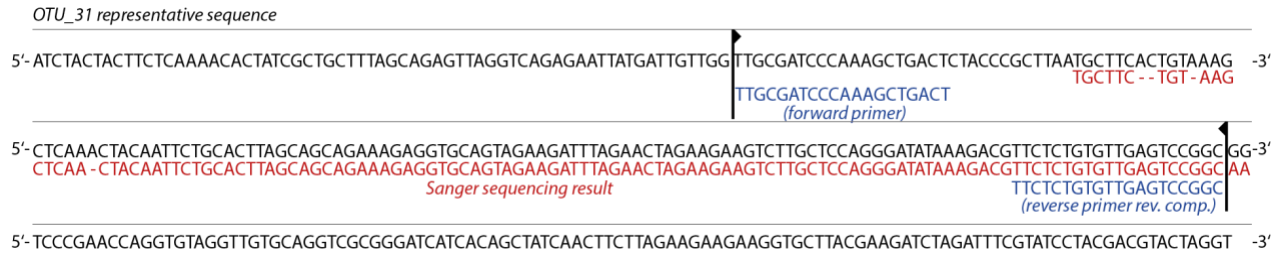
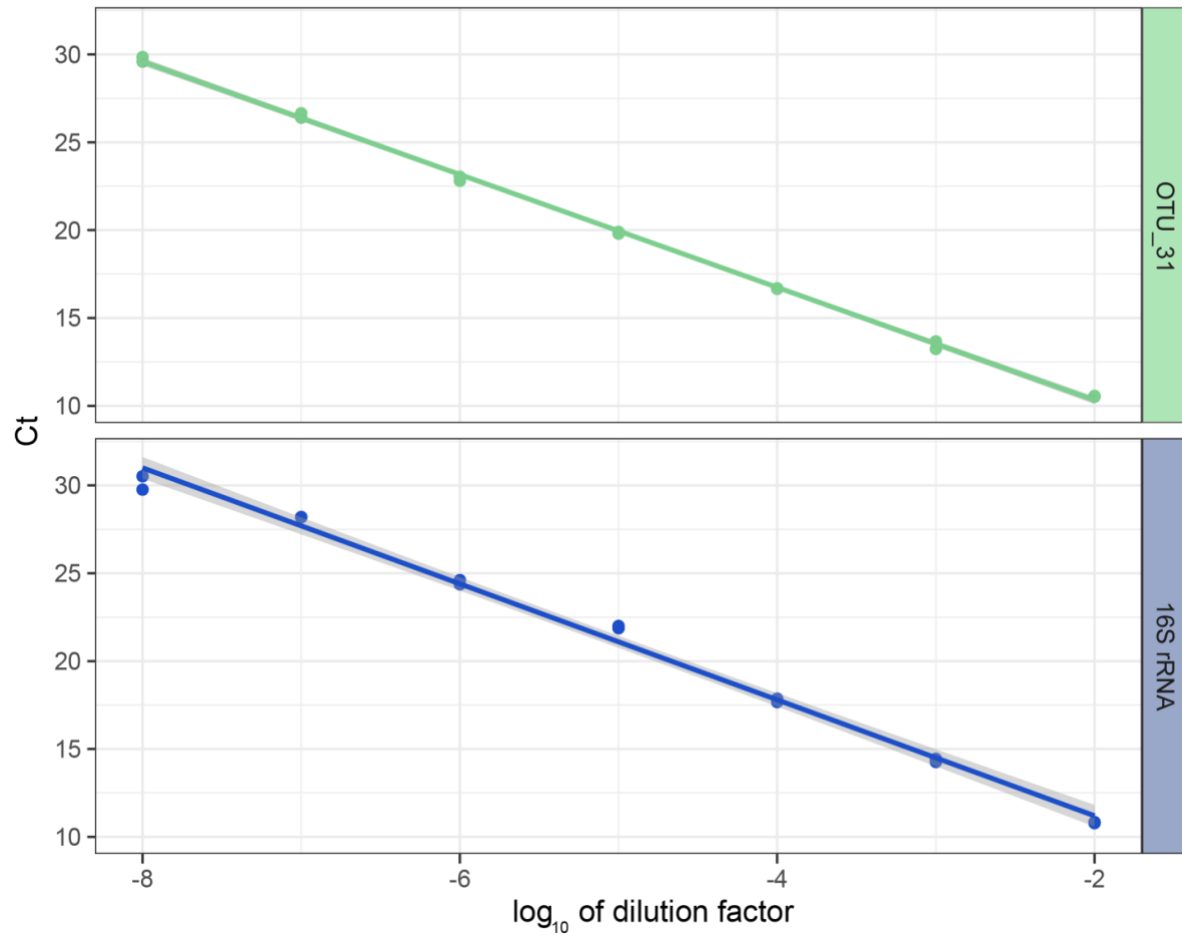


