

Table 1. Summary of probiotic trial information and sequencing data for all three trials.

	Trial 1	Trial 2	Trial 3
Sample Types	Water, Swabs, Oysters	Water, Swabs, Oysters	Water
Sampling Days (0=spawn)	W:1,12 / OS:5,12	W:1,9 / OS:6,9	W: 5,8,12
Water Filtered	410-750ml	7-10ml	1300-1700ml
Trial Dates	July 11-23, 2012	Jan 9-18, 2013	June 3-15, 2016
Bacterial reads from 12 water samples	1.3 million	1.8 million	5.7 million
Methods	MoBio extraction MiSeq, 2x250 PE	MoBio extraction MiSeq, 2x250 PE	Puregene extraction HiSeq, 2x100 PE
16S region	V4	V4	V6

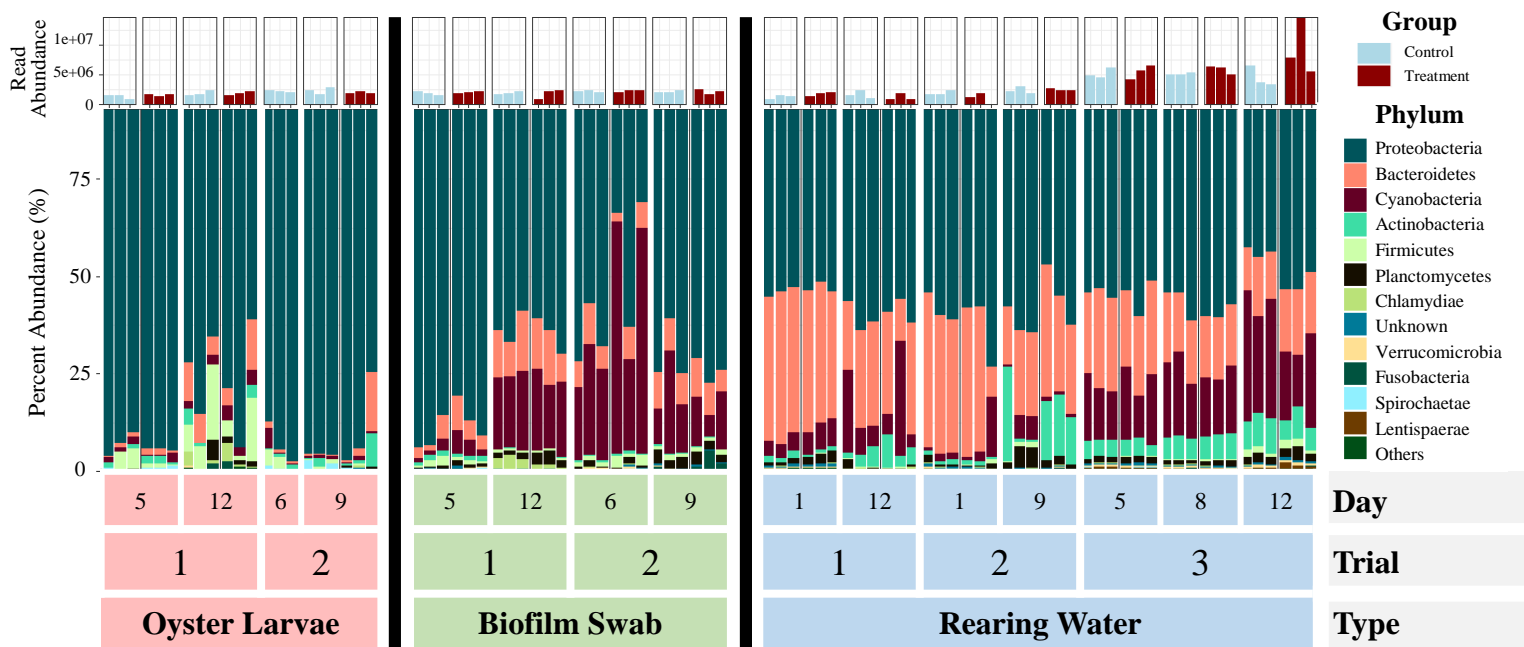


Figure 1. Percent abundances of the 12 most abundant phyla in all oyster larvae, biofilm swab, and rearing water samples from all 3 Trials based on 16S rDNA amplicon sequencing data (bottom). The total abundance of quality filtered sequencing reads is shown in the bar graph (top). The 12 dominant phyla include *Actinobacteria*, *Bacteroidetes*, *Cyanobacteria*, *Deferribacteres*, *Firmicutes*, *Fusobacteria*, *Lentisphaerae*, *Planctomycetes*, *Proteobacteria*, *Spirochaetae*, *Verrucomicrobia*, and *Unknown*. Note: there are no treated oyster larvae samples from Trial 2, Day 6.

