Table 3. Split-plot analysis of variance for the abundance of *amoA* genes in the Jasper Ridge Global Change Experiment

Source	df	Sum of squares	Mean square	*F*	*P*
Main plot comparisons					
C	1	2.3990	2.3990	4.71	0.0387*
H	1	0.0019	0.0019	0.00	0.9523
C × H	1	1.5651	1.5651	3.07	0.0907
Error (plot{H × C})	28	14.2738	0.5098		
Subplot comparisons					
N	1	0.1267	0.1267	0.64	0.4315
N × C	1	0.0162	0.0162	0.08	0.7771
N × H	1	0.1673	0.1673	0.84	0.3669
N × C × H	1	0.0907	0.0907	0.46	0.5050
Error (N × plot{H × C})	28	5.5689	0.1989		
W	1	0.1600	0.1600	0.61	0.4414
W × N	1	0.3382	0.3382	1.29	0.2658
W × C	1	1.4012	1.4012	5.34	0.0284*
W × H	1	5.0788	5.0788	19.36	0.0001****
W × H × C	1	0.0050	0.0050	0.02	0.8910
Error (W × plot{H × C})	28	7.3441	0.2623		
N × W × C	1	0.0234	0.0234	0.13	0.7211
N × W × H	1	0.1962	0.1962	1.09	0.3061
N × W × H × C	1	0.4842	0.4842	2.69	0.1130
Error (N × W × plot{H × C})	26	4.6809	0.1800		

Two missing data points (for plots 47 and 123) were deleted. Split-plot ANOVA was performed by using the general linear model (GLM) in the SAS statistical package (SAS Institute, Cary, NC). *, $P < 0.05$; ****, $P < 0.0001$; N, nitrogen; H, heat; W, water; C, CO_2.