Supplementary Material

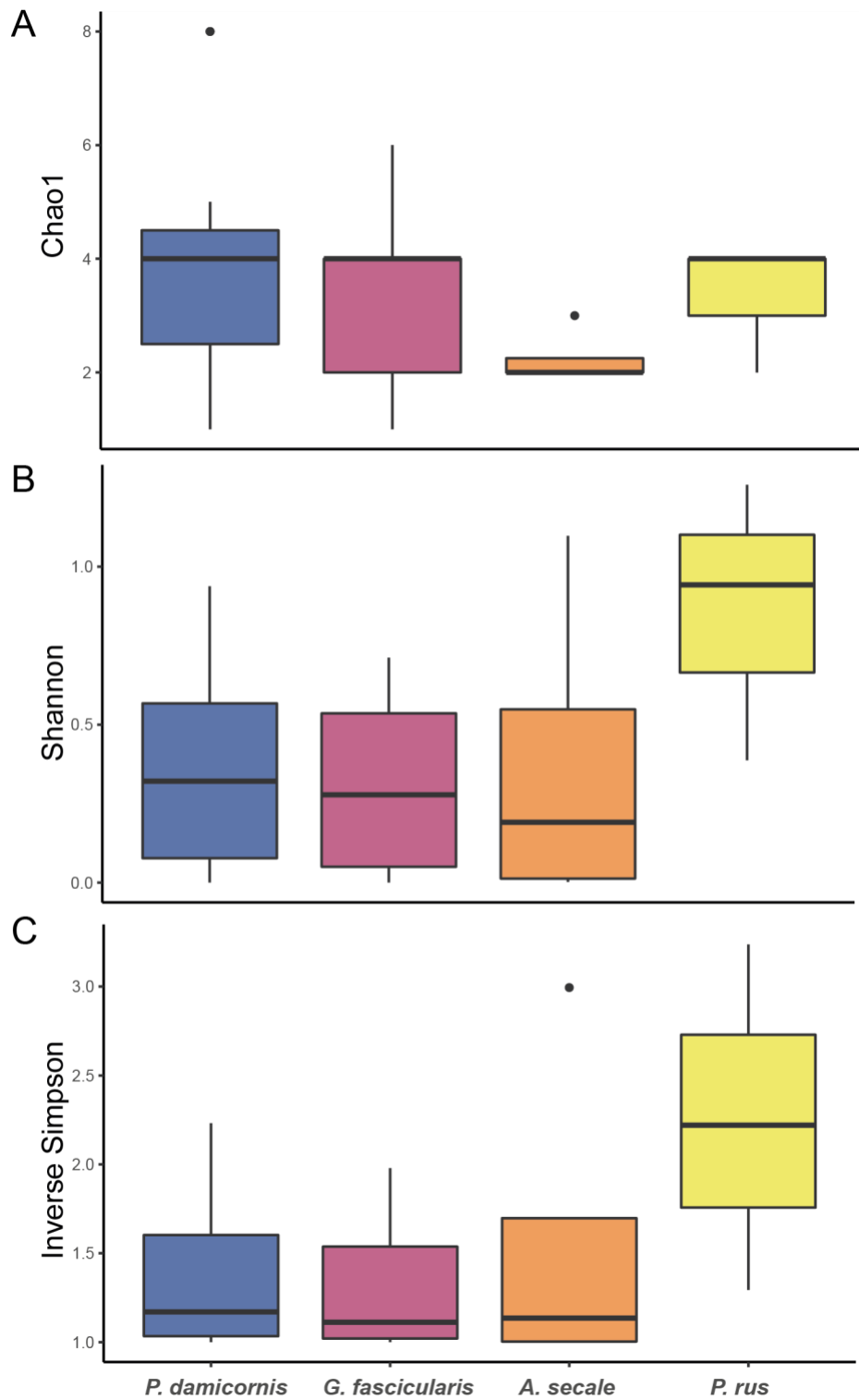
Supplementary Figures



Supplementary Figure 1. OTU_31 (Cyanobacteria) representative sequence (black) and specific primer pair (blue). Sanger sequencing result (red) shows accuracy of amplification within the target range of the *nifH* amplicon.



Supplementary Figure 2. qPCR standard curves for OTU_31 specific primer pair (top, green) and 16S rRNA gene primer pair (bottom, blue).



Supplementary Figure 3. Boxplot visualization of alpha diversity measures across all samples from each coral host species. A) Chao1 estimator of richness; B) Shannon diversity index; C) Inverse Simpson diversity index.

Supplementary Tables

Supplementary Table 1. Overview of minimum entropy decomposition (MED).

<i>nifH</i> Cluster	I	II	III	IV-V
Number of final nodes	36	1	1	159
Decomposition steps	1.67±0.098	2	1	2.24±0.081
Median Size	4773	3970	5121	6791
Mean Size	17453	3790	5121	24490.34

Supplementary Table 2. Host pairwise PERMANOVA results.

Host comparisons	Sums of Sqs	F Model	R2	P value	P adjusted
<i>G. fascicularis</i> vs. <i>P. rus</i>	0.724918344	1.739134614	0.178571781	0.076	0.0912
<i>G. fascicularis</i> vs. <i>P. damicornis</i>	1.132235971	2.841022018	0.150789167	0.005	0.03*
