Fig. S1. Temperature. Continuous (every 30 min) measurements of temperature at the surface of the water column in a control microcosm.

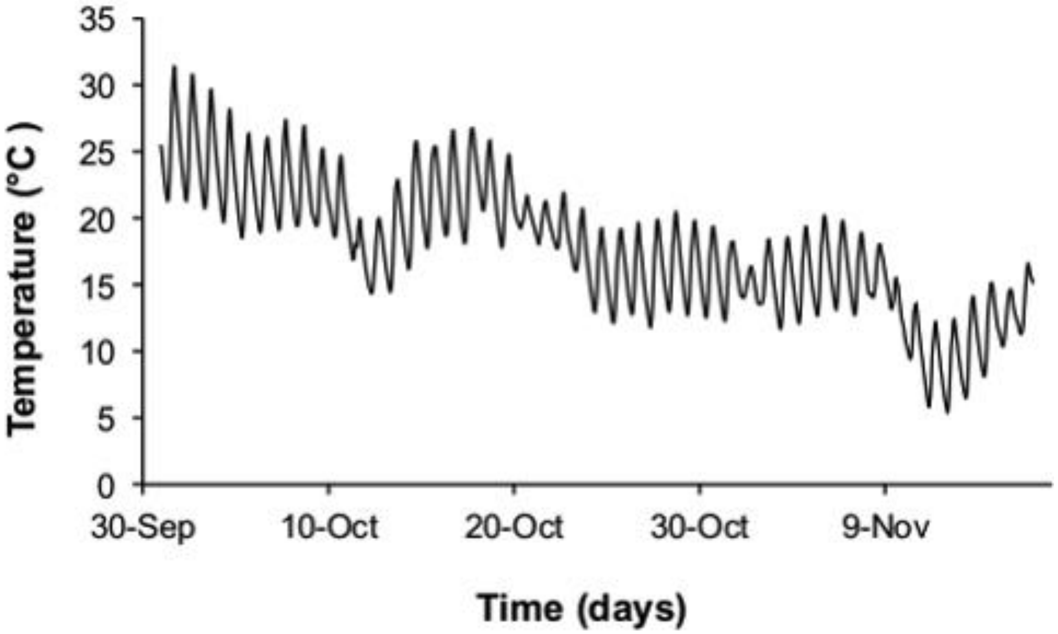

Fig. S2. Colour of water. Water samples from untreated controls (A) and microcosms treated with low (B) and high *Bti* (C) at 44 days after *Bti* application in autumn 2012.

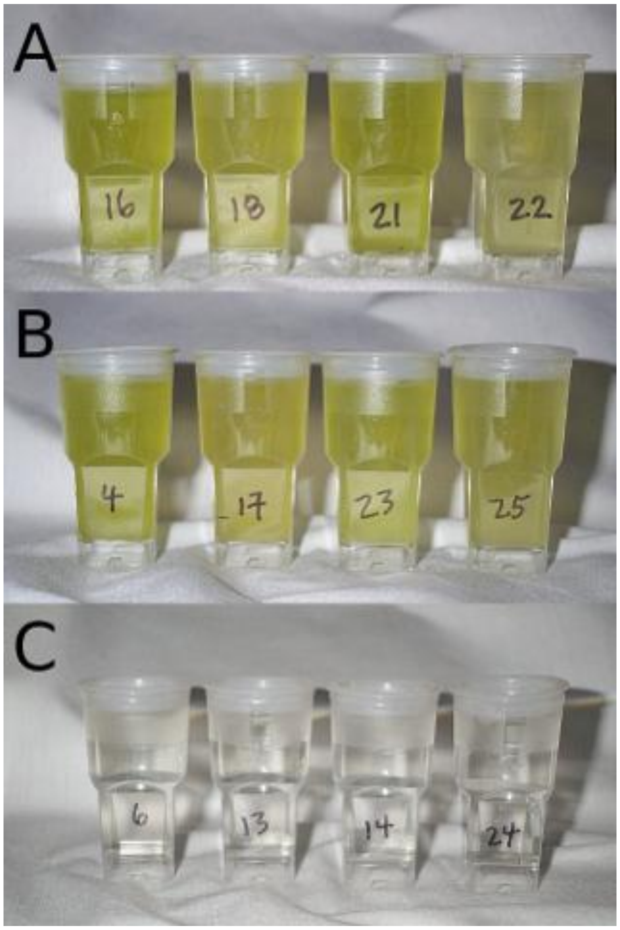

Fig. S3. Bioavailable nitrogen species. Ammonium nitrogen (A), nitrite (B), and nitrate (C) concentration (mg L^{-1}: mean ± SE) in the water column of microcosms assigned to two application rates of mosquito larvicide treatments and an untreated control.

