

Supplementary Table S1. Significance values from analysis of DNA concentration, 16S rRNA gene qPCR, cyanobacteria 16S rRNA gene qPCR, and chlorophyll *a* concentration comparisons. Each measurement was averaged over 6 field replicate values. The Arches and ISKY control vs. trampled values were compared using a two-sided t-test. The CV experiment was analyzed using a factorial model.

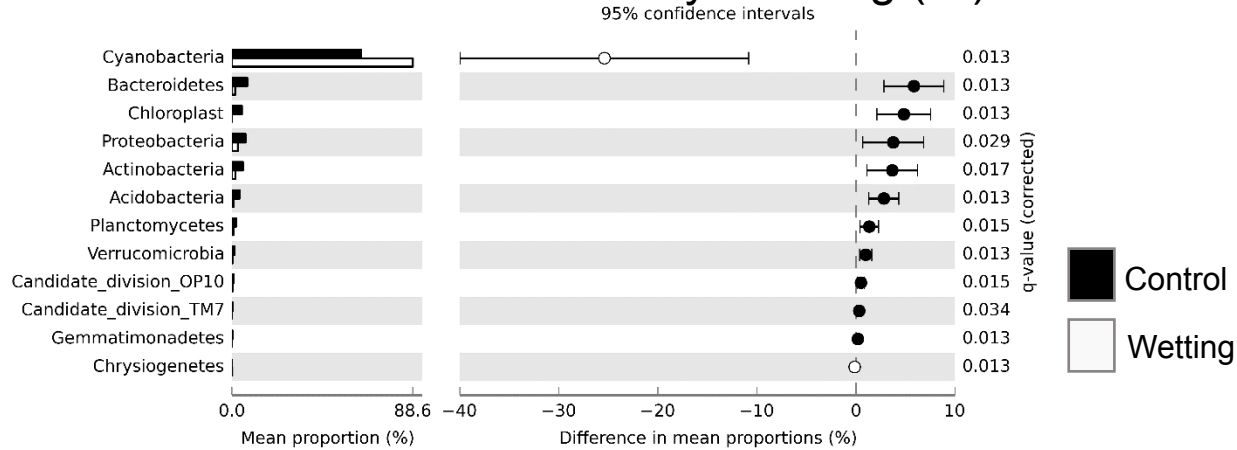
Field experiment		DNA concentration	16S rRNA gene qPCR	Cyanobacteria 16S rRNA gene qPCR	Chlorophyll <i>a</i> concentration
ARCHES		0.2702	0.0388	0.0699	<0.0001
ISKY		0.0367	0.0031	0.019	<0.0001
CV	model	0.0003	0.4555	0.0168	<0.0001
	IR	0.0049	0.1741	0.0059	<0.0001
	W	0.0285	0.4133	0.7202	0.9381
	IR X W	0.0009	0.8538	0.0837	<0.0001

Supplementary Table 4. ANOSIM comparisons of 16S rRNA gene communities

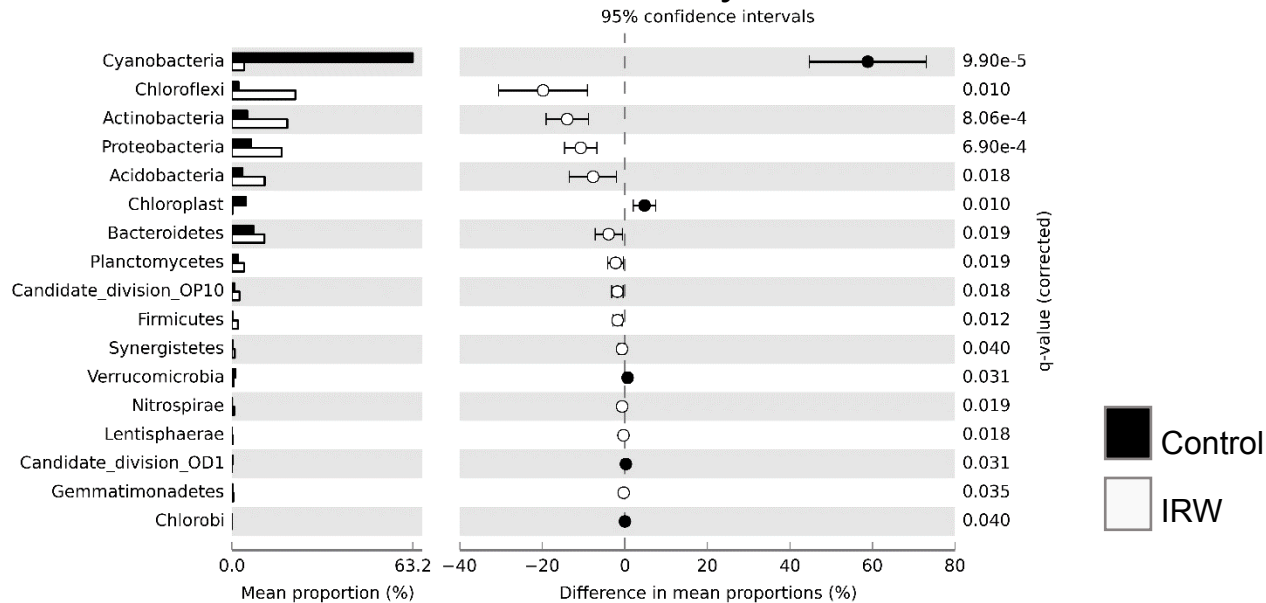
Comparisons	r²-value	p-value
<i>Between control plots</i>		
Arches and ISKY	0.343	0.006
Arches and CV	0.021	0.296*
ISKY and CV	0.185	0.030
<i>Between control and treatment plots</i>		
<i>Arches</i>		
Control and T	0.081	0.035
<i>ISKY</i>		
Control and T	0.595	<0.001
<i>Castle Valley</i>		
Control and IR	0.015	0.349*
Control and W	0.372	0.016
Control and IRW	0.932	0.002
<i>Between different treatment plots</i>		
<i>Trampled sites</i>		
Arches and ISKY	0.076	0.182*
<i>Castle Valley</i>		
IR and W	0.375	0.004
IR and IRW	0.963	0.003
W and IRW	0.991	0.004
<i>Castle Valley and Trampling</i>		
Arches T and IR	0.264	0.026
Arches T and W	0.562	0.003
Arches T and IRW	0.959	0.002
ISKY T and IR	0.395	0.004
ISKY T and W	0.524	0.005
ISKY T and IRW	0.981	0.002

