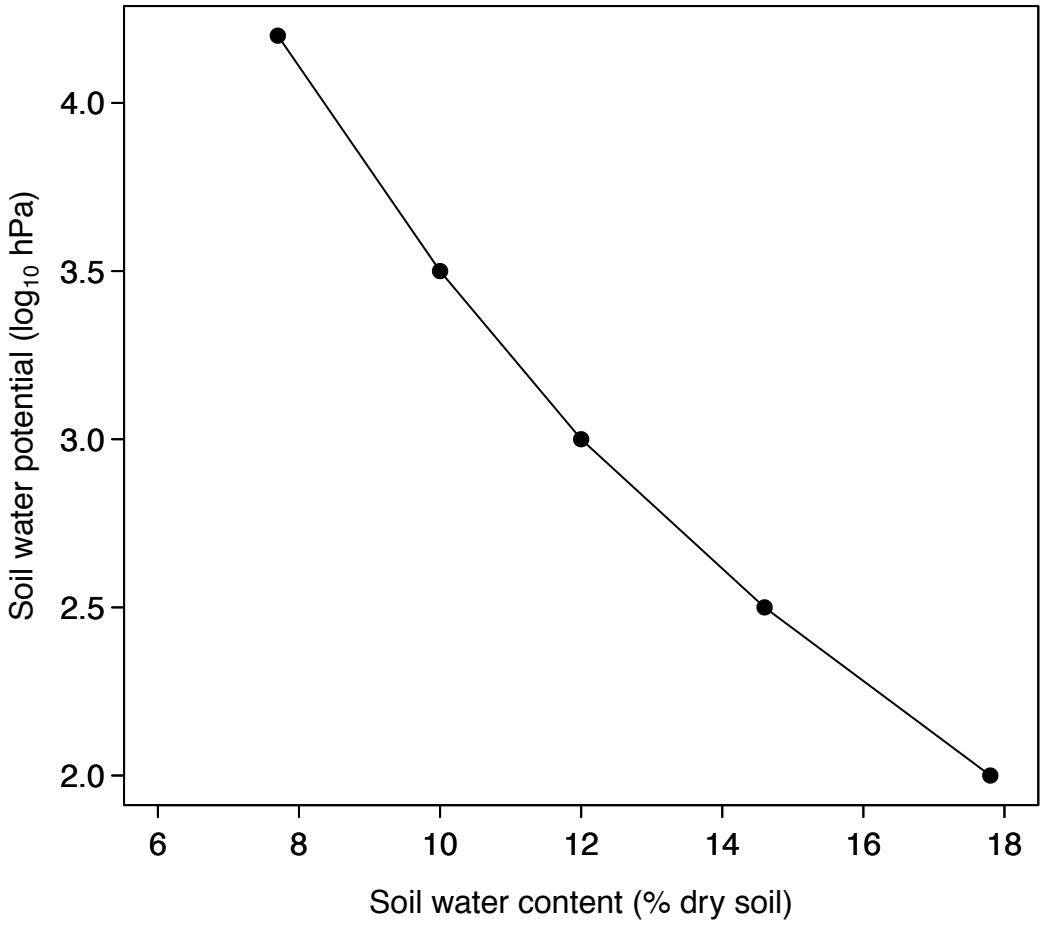

Fig. S2. Theoretical soil water retention curve for our soil, based on pedotransfer functions that used soil texture, bulk density as well as soil horizon (Al Majou *et al.*, 2008).

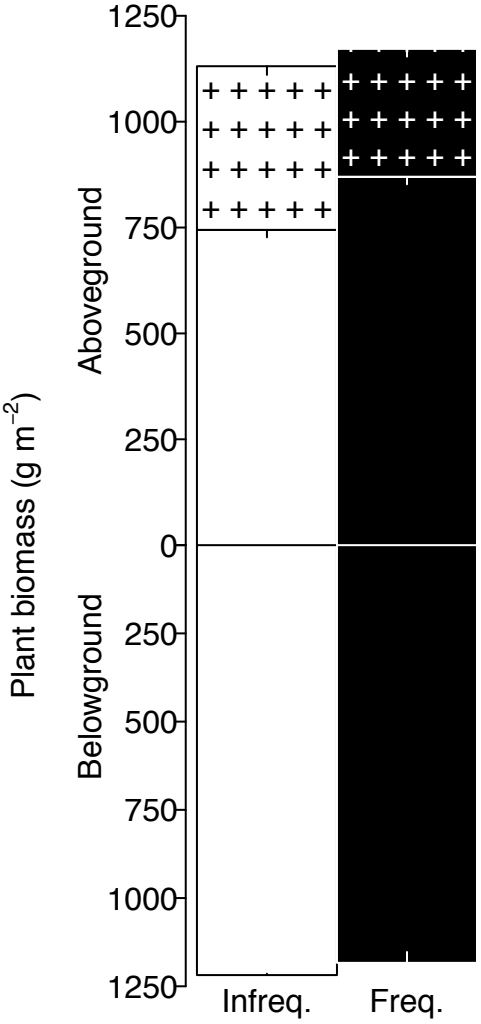

Fig. S3. Plant biomass in the infrequent watering (open bars) and frequent watering (closed bars) treatments. The polygons filled with crosses indicate dead aboveground biomass. Bars indicate mean, ticks inside the bars indicate standard error (n=5).