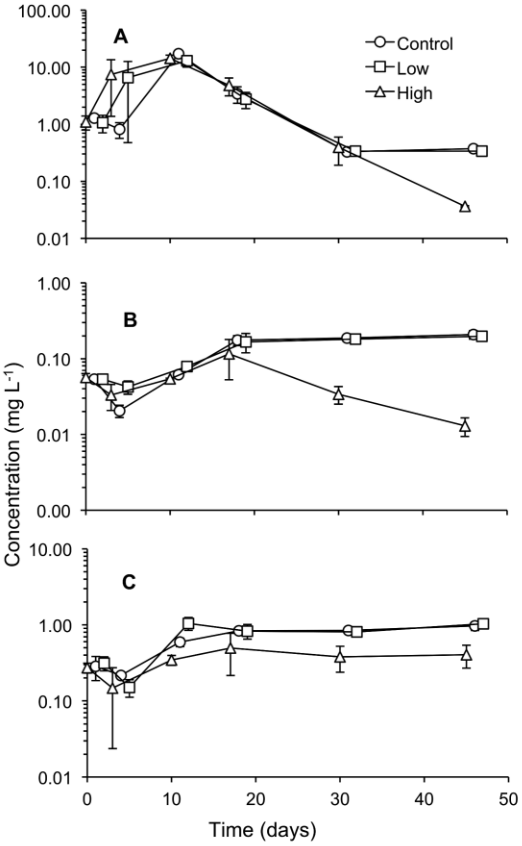

Fig. S4. pH level. pH levels in the water column of microcosms assigned to two application rates of mosquito larvicide treatments and an untreated control at two time points (AM: 08:30; PM: 15:30).

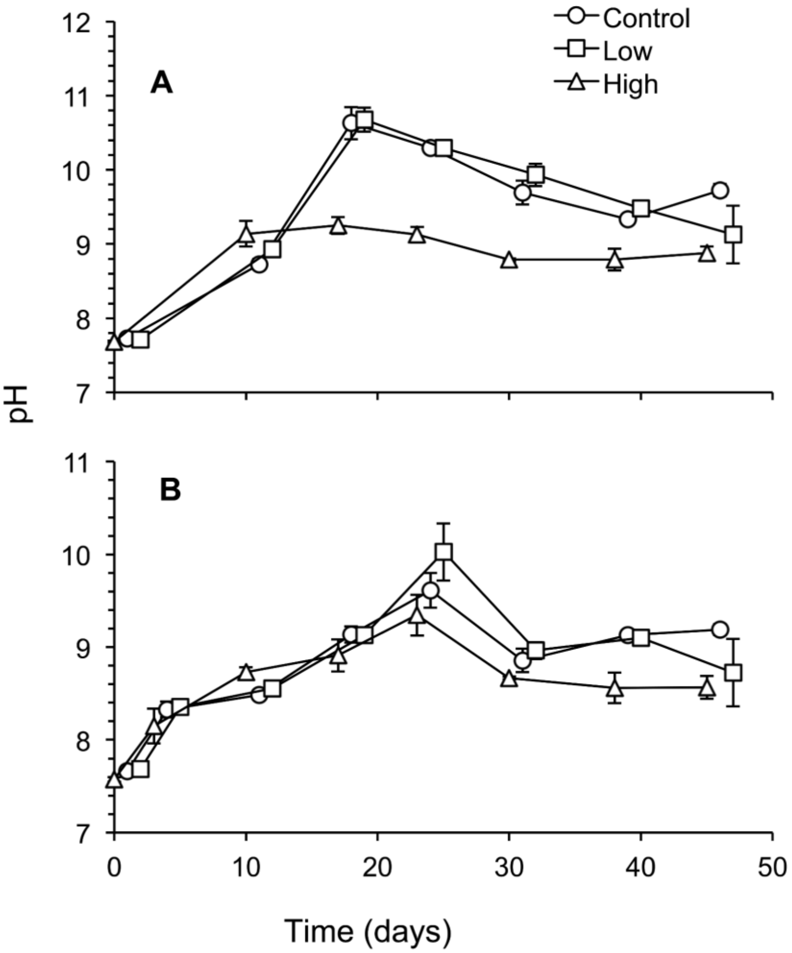

Fig. S5. Dissolved oxygen concentration in water column. Dissolved oxygen levels (mg L^{-1}: mean ± SE) in the water column of microcosms assigned to two application rates of mosquito larvicide treatments and an untreated control at two time points (AM: 08:30; PM: 15:30).

