

**S13 Table.** Three-way ANOVA <sup>a</sup> to assess alpha diversities <sup>b</sup> at different levels for experiment II.

	Df	Shannon measurement (H')				Number of OTUs				Pielou evenness (J)			
		With singletons		Singletons removed		With singletons		Singletons removed		With singletons		Singletons removed	
		F <sup>c</sup>	P <sup>d</sup>	F	P	F	P	F	P	F	P	F	P
Technical replicate	2	1.343	0.271	1.262	0.292	2.771	0.073	2.085	0.135	1.011	0.371	1.062	0.354
Location	2	6.389	0.003**	5.625	0.006**	12.702	4.E-05**	10.681	1.5E-04**	4.904	0.012*	4.36	0.018*
Treatment	1	14.116	4.7E-04**	12.674	0.001**	9.667	0.003**	8.506	0.005**	15.301	2.9E-04**	13.80	0.001**
Residuals	48												

<sup>a</sup> The model used for the three-way ANOVA:  $(\alpha \text{ diversity})_{ijk} = (\text{technical replicate})_i + (\text{location})_j + (\text{treatment})_k + (\text{error})_{ijk}$ .

<sup>b</sup> The Shannon entropy index, number of OTUs, and the Pielou evenness were used to measure the alpha diversity for each tagged PCR library.

<sup>c</sup> F-value

<sup>d</sup> P-value (>F)

\* p<0.05

\*\* p<0.01