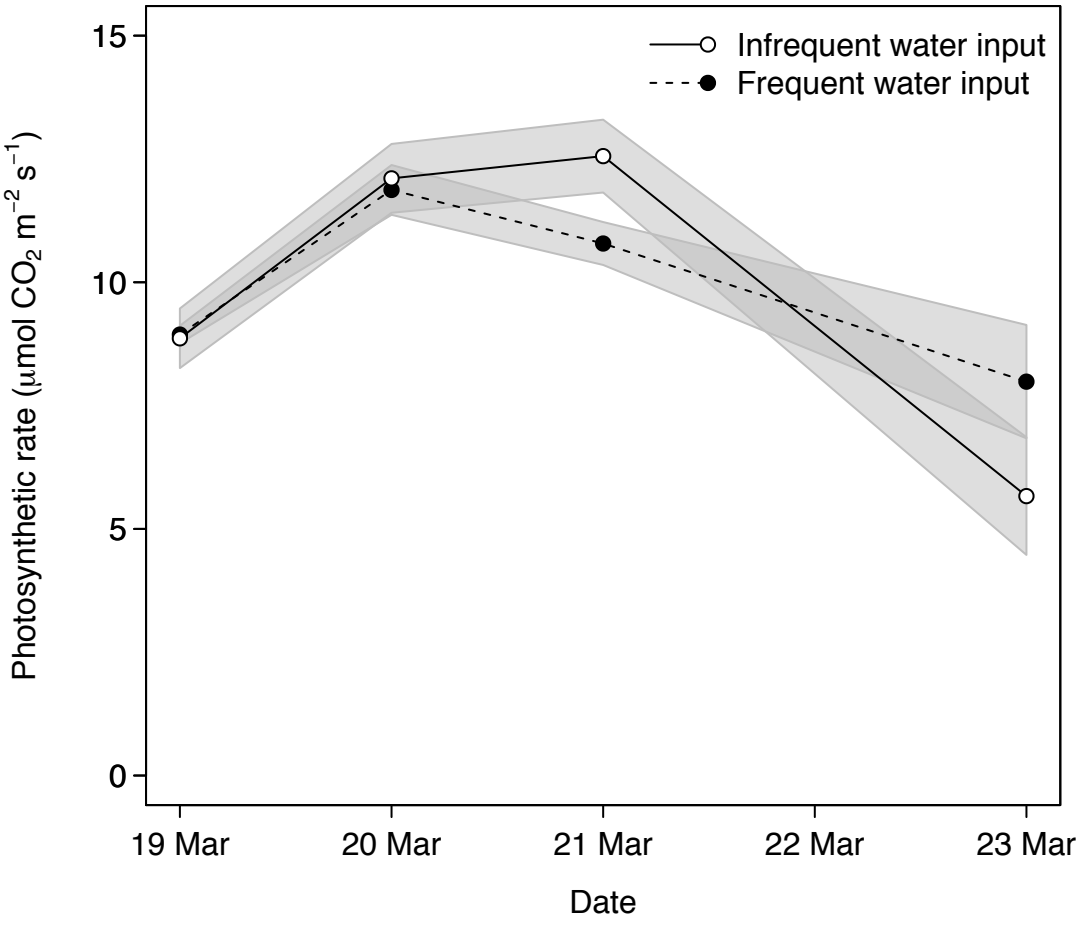

Fig. S4. Plant photosynthetic rate, scaled by plant leaf area for each experiment treatment (infrequent and frequent water input, full and dashed curves, respectively). Shaded polygons indicate ±standard error of the mean.