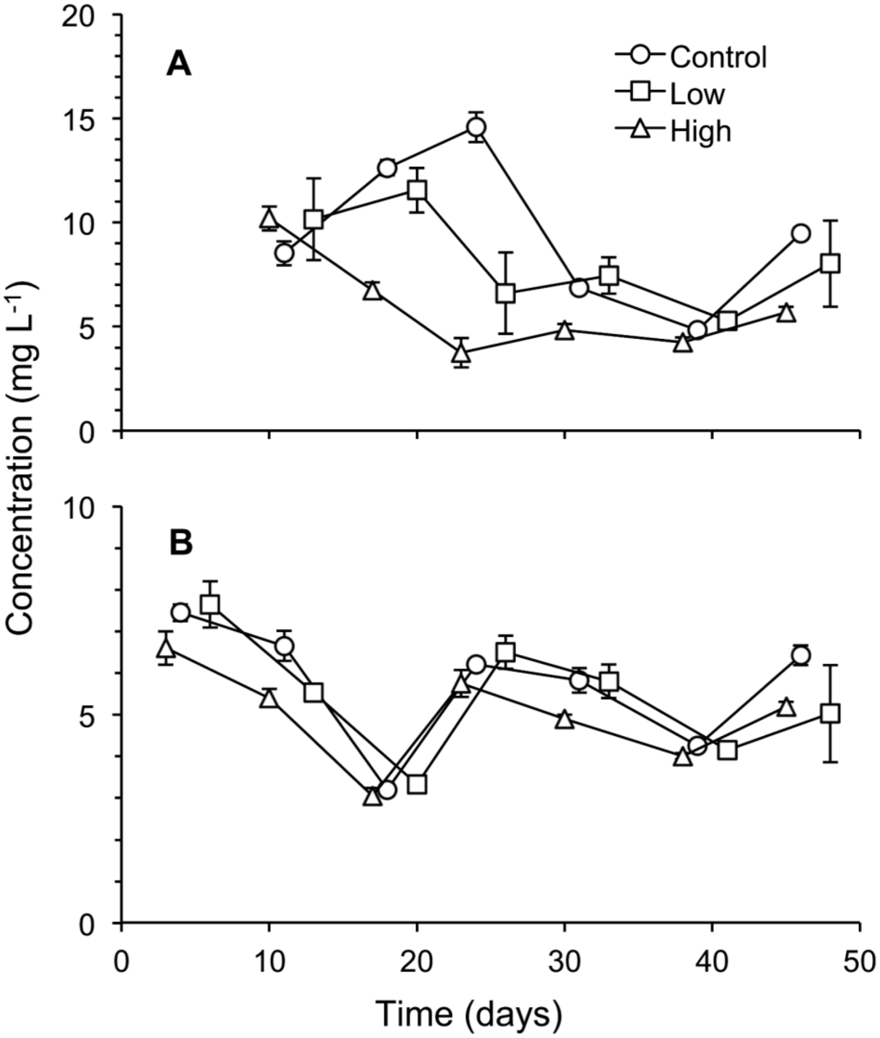

Fig. S6. Major *Bacteria* phyla found in water column. Proportion (≥1%) of *Bacteria* phyla found in each of the 41 samples taken from the water column of experimental microcosms. On October 11, half of the bacterial samples did not amplify during PCR.

