

Supplementary Material

Rethinking the Coral Microbiome. Simplicity exists within a diverse microbial biosphere

Alejandra Hernandez-Agreda^{a,b,#}, William Leggat^{a,b,c}, Pim Bongaerts^{d,e}, César Herrera^{f,g}, Tracy D. Ainsworth^{a,h}

^aAustralian Research Council Centre of Excellence for Coral Reef Studies, James Cook University, Townsville, Australia

^bThe College of Public Health, Medical and Veterinary Sciences, James Cook University, Townsville, Australia

^cSchool of Environmental and Life Sciences, University of Newcastle, Ourimbah, Australia

^dGlobal Change Institute, The University of Queensland, Brisbane, Australia

^eCalifornia Academy of Sciences, San Francisco, California, USA

^fTropWATER, Centre for Tropical Water & Aquatic Ecosystem Research, James Cook University, Townsville, Australia

^gCollege of Science and Engineering, James Cook University, Townsville, Australia

^hSchool of Biological, Earth and Environmental Sciences, University of New South Wales, Sydney, Australia

Running Head: Rethinking the coral microbiome

#Address correspondence: alejandra.hernandezagreda@my.jcu.edu.au

1.1 Supplementary Figures

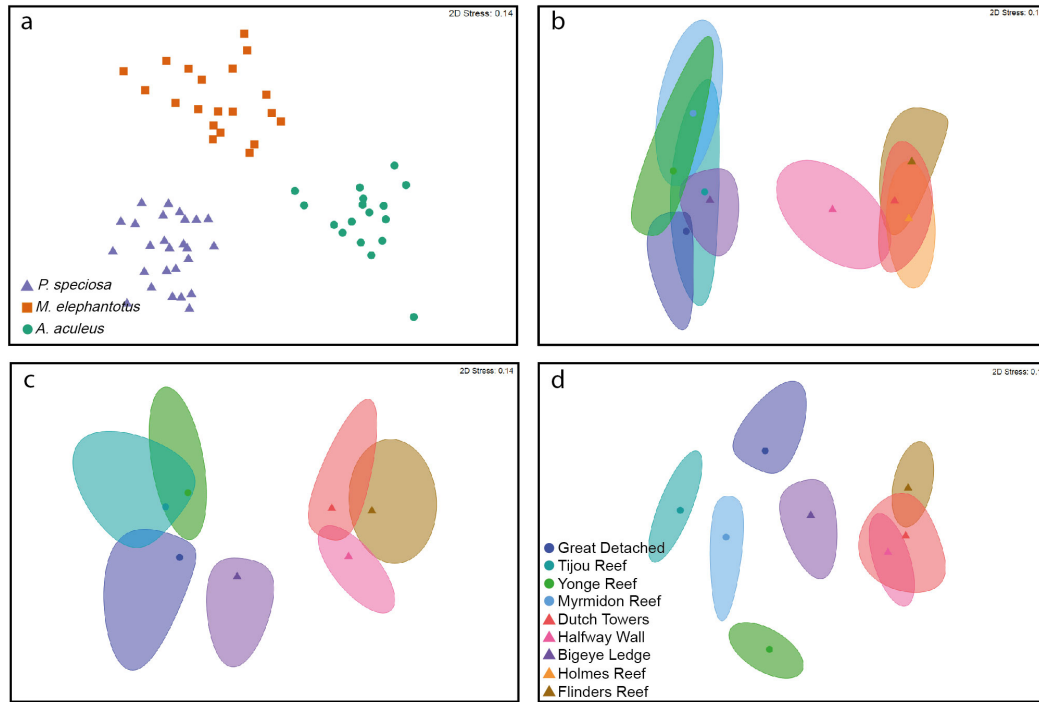


Fig. S1. Non-metric MDS based on composition data to illustrate differences between coral species (a; PERMANOVA, $p < 0.01$, Table S4) and between reefs for *P. speciosa* (b), *M. elephantotus* (c; excluding Myrmidon reef), and *A. aculeus* (d; excluding Holmes reef). NMDS based on Sorensen dissimilarity data. (a) Centroids, (b-d) bootstrap area and average for reefs. Circles denote GBR reefs, triangles CS reefs.