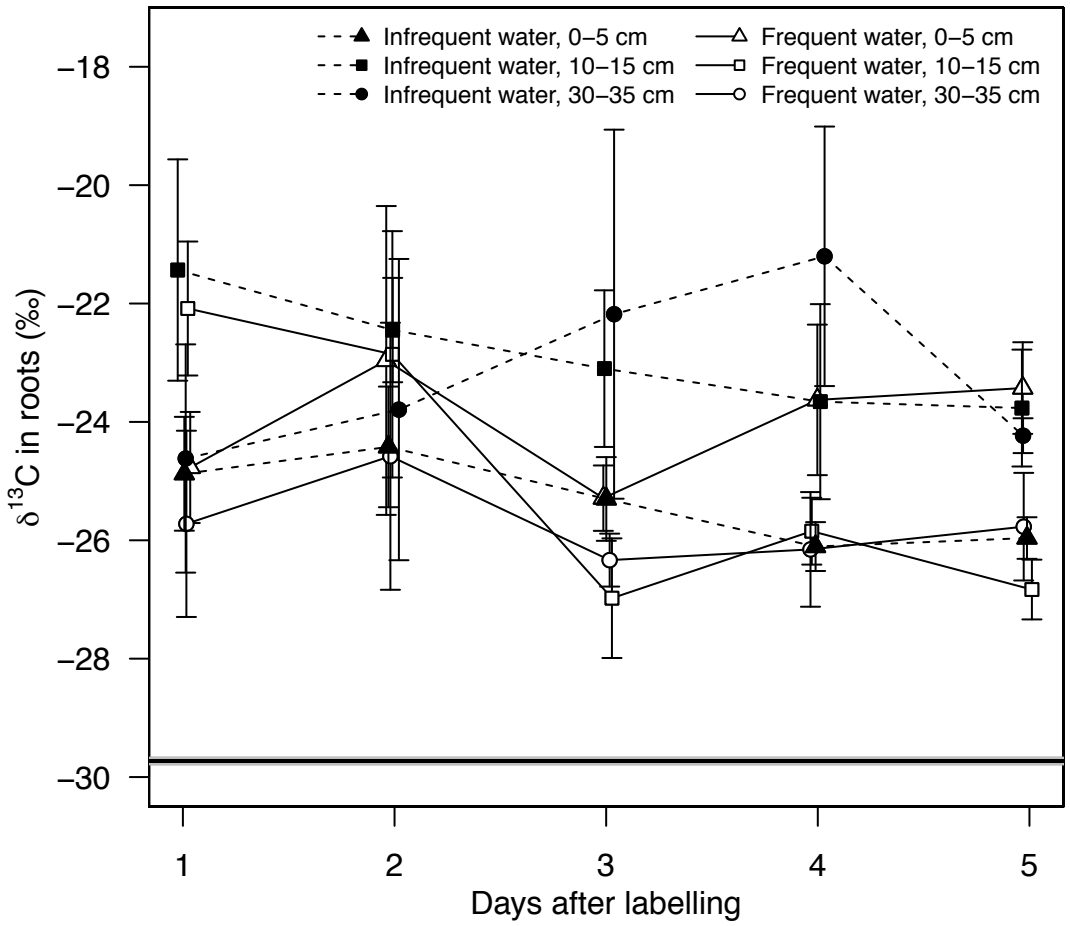

Fig. S5. ^{13}C signature in roots (mean±se), over 5 days after plant ^{13}C-CO_2 labeling, in the infrequent (open symbols) and frequent (closed symbols) water input treatments, at three depths (top: 0-5 cm, triangles; middle: 10-15 cm, squares, bottom: 30-35 cm, circles). Background root ^{13}C signature mean ± standard error is shown (horizontal line and grey polygon).