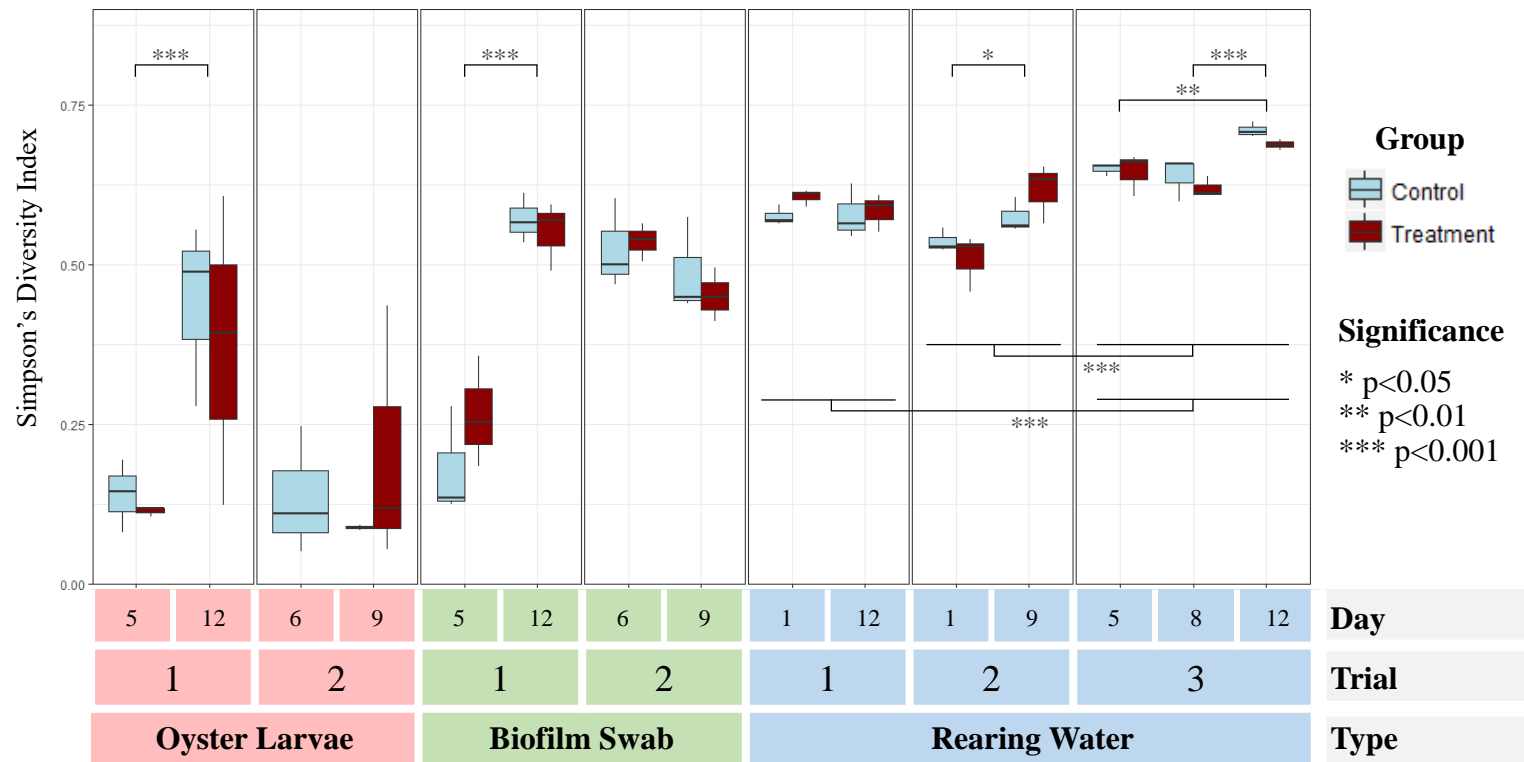


Figure 2. Simpson's index of diversity of bacterial communities in all samples from all 3 trials. The control group is indicated by light blue and the probiotic treated group is indicated by dark red. No significant differences were found between control and treatment samples, due to high variation in the replicate tanks. The diversity significantly increases over time in larvae, swab, and water samples from Trial 1, and water samples from Trial 3. The rearing water is significantly more diverse in Trial 3 than Trials 1 and 2. Note: there are no treated oyster larvae samples from Trial 2, Day 6.

