

1 **Table S6. ANOVA statistics for changes in relative abundance of 18 bacterial families in Looe Key**
 2 **Reef triclosan microcosms.**

3 If differences by ANOVA were determined to be statistically significant, Tukey multiple comparisons test
 4 was run comparing treatments (noadd, lowt, high) to relative abundance at time zero (zero).

Bacterial Family	ANOVA		Tukey Multiple Comparisons p-values		
	F _{3,8} =	p-value	zero v noadd	zero v lowt	zero v high
Alteromonadaceae	58.72	< 0.0001	0.4562	0.2779	<0.0001
Bradyrhizobiaceae	3.801	0.0581	-	-	-
Colwelliaceae	35.22	< 0.0001	0.9999	0.9751	0.0001
Cryomorphaceae	27.36	0.0001	0.1178	0.3202	0.0001
Flavobacteriaceae	33.47	< 0.0001	0.9992	0.8447	0.0001
Halomonadaceae	10.44	0.0039	0.9972	0.8046	0.0122
Oceanospirillaceae	59.8	< 0.0001	0.6576	0.6466	< 0.0001
OCS155	2.433	0.14	-	-	-
OM60	43.35	< 0.0001	0.0046	0.0002	0.1545
Pelagibacteraceae	7.45	0.0105	0.5474	0.8998	0.0101
Pseudoalteromonadaceae	82.12	< 0.0001	0.1177	0.4241	< 0.0001
Puniceicoccaceae	12.47	0.0022	0.2636	0.7945	0.0066
Rhodobacteraceae	30.95	< 0.0001	0.001	0.9852	0.0849
Saprospiraceae	8.731	0.0066	0.3409	>0.9999	0.0485
Sphingobacteriales; other	14.26	0.0014	0.3269	0.8177	0.0038
Synechococcaceae	1.435	0.3028	-	-	-
Verrucomicrobiaceae	5.544	0.0235	0.9965	0.5763	0.1058
Vibrionaceae	17.65	0.0007	0.9925	0.9783	0.002

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