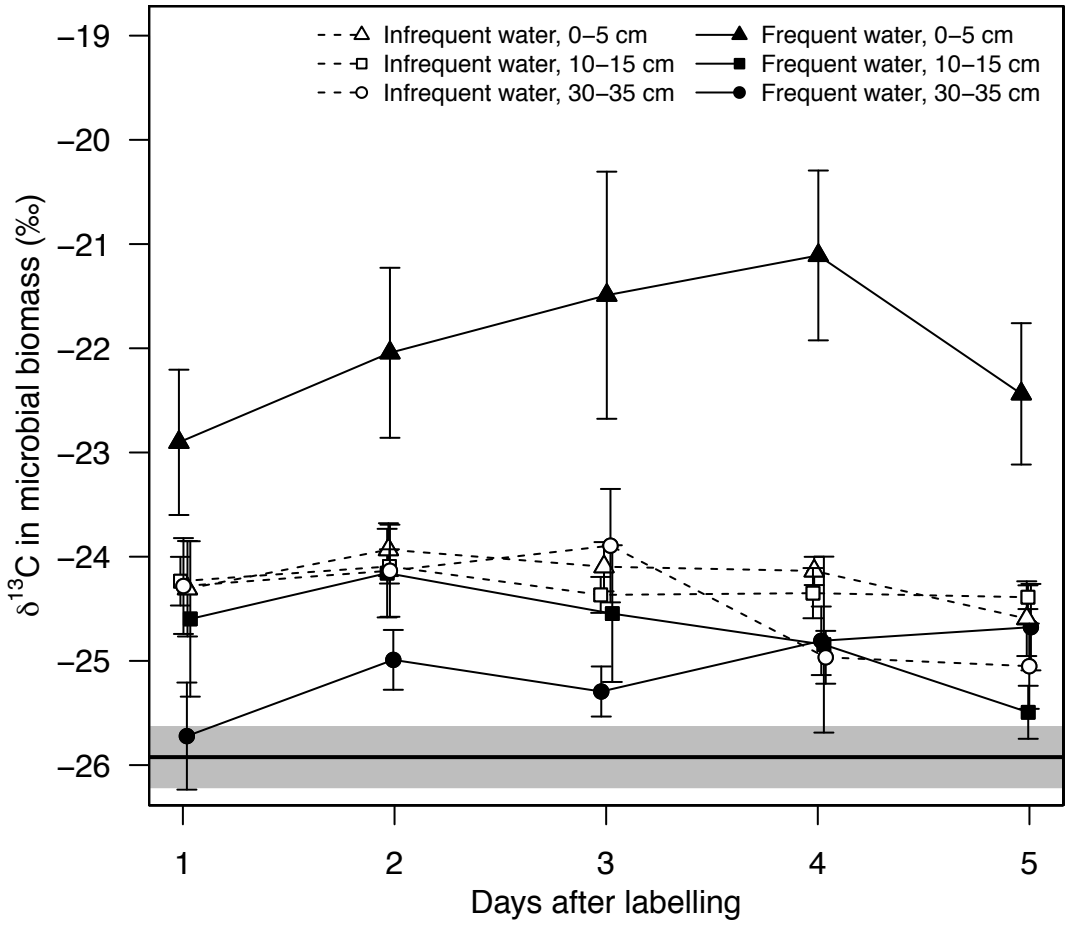

Fig. S6. ^{13}C signature in microbial biomass (mean±se), over 5 days after plant ^{13}C-CO_2 labeling, in the infrequent (open symbols) and frequent (closed symbols) water input treatments, at three depths (top: 0-5 cm, triangles; middle: 10-15 cm, squares, bottom: 30-35 cm, circles). Background microbial biomass ^{13}C signature mean ± standard error is shown (horizontal line and grey polygon).

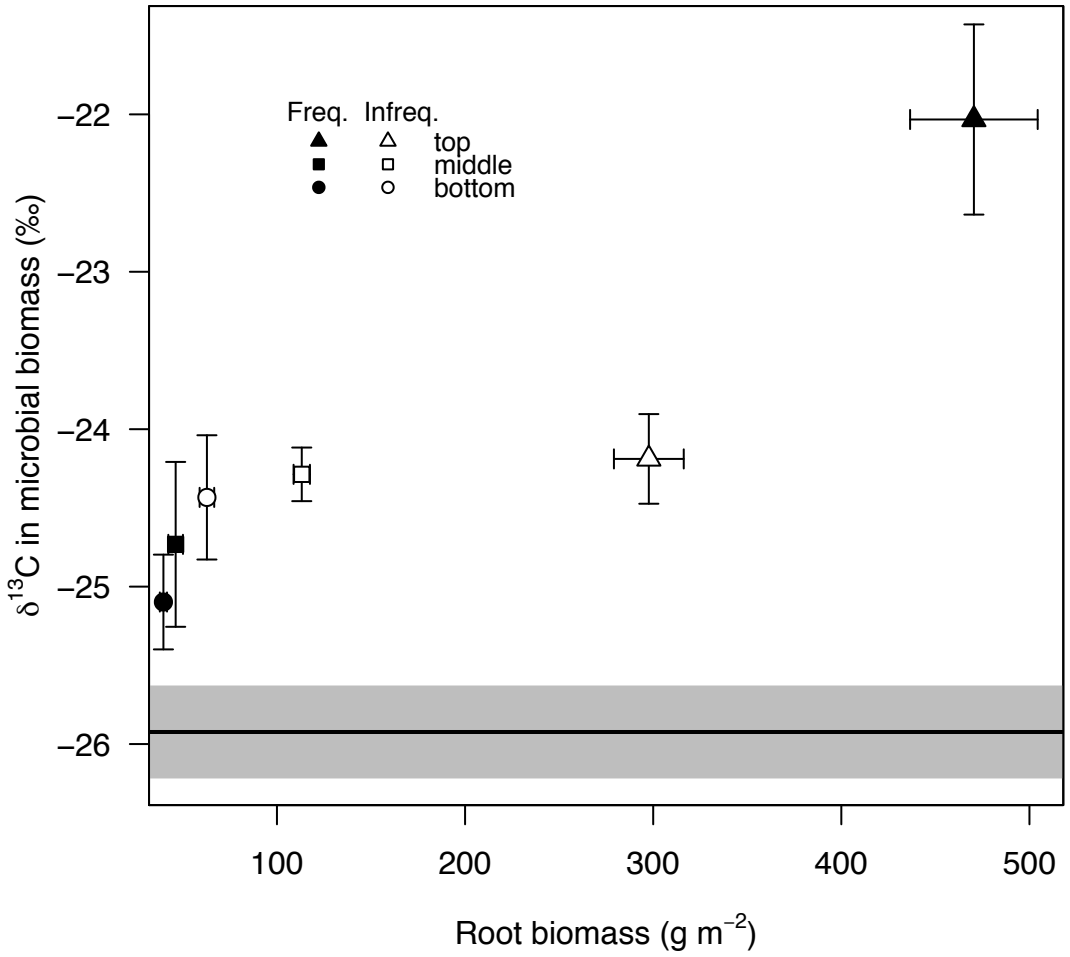

Fig. S7. ^{13}C signature in microbial biomass against root biomass (mean ± standard error) in the frequent (closed symbols) and infrequent (open symbols) water input treatments, at three depths (top: 0-5 cm, triangles; middle: 10-15 cm, squares, bottom: 30-35 cm, circles). Microbial biomass $\delta^{13}C$ was averaged over 5 days after plant ^{13}C-CO_2 labeling. Background microbial biomass ^{13}C signature is shown (line and grey polygon indicate mean ± standard error).