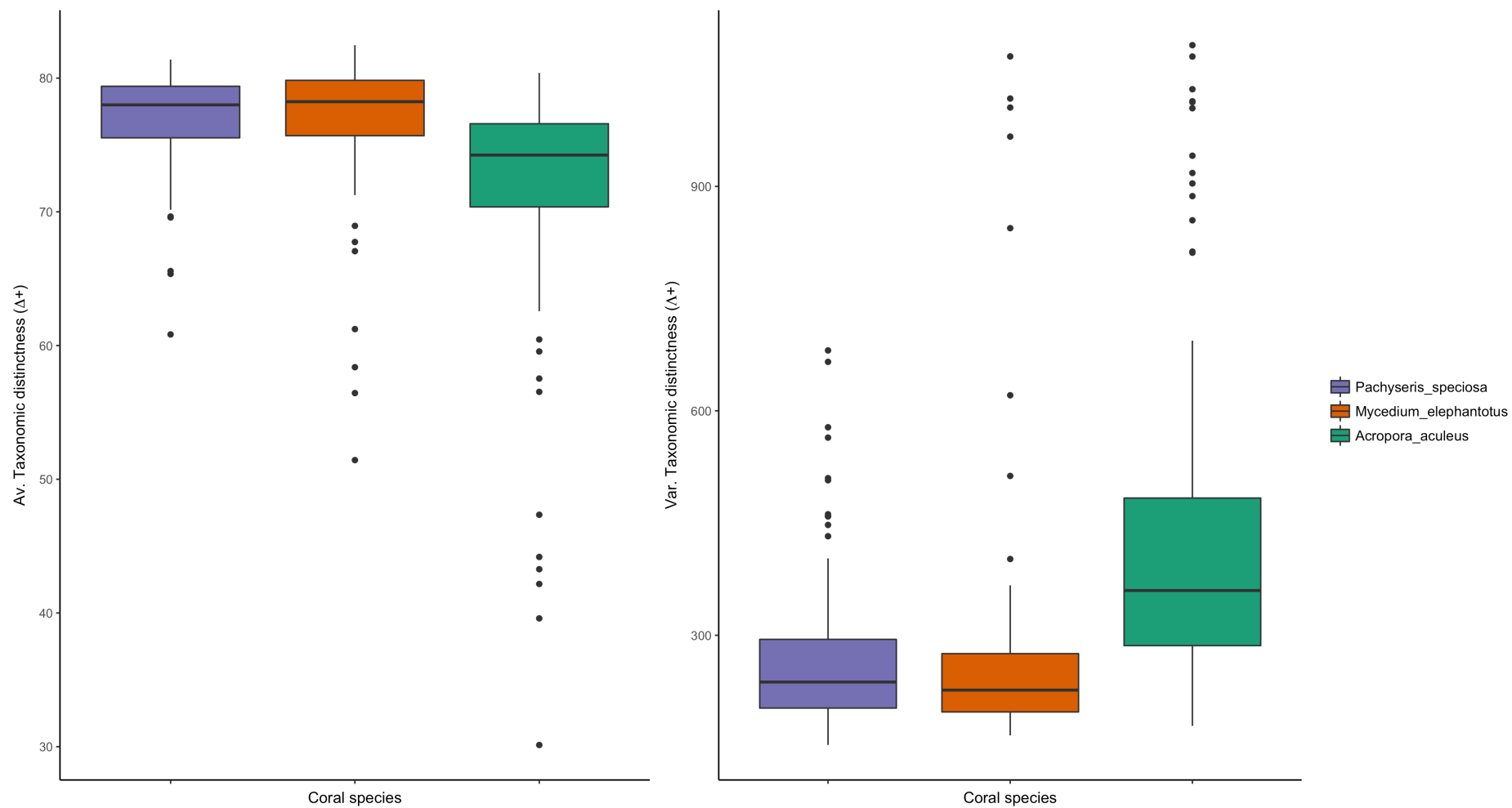


Fig. S2. Average and Variation of Taxonomic distinctness of bacterial assemblages in the three coral species. Indexes of distinctness are used as a metric of taxonomic breadth in bacterial assemblages. Note the similarity in the median between *P. speciosa* and *M. elephantotus* compared to *A. aculeus*.

