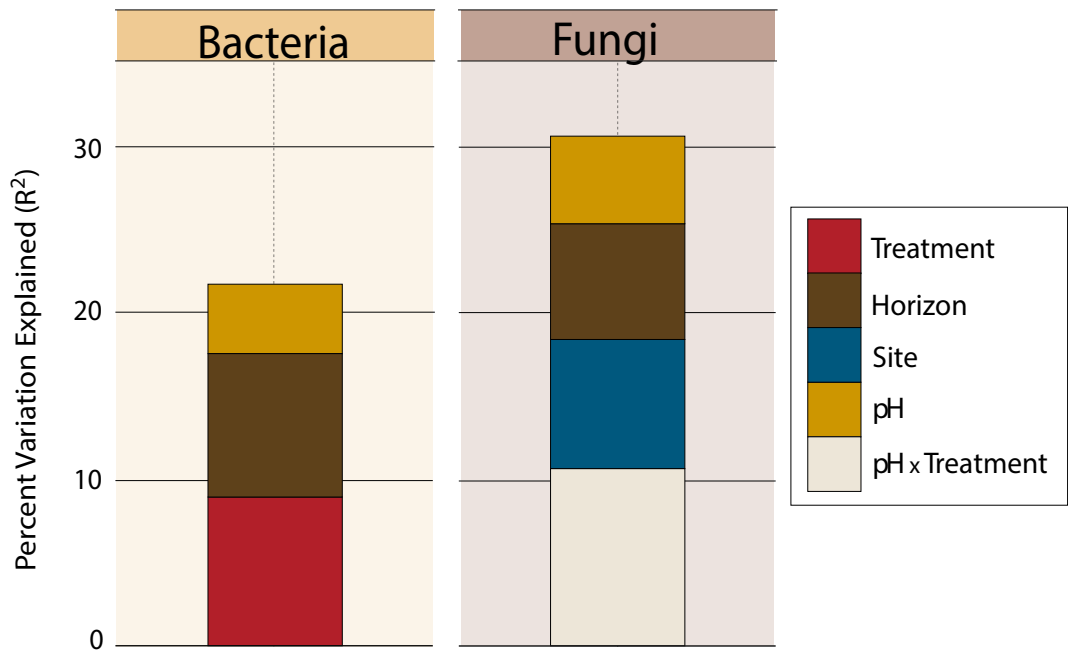


Figure S4. Barplot of the percent variance (R^2) explained by each factor based on perMANOVA ($n_{\text{perm}} = 1000$) using Bray-Curtis dissimilarities for either 16S rRNA gene or ITS pyrotag libraries. Only factors with statistical support ($p < 0.05$) factors were included in the plot. The full tabular perMANOVA results are included.



Fungi	Df	Sum of Sqs	F.Model	R ²	p-value
pH	1	0.56	2.64	0.062	0.005
Treatment	3	0.92	1.43	0.102	0.091
Horizon	1	0.70	3.28	0.078	0.006
C:N	1	0.36	1.66	0.040	0.095
Site	2	0.77	1.80	0.086	0.041
pH x Treatment	3	0.99	1.54	0.110	0.053
pH x Horizon	1	0.19	0.90	0.021	0.500
Treatment x Horizon	2	0.61	1.42	0.068	0.130
pH x C:N	1	0.12	0.57	0.014	0.850
Treatment x C:N	3	0.35	0.81	0.039	0.68
Residuals	16	9.00	-	0.381	-

Bacteria	Df	Sum of Sqs	F.Model	R ²	p-value
pH	1	0.63	1.90	0.046	0.002
Treatment	3	1.30	1.30	0.094	0.036
Horizon	1	1.24	3.74	0.090	0.001
C:N	1	0.36	1.09	0.026	0.301
Site	2	0.76	1.14	0.055	0.182
pH x Treatment	3	1.08	1.08	0.078	0.278
pH x Horizon	1	0.38	1.15	0.028	0.224
Treatment x Horizon	2	0.57	0.85	0.041	0.831
pH x C:N	1	0.29	0.88	0.021	0.666
Treatment x C:N	3	0.83	0.83	0.060	0.887
Residuals	19	6.32	-	0.459	-