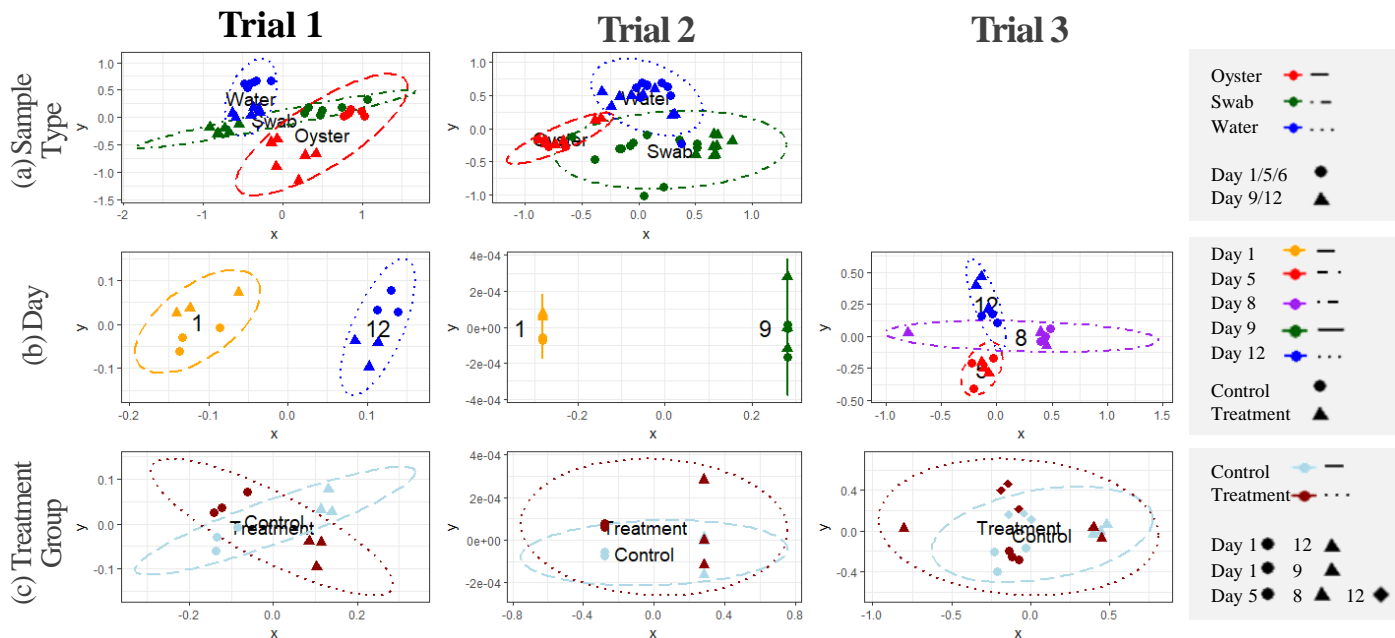


Figure 3. NMDS plots calculated using Bray-Curtis beta-diversity ($k=2$) at the Order level by (a) Sample Type, (b) Sampling Day, and (c) Probiotic Treatment Group. (b) and (c) were calculated using only water samples. The ellipse lines show the 95% confidence interval. (a) The different types of samples are indicated by colors (Oyster=dashed red, Swab=dashdot green, Water=dotted blue) and the days are indicated by symbols (Timepoint 1=circle, Timepoint 2=triangle). The water and swab communities are significantly distinct from each other in both trials. (b) The sampling timepoints are indicated by colors (1=longdash yellow, 5=shortdash red, 8=dashdot purple, 9=solid green, 12=dotted blue) and the treatment group is indicated by symbols (Control=circle, Probiotic treatment=triangle). The water community is significantly different between timepoints. (c) The treatment group is indicated by colors (Control=light blue dashed, Probiotic treatment=dark red dotted) and sampling timepoints are indicated by symbols. The water community is not significantly different according to treatment.