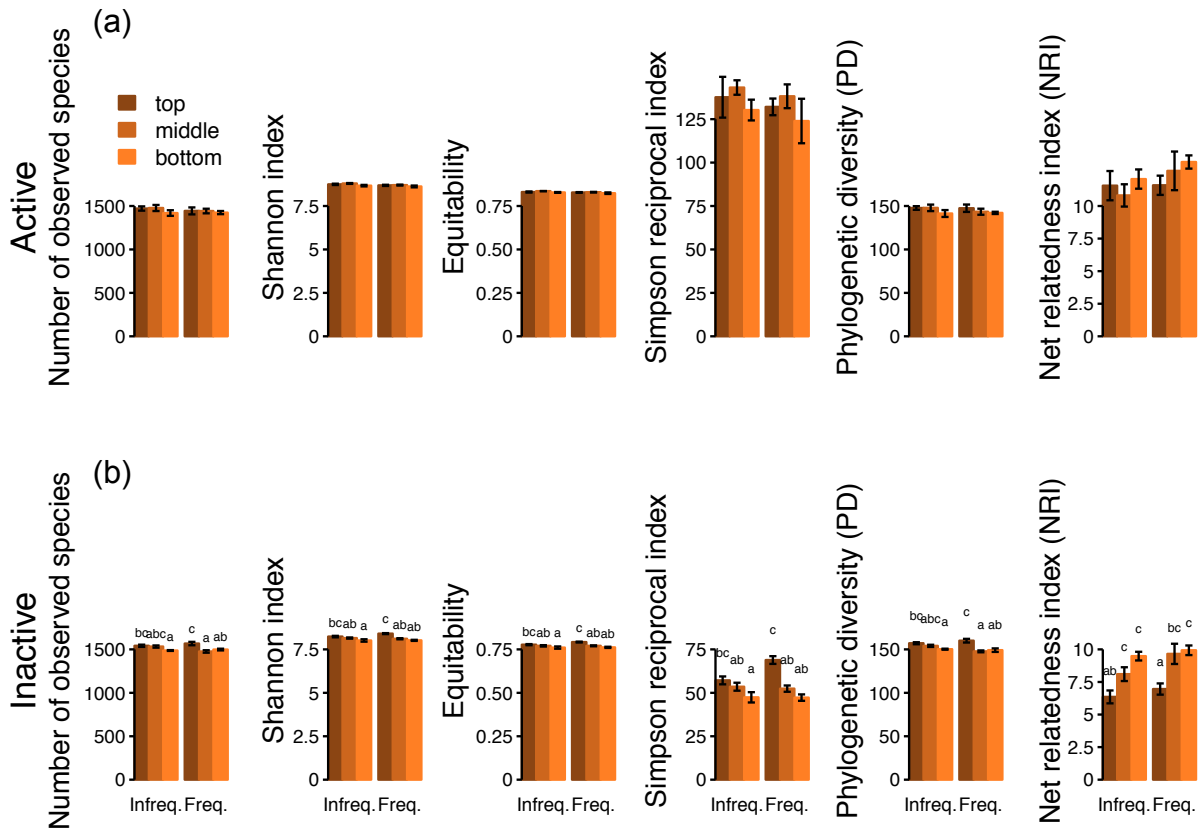

Fig. S8. Bacterial diversity indices in the active (a) and inactive (b) bacterial communities in the infrequent watering (left bar triplets) and frequent watering (right bar triplets) treatments, at three soil depths (top: 0-5 cm, brown; middle: 10-15 cm, light brown, bottom: 30-35 cm, orange). Within an index, bars that share a letter are not significantly different. Bars indicate mean ± standard error.