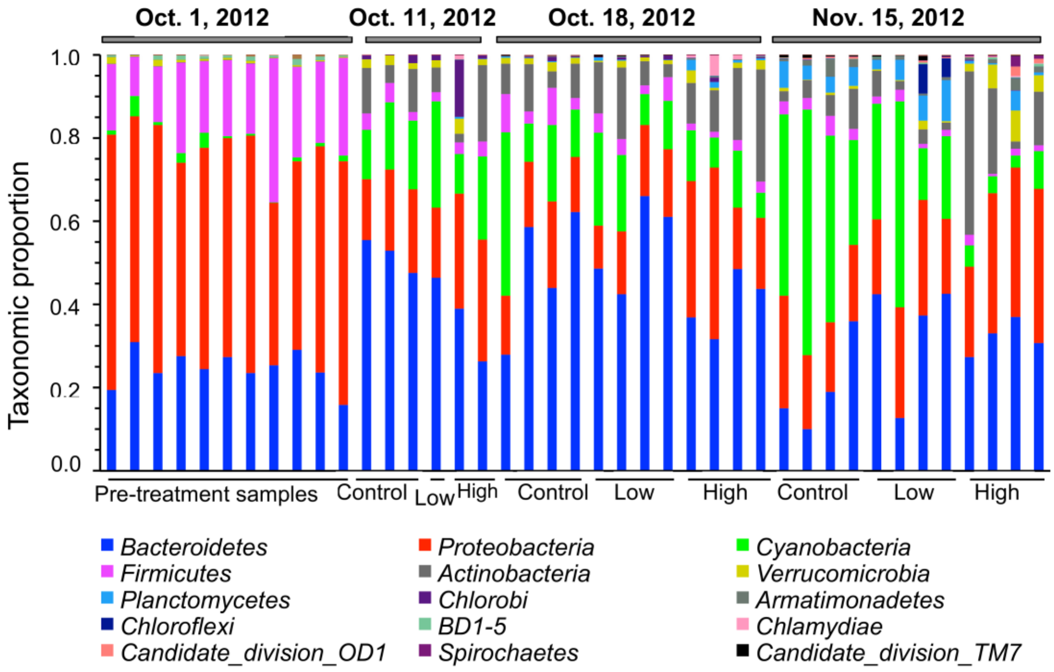

Fig. S7. Nonmetric multidimensional scaling plot. NMDS ordination of bacterial communities by sampling date based on a Bray-Curtis distance matrix. Pre-treatment samples distinctly separated from post-treatment samples. Stress value was 0.10.