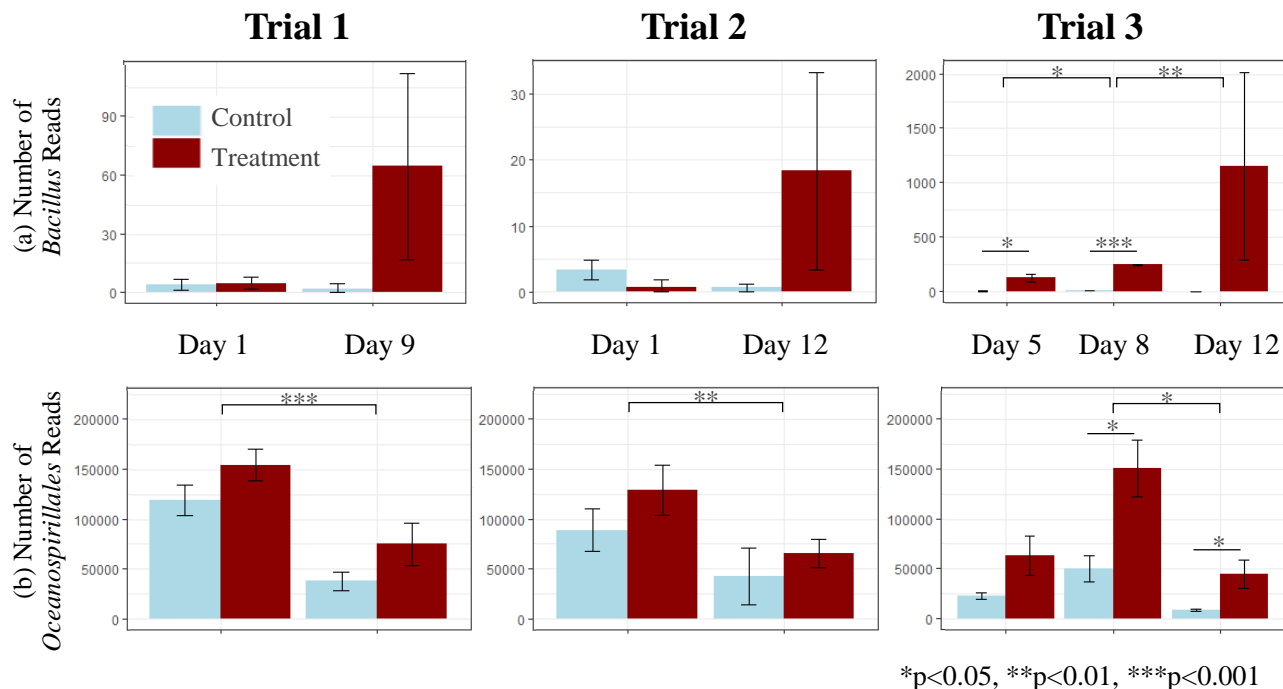


Figure 4. Number of (a) *Bacillus* and (b) *Oceanospirillales* reads in treated and control water samples (n=3) on Days 1 and 12 (Trial 1), Days 1 and 9 (Trial 2), and Days 5, 8 and 12 (Trial 3). Control is indicated by light blue boxplots and probiotic treatment is indicated by dark red boxplots. (a) *Bacillus* is significantly more abundant in the treated than the control water on the first and second timepoint in Trial 3, and increases over time. (b) *Oceanospirillales* are consistently more abundant in probiotic-treated tank rearing water, and decrease with time.

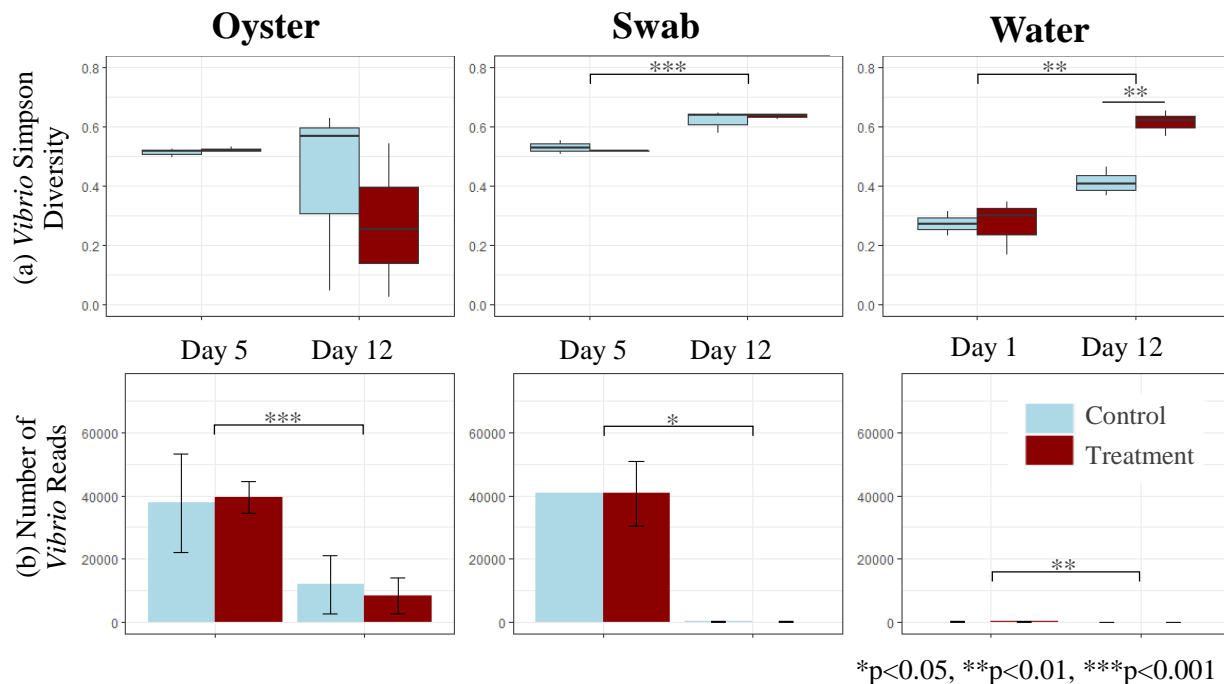


Figure 5. Total *Vibrio* read abundance (a, bar graph) and Simpson's Index of Diversity (b, boxplots n=3) in all samples types on Days 1/5 and 12 from Trial 1. Total *Vibrio* reads are the most diverse in the tank biofilms (swab), and most abundant in the oyster and swab samples on Day 5. Total *Vibrio* reads are significantly more diverse over time in the swab and water samples, and significantly less abundant over time in all samples.