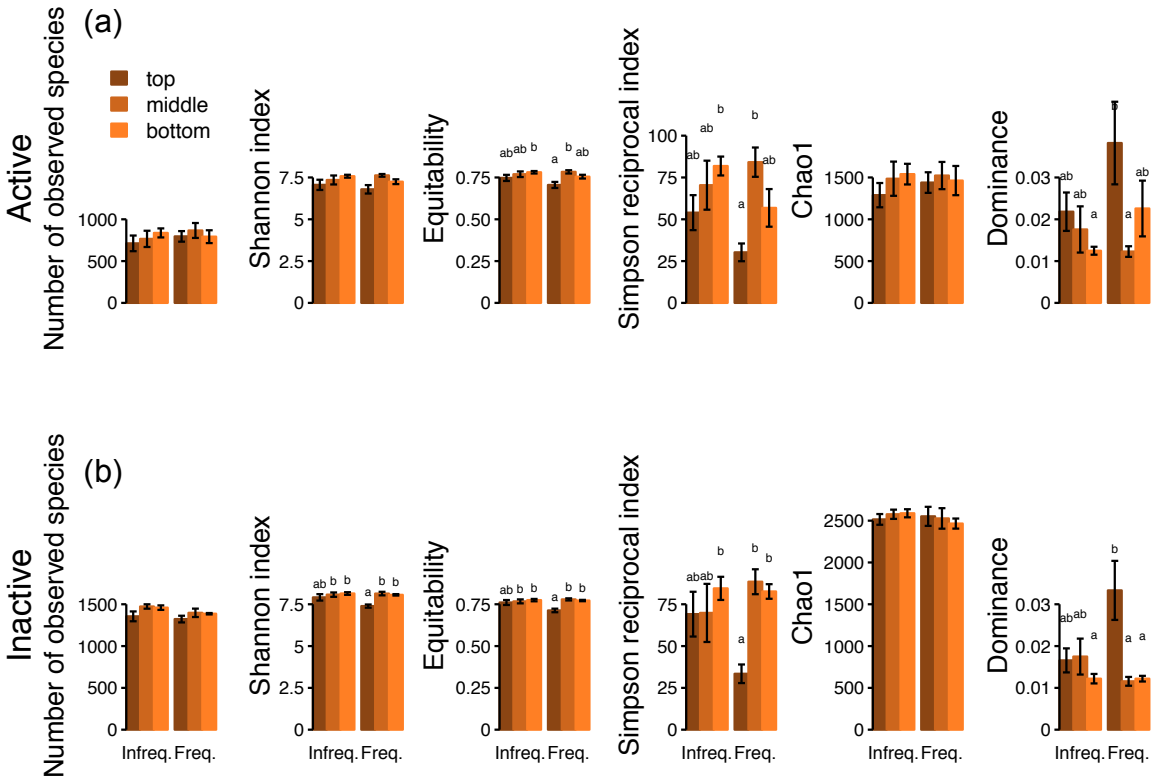

Fig. S9. Fungal diversity indices in the active (a) and inactive (b) fungal communities in the infrequent watering (left bar triplets) and frequent watering (right bar triplets) treatments, at three soil depths (top: 0-5 cm, brown; middle: 10-15 cm, light brown, bottom: 30-35 cm, orange). Within an index, letters indicate significant differences among the means: bars that share a letter are not significantly different. Bars indicate mean ± standard error.

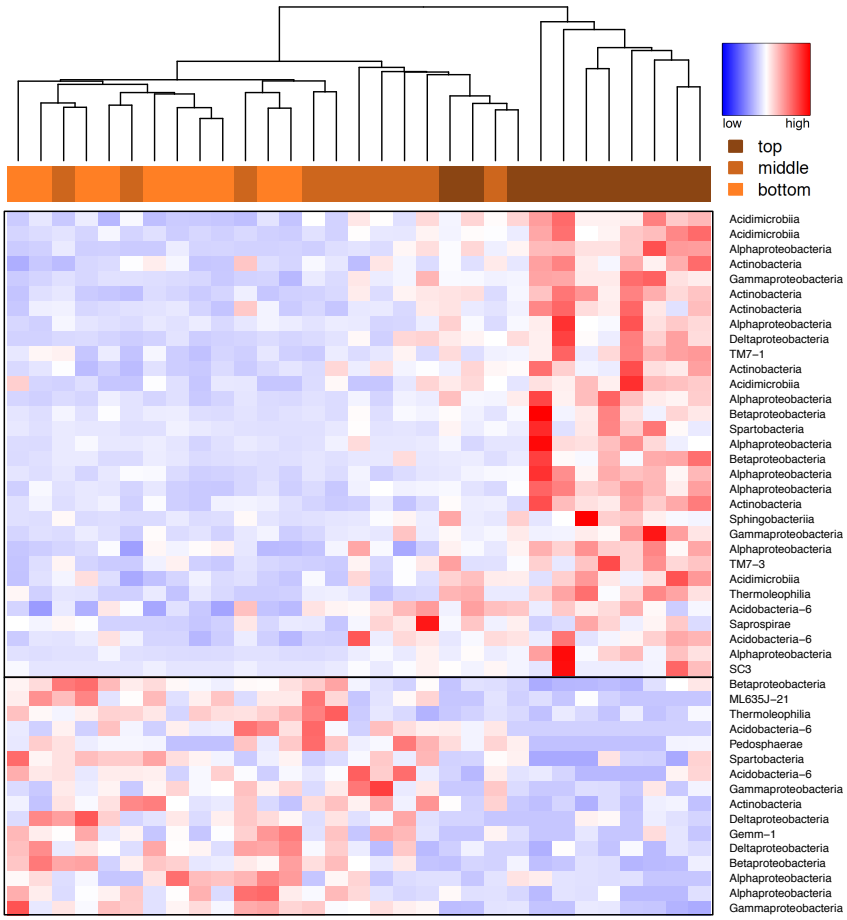

Fig. S10. Heatmap of the OTUs (labeled by class) that responded significantly to soil depth in the active bacterial community (lines, class assignment provided), across all samples (top: 0-5 cm, brown; middle: 10-15 cm, light brown, bottom: 30-35 cm, orange). The relative abundance of the OTUs across samples ranges from blue to white to red (low to medium to high relative abundance). The OTUs clustered into a “top” group and a “bottom” group, delineated by a black line.