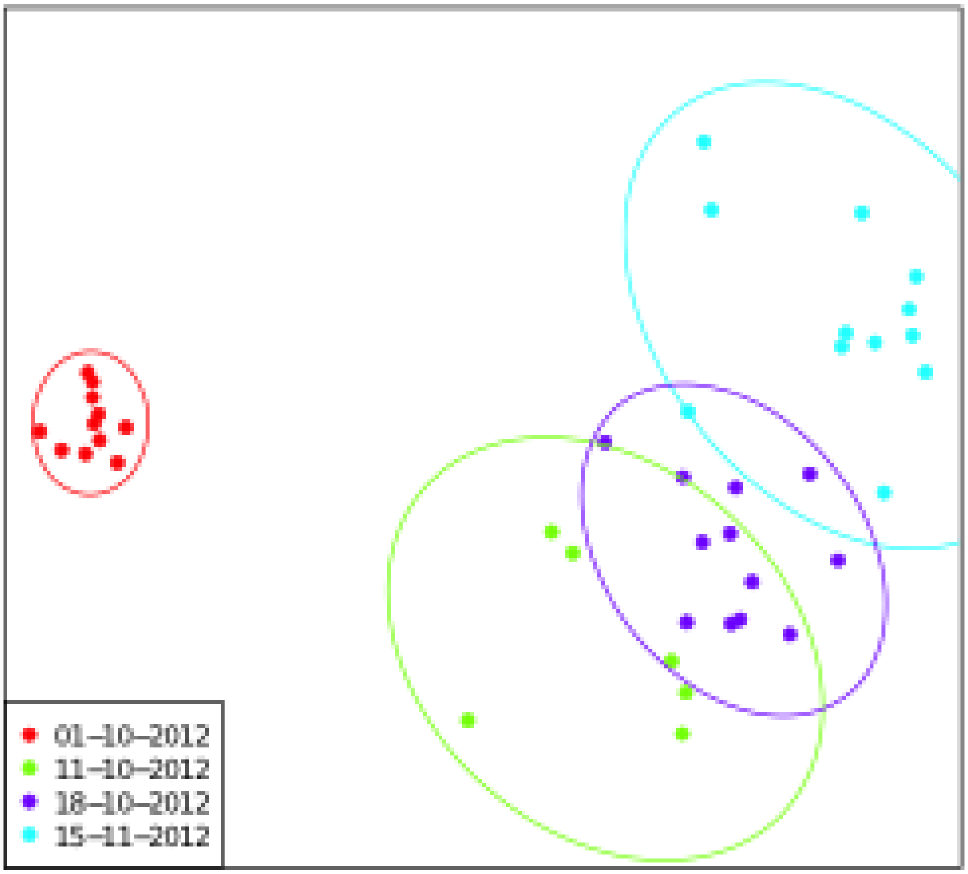

Fig. S8. Alpha diversity comparisons. Box and whisker plots indicating median (middle line), upper and lower quartiles (box top and bottom), outliers (circles), min to max (whiskers), and statistical significance (asterisks) for alpha diversity calculations. Diversity for each time point is shown for different diversity metrics: observed species, Shannon index, and phylogenetic diversity (PD). Comparisons were made between treatment groups using ANOVA and Tukey's method (* = *p*<0.05, ** = *p*<0.01).

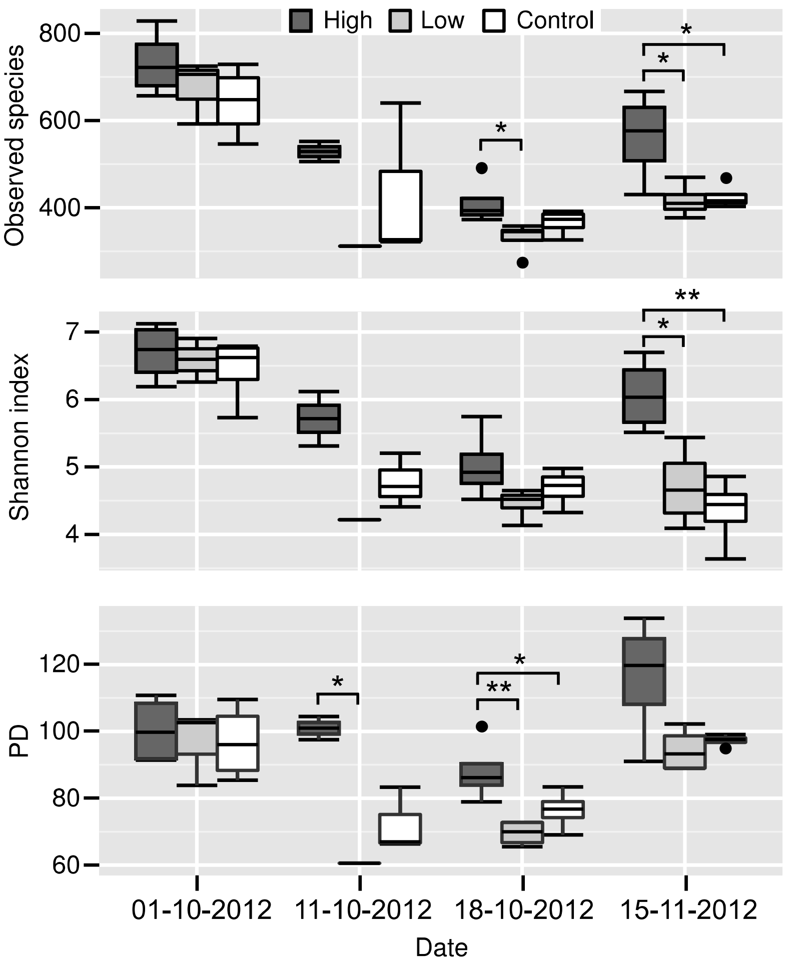

Fig. S9. Principal coordinate analysis. Principal coordinate analysis (PCoA) ordination plot based on a Bray-Curtis dissimilarity matrix, comparing bacterial communities from different *Bti* treatments (Panel A), and three sampling dates (Panel B).