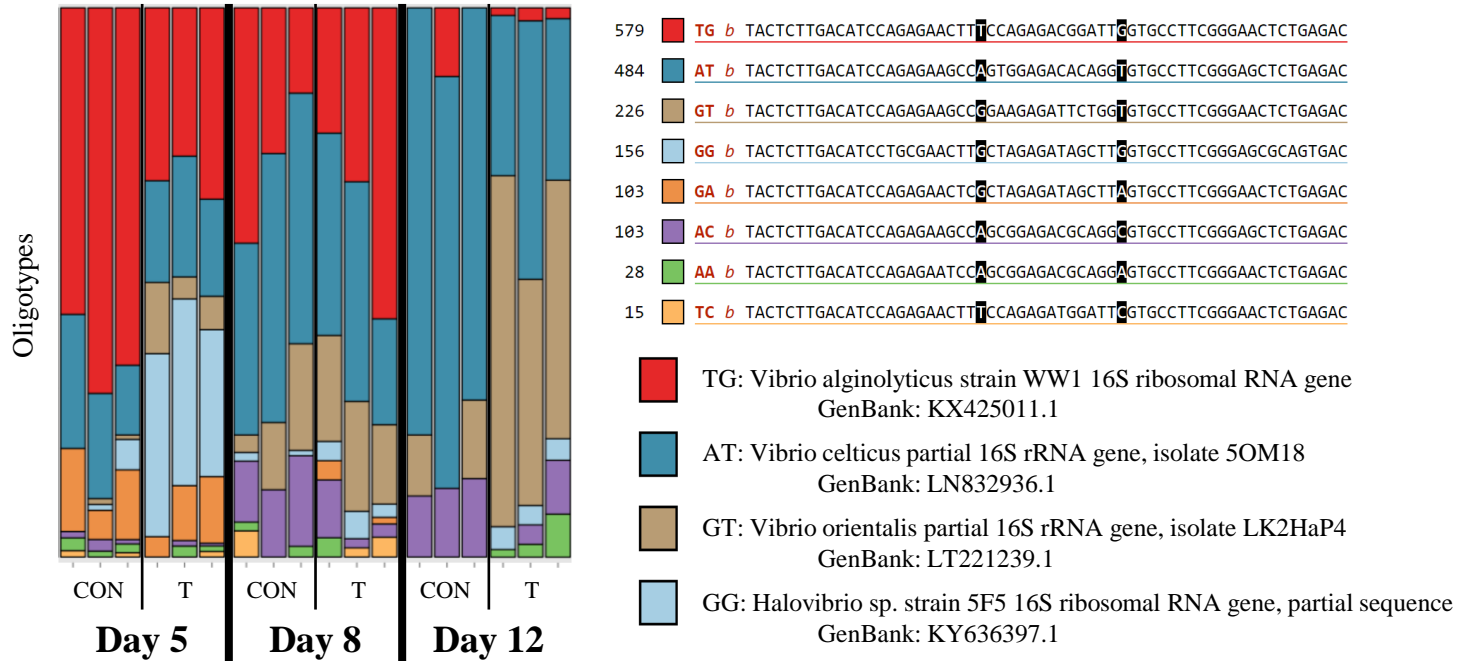
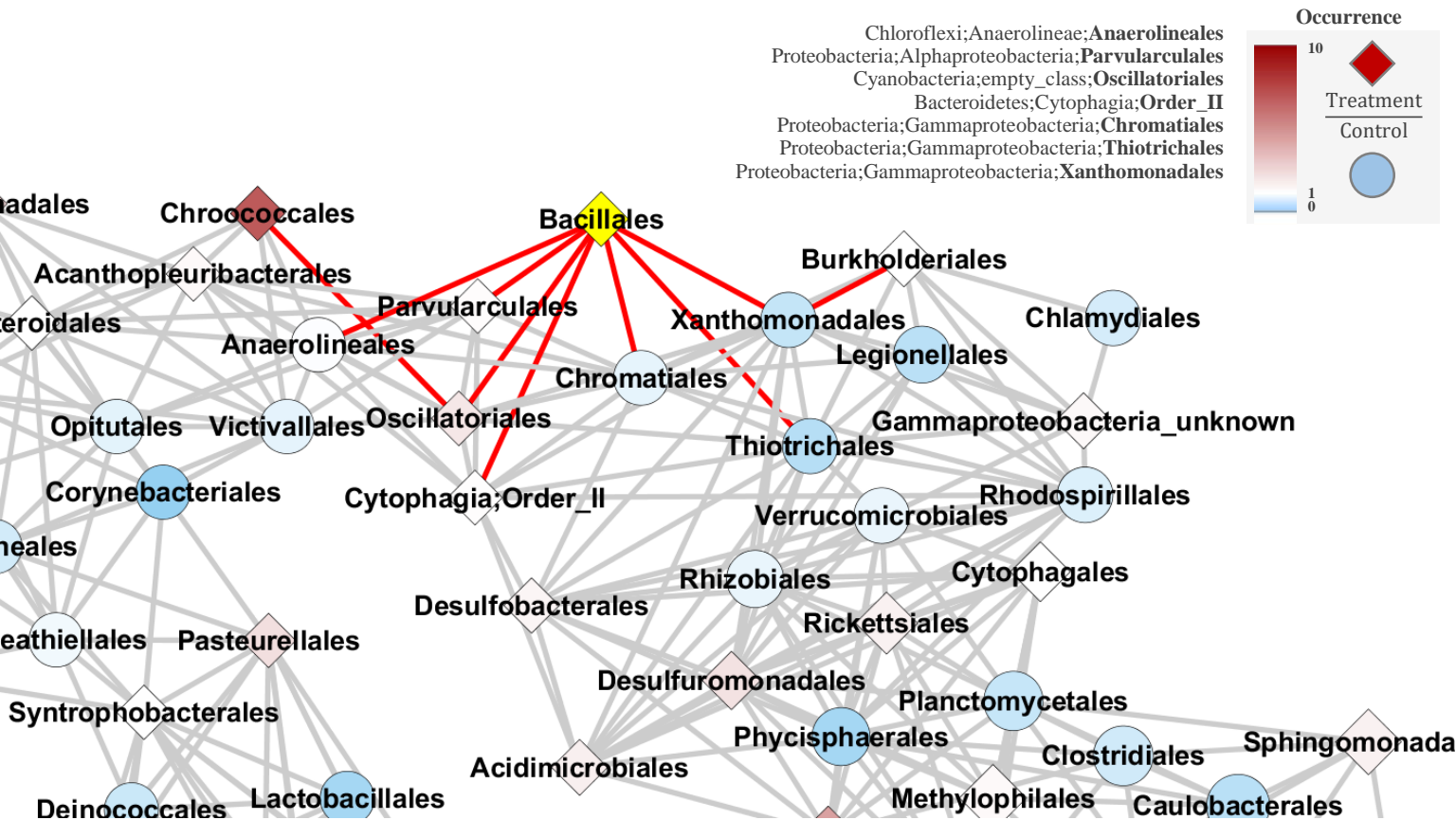