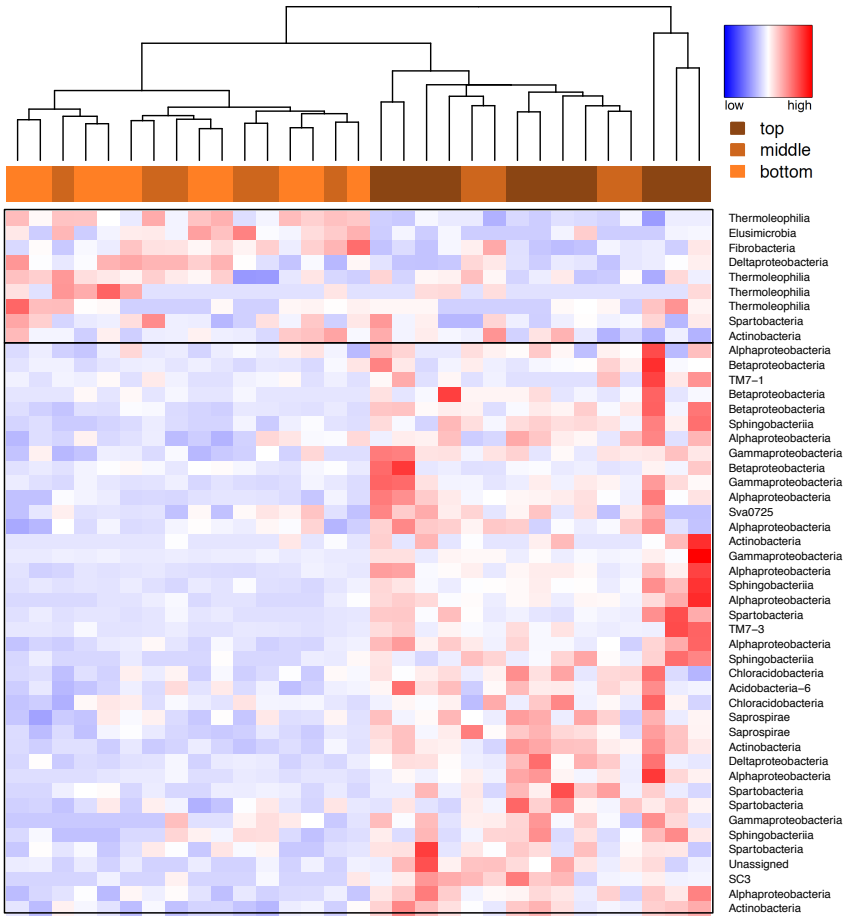

Fig. S11. Heatmap of the OTUs (labeled by class) that responded significantly to soil depth in the inactive bacterial community (lines, class assignment provided), across all samples (top: 0-5 cm, brown; middle: 10-15 cm, light brown, bottom: 30-35 cm, orange). The relative abundance of the OTUs across samples ranges from blue to white to red (low to medium to high relative abundance). The OTUs clustered into a “bottom” group and a “top” group, delineated by a black line.