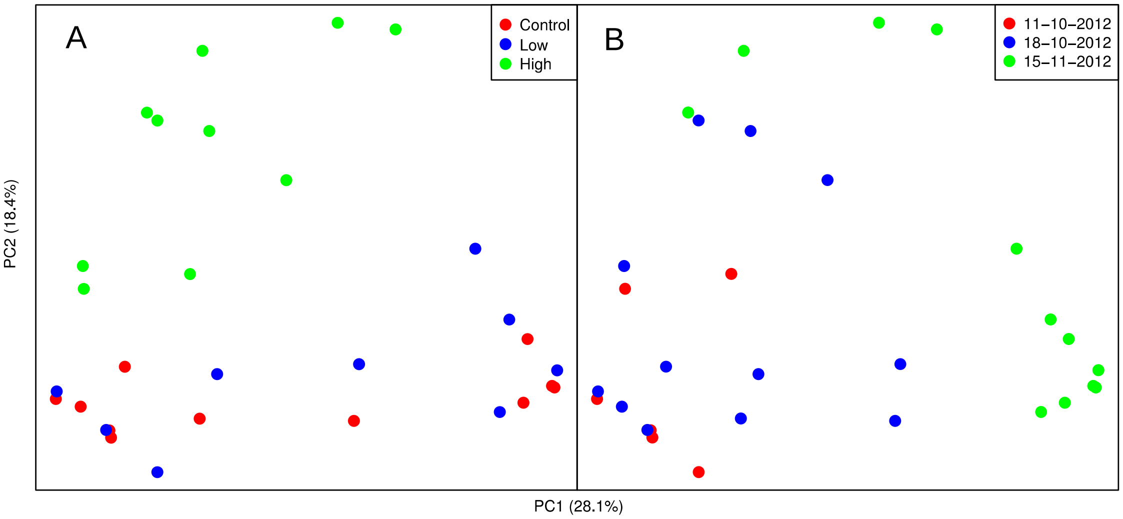

Table S1. Sampling schedule of *Bacteria*, Phytoplankton, particles and other water quality parameters during Fall 2012

Parameters	**1-Oct**	**2-Oct**	**4-Oct**	**5-Oct**	**11-Oct**	**12-Oct**	**18-Oct**	**19-Oct**	**25-Oct**	**1-Nov**	**9-Nov**	**15-Nov**	**16-Nov**
Bacteria (DNA)	X				X		X					X	
Particles		X		X	X		X			X		X	
Chlorophyll		X		X	X		X			X		X	
TN		X		X		X		X		X	X		X
SRP		X		X		X		X		X	X		X
TP		X		X		X		X		X	X		X
Nitrite		X		X		X				X	X		X
Nitrate		X		X		X				X	X		X
Ammonia		X		X		X				X	X		X
pH		X				X		X	X	X	X		X
DO		X		X		X		X	X	X	X		X
Sulfate											X		X
COD													X

Table S2. Mean (±SE, n=4) sulfate and chemical oxygen demand concentration (mg L^{-1}).

Parameters	**Treatment T**		**Time (days)**
		38	**44**
	Control	445.8 (13.24)a	425.3 (6.69)a
Sulfate	Low	400.3 (14.10)a	400.0 (14.02)a
	High	342.0 (18.83)b	363.0 (13.74)b
	Control	N/A	[1]549.3 (18.0)a
COD	Low	N/A	482.3 (10.66)a
	High	N/A	137.5 (8.0)b

[1]n= 3

Means followed by same letters within a column are not significantly different (ANOVA: Tukey's test, *p*>0.05).

Table S3. Mean (±SE) abundance (percentage per sample) of 11 bacterial taxa found in all samples 44 days after *Bti* treatment.

Phylum	Class	Species	Treatments		
			Control [n=4]	Low [n=4]	High [n=4]
Actinobacteria	*Micrococcales*	*Candidatus* Aquiluna	3.4 (0.6)	2.0 (0.3)	7.3 (3.4)
		Agrococcus jejuensis	1.8(1.0)	1.1 (0.7)	0.8 (0.3)
Bacteroidetes	*Sphingobacteria*	*Sediminibacterium*	0.1 (0.02)	0.1 (0.02)	4.7 (3.35)
		Sphingobacterium	0.1 (0.03)	0.2 (0.08)	0.9 (0.7)
	Cytophagia	*Cyclobacteriaceae*	2.8 (1.3)	6 (4.4)	0.2 (0.03)
Cyanobacteria	Chloroplast	*Proteomonas* sp.	41.7(6.9)a	26.2 (8.3)ab	1.7 (0.3)c
		Eutreptiella sp. *LIS2000*	0.2 (0.07)	0.05 (0.02)	0.1 (0.1)
Firmicutes	*Bacilli*	*Bacillus*	1.1(0.2)	0.5 (0.3)	0.2 (0.1)
	Clostridia	*Clostridium*	0.3 (0.1	0.2(0.05)	0.3 (0.2)
Proteobacteria	*Alphaproteobacteria*	*Sphingomonas* sp.	0.1 (0.03)	0.1 (0.04)	0.7 (0.4)
	Betaproteobacteria	*Polaromonas*	4.8 (1.4)	5.4 (1.4)	6.1 (2.0)

Means followed by same letters within a row are not significantly different (ANOVA: Tukey's test, *p*>0.004