*Highlights comparisons where the anosim comparison resulted in a non-significant difference (p>=0.05).

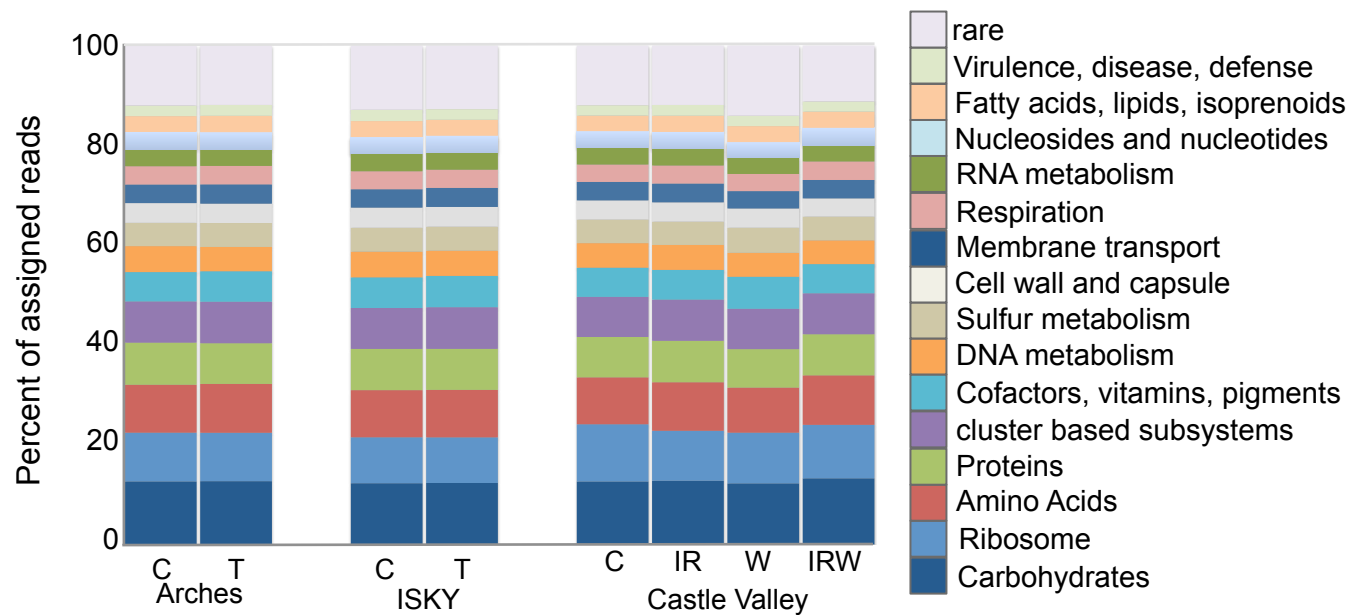
A. Castle Valley: Wetting (W)



B. Castle Valley: IRW



Supplementary Figure 1. Phyla showing significant differences in relative abundance between control and treatment plots. Significant differences were only found in the W and IRW treatments. Values and figures were generated employing Welch's t-test with Storey's FDR method of multiple test correction within the STAMP software package.



Supplementary Figure 2. Functional bins (MG-RAST level 1) in the shotgun metagenomes. Each bar represents the average value of two sequence datasets derived from replicate field plots. The category “rare” represents the sum total of subsystems that individually accounted for <1% of the total sequences.