<i>G. fascicularis</i> vs. <i>A. secale</i>	0.941841821	2.383581436	0.209387656	0.01	0.03*
<i>P. rus</i> vs. <i>P. damicornis</i>	0.780117934	1.921331574	0.138013491	0.058	0.087
<i>P. rus</i> vs. <i>A. secale</i>	0.704068771	1.715488823	0.255452562	0.046	0.087
<i>P. damicornis</i> vs. <i>A. secale</i>	0.357628654	0.912680331	0.065600611	0.429	0.429

Supplementary Table 3. Wilcoxon test results on alpha diversity measures.

All coral samples

Diversity/Richness Index	Control mean	Seeps mean	Wilcoxon W	P value
Shannon	0.527	0.289	45.5	0.081
Inverse Simpson	1.660	1.329	44.5	0.073
Chao1	4.083	2.846	54.5	0.195

P. damicornis

Diversity/Richness Index	Control mean	Seeps mean	Wilcoxon W	P value
Shannon	0.423	0.289	9	0.329
Inverse Simpson	1.457	1.281	9	0.329
Chao1	5.200	3.000	8	0.229

G. fascicularis

Diversity/Richness Index	Control mean	Seeps mean	Wilcoxon W	P value
Shannon	0.406	0.180	4	0.629
Inverse Simpson	1.470	1.109	4	0.629
Chao1	3.250	3.333	6.5	1

Supplementary Data

Supplementary Data 1. Zehr database and BLAST nr annotation, reference sequences, and abundance counts of 88 OTUs, based on CD-HIT-EST clustering at a 91.9% sequence identity threshold of 197 determined MED nodes.