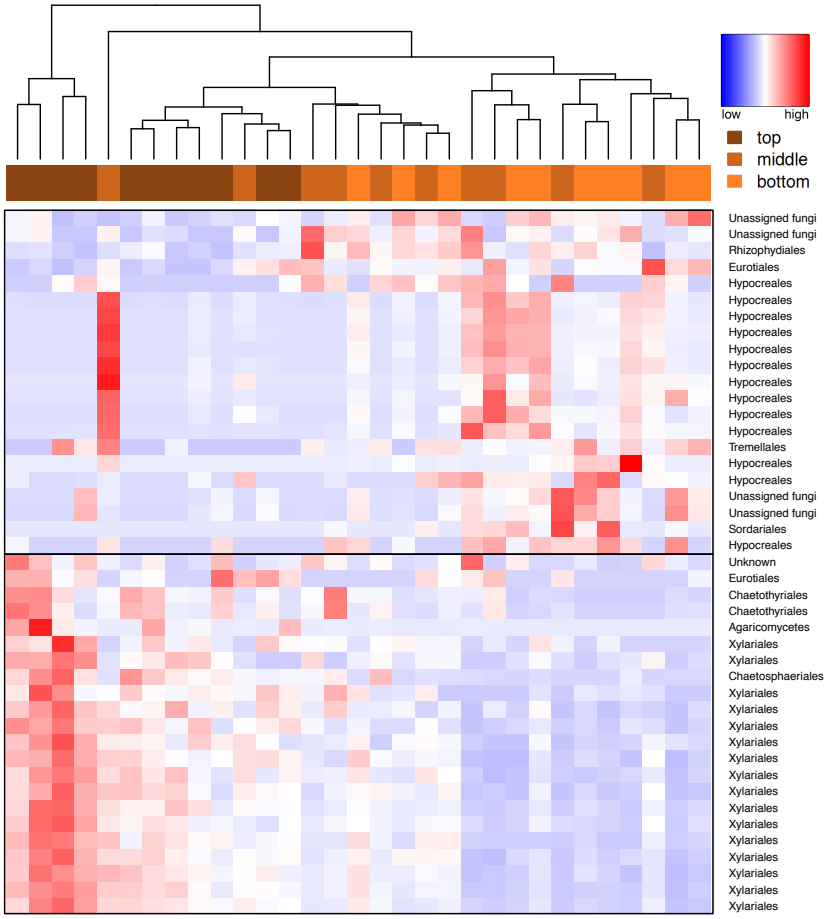

Fig. S12. Heatmap of the OTUs (labeled by order) that responded significantly to soil depth in the active fungal community (lines, class assignment provided), across all samples (top: 0-5 cm, brown; middle: 10-15 cm, light brown, bottom: 30-35 cm, orange). The relative abundance of the OTUs across samples ranges from blue to white to red (low to medium to high relative abundance). The OTUs clustered into a “top” group and a “bottom” group, delineated by a black line.

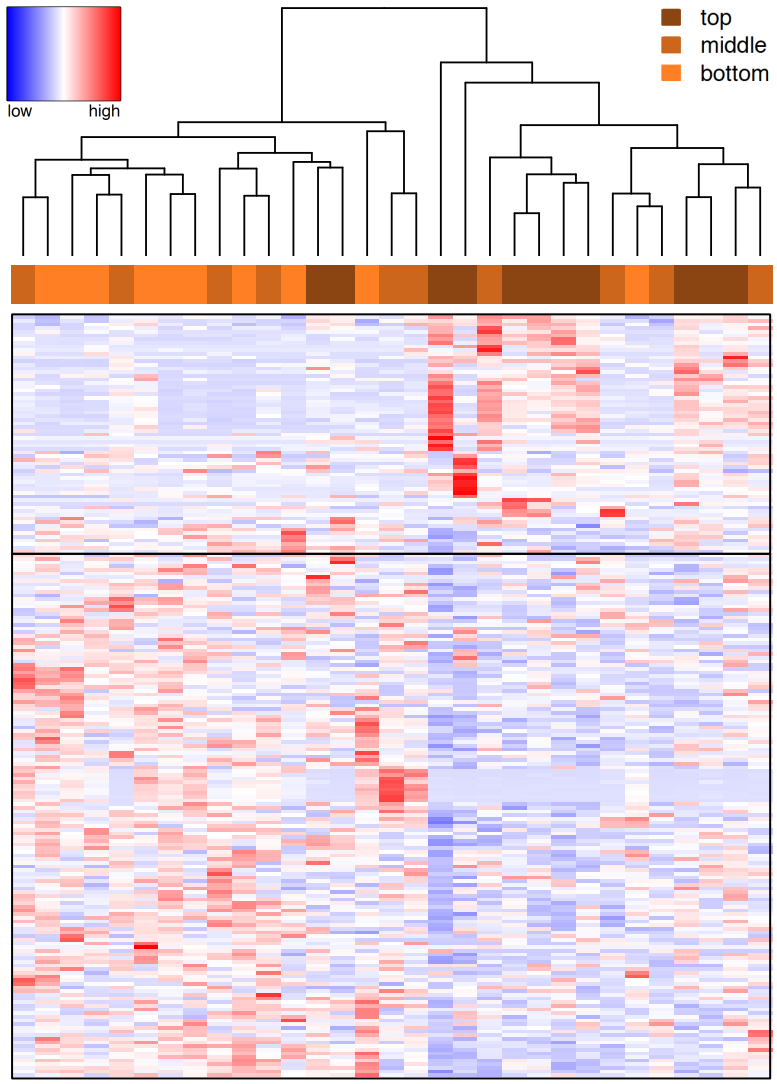

Fig. S13. Heatmap of the OTUs (no label for clarity) that responded significantly to soil depth in the inactive fungal community (lines, class assignment provided), across all samples (top: 0-5 cm, brown; middle: 10-15 cm, light brown, bottom: 30-35 cm, orange). The relative abundance of the OTUs across samples ranges from blue to white to red (low to medium to high relative abundance). The OTUs clustered into a “bottom” group and a “top” group, delineated by a black line.