Figure 6. *Vibrio* spp. oligotypes in Control (CON) and Treatment (T) water samples on Days 5, 8, and 12 from Trial 3. These 8 oligotypes were generated from changes in positions 23 and 37 in a total of 1727 sequences. *Vibrio* oligotypes show differences in succession of species over time between control and treatment rearing water.



Supplementary Figures

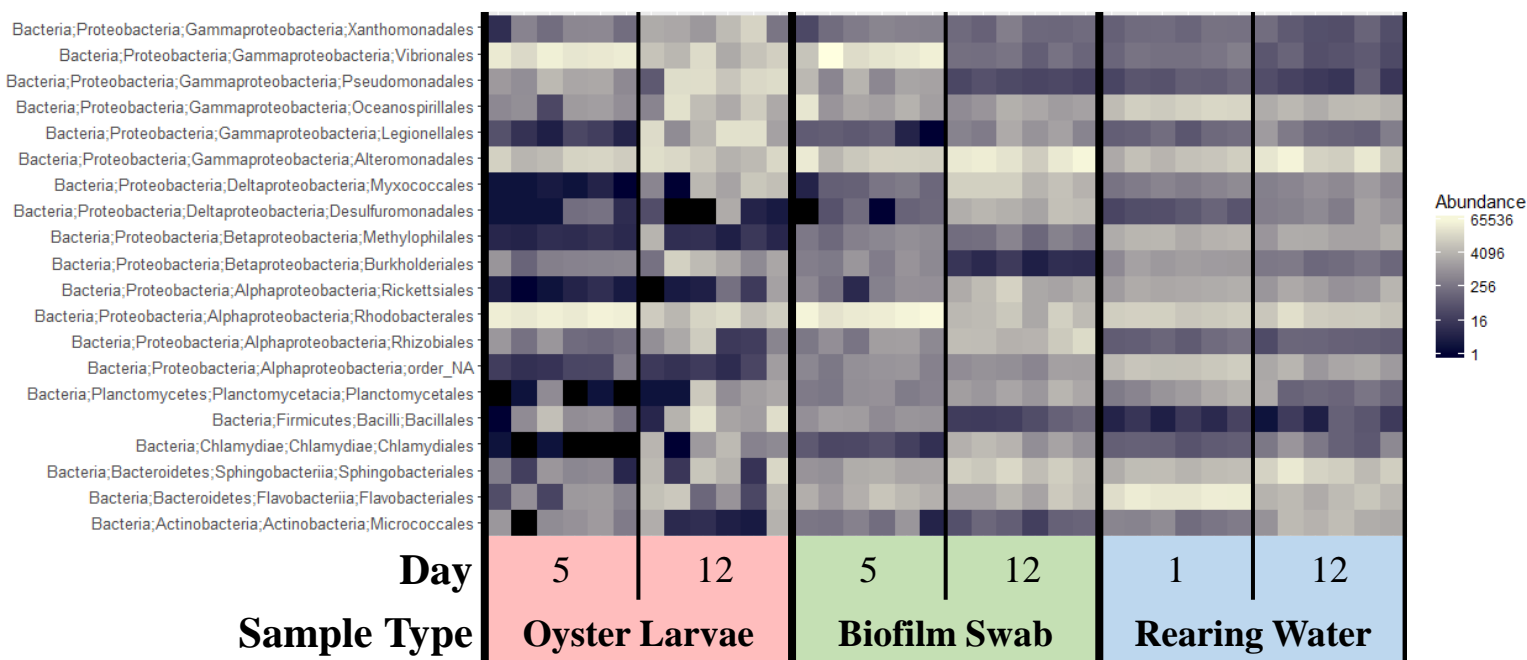


Figure S1. The relative abundances of the 20 most abundant orders in oyster, swab, and water samples from Trial 1.

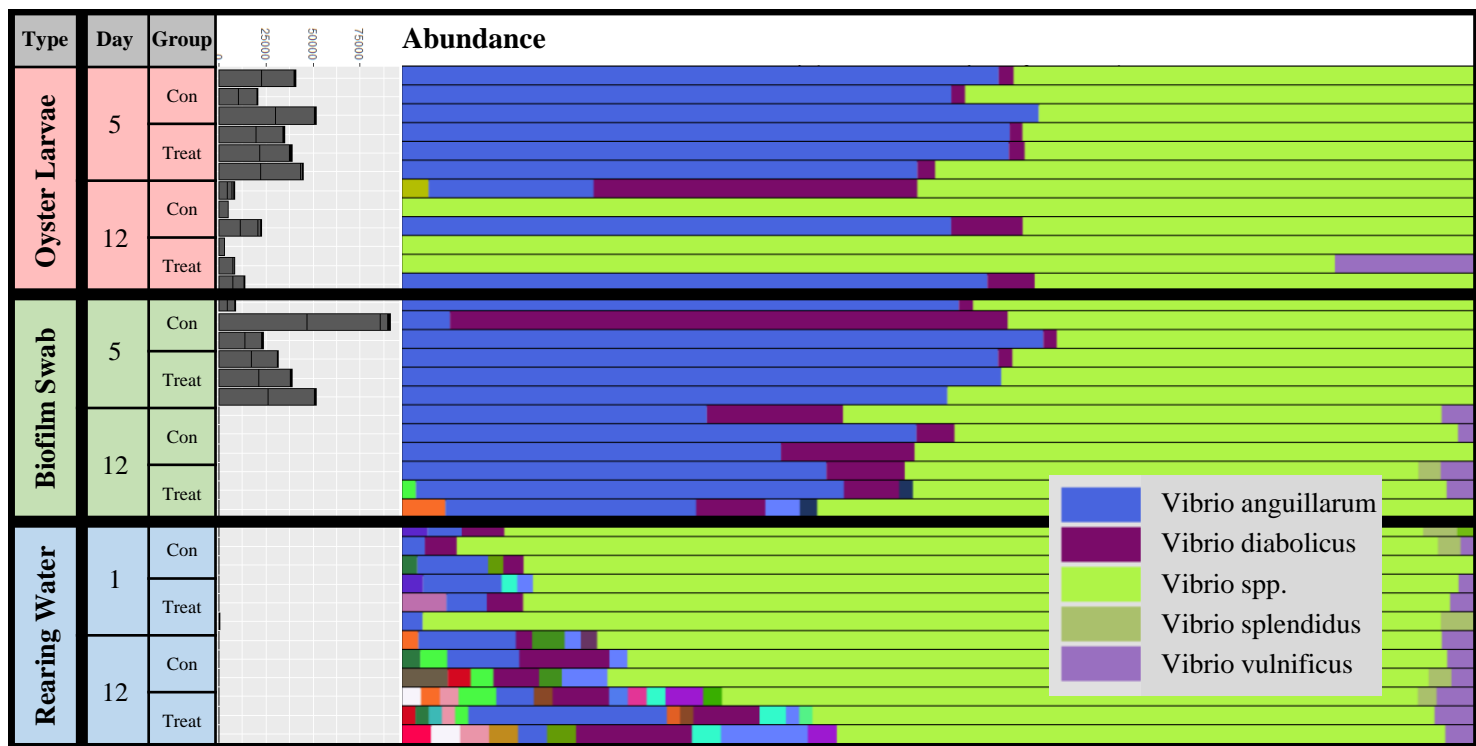


Figure S2. Percent abundances of *Vibrio* species in all sample types in Trial 1. The total abundance of sequencing reads is shown in the bar graph. The structure of total *Vibrios* is different based on the sample type and time point.

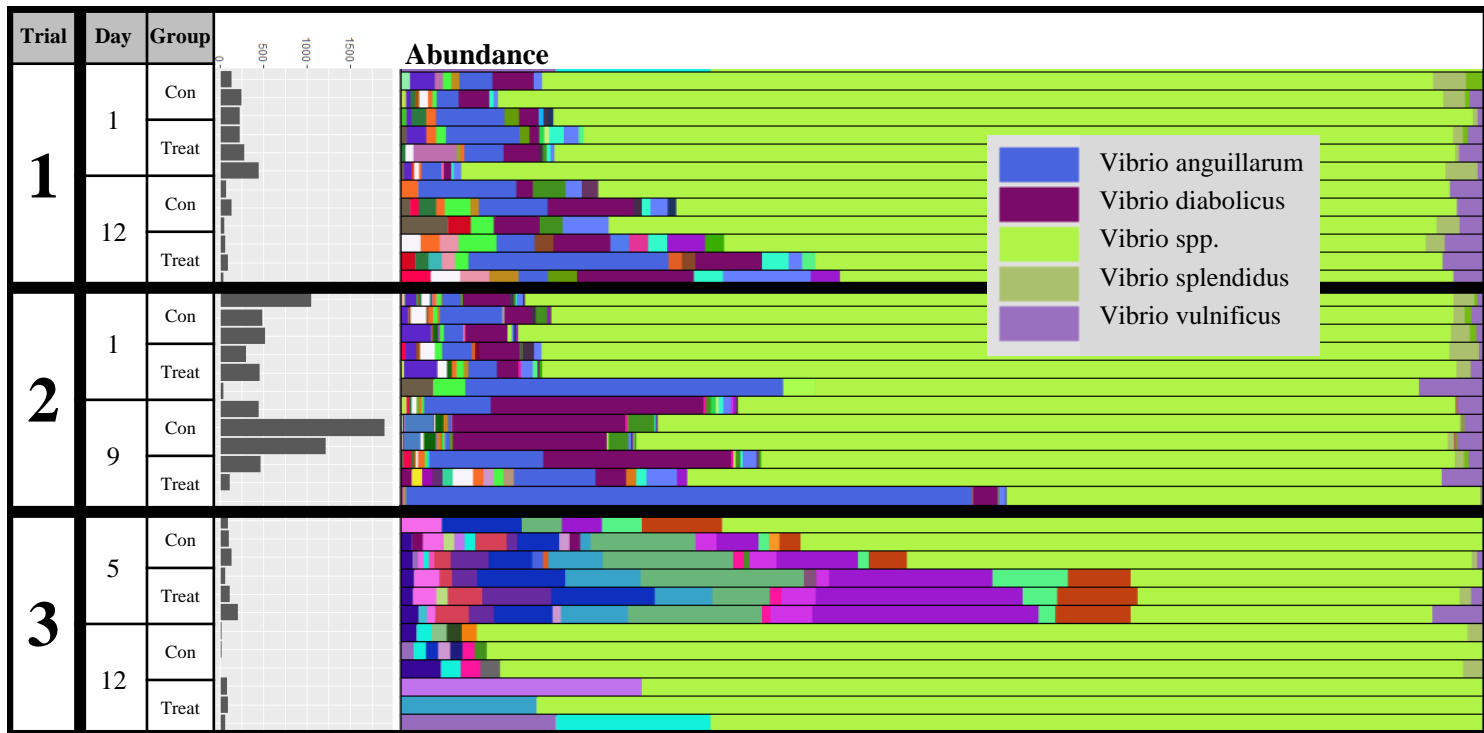


Figure S3. Percent abundances of *Vibrio* species in rearing water samples from all 3 Trials. The total abundance of sequencing reads is shown in the bar graph. The structure of total *Vibrio* counts in the rearing water is different between Trials and changes over time.