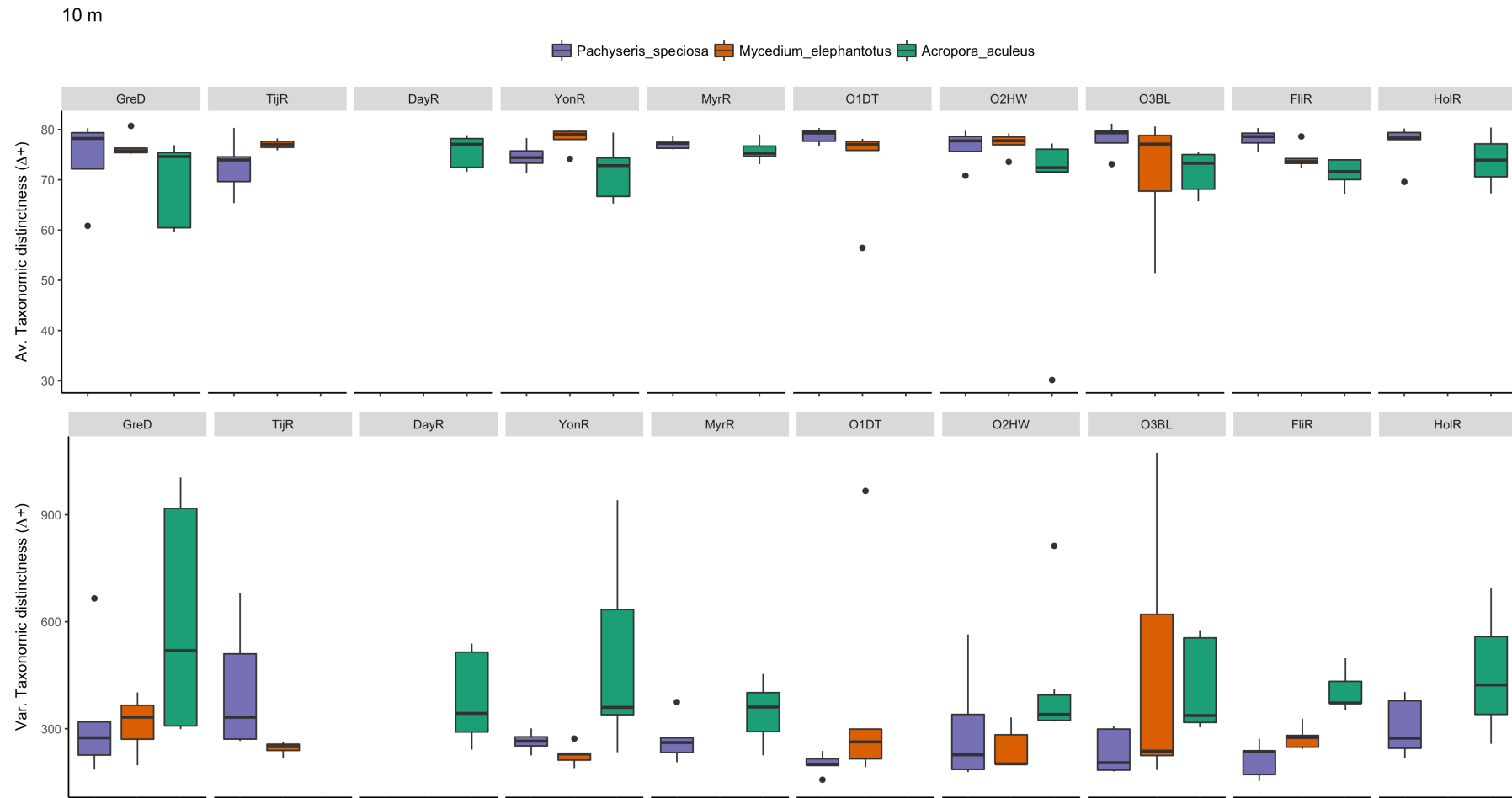


Fig. S3. Average and Variation of Taxonomic distinctness of bacterial assemblages per reef at 10 m depth. Index Average of Taxonomic distinctness is comparable between species and reefs at 10 m depth. Variation of Taxonomic distinctness (shape of the tree) shows a more broad distribution in the distinct bacterial assemblages across 10 m reefs. GreD: Great Detached, TijR: Tjouw Reef, DayR: Day Reef, YonR: Yonge Reef, MyrR: Myrmidon Reef, O1DT: Dutch Towers (Osprey), O2HW: Halfway Wall (Osprey), O3BL: Bigeye Ledge (Osprey), FliR: Flinders Reef, HolR: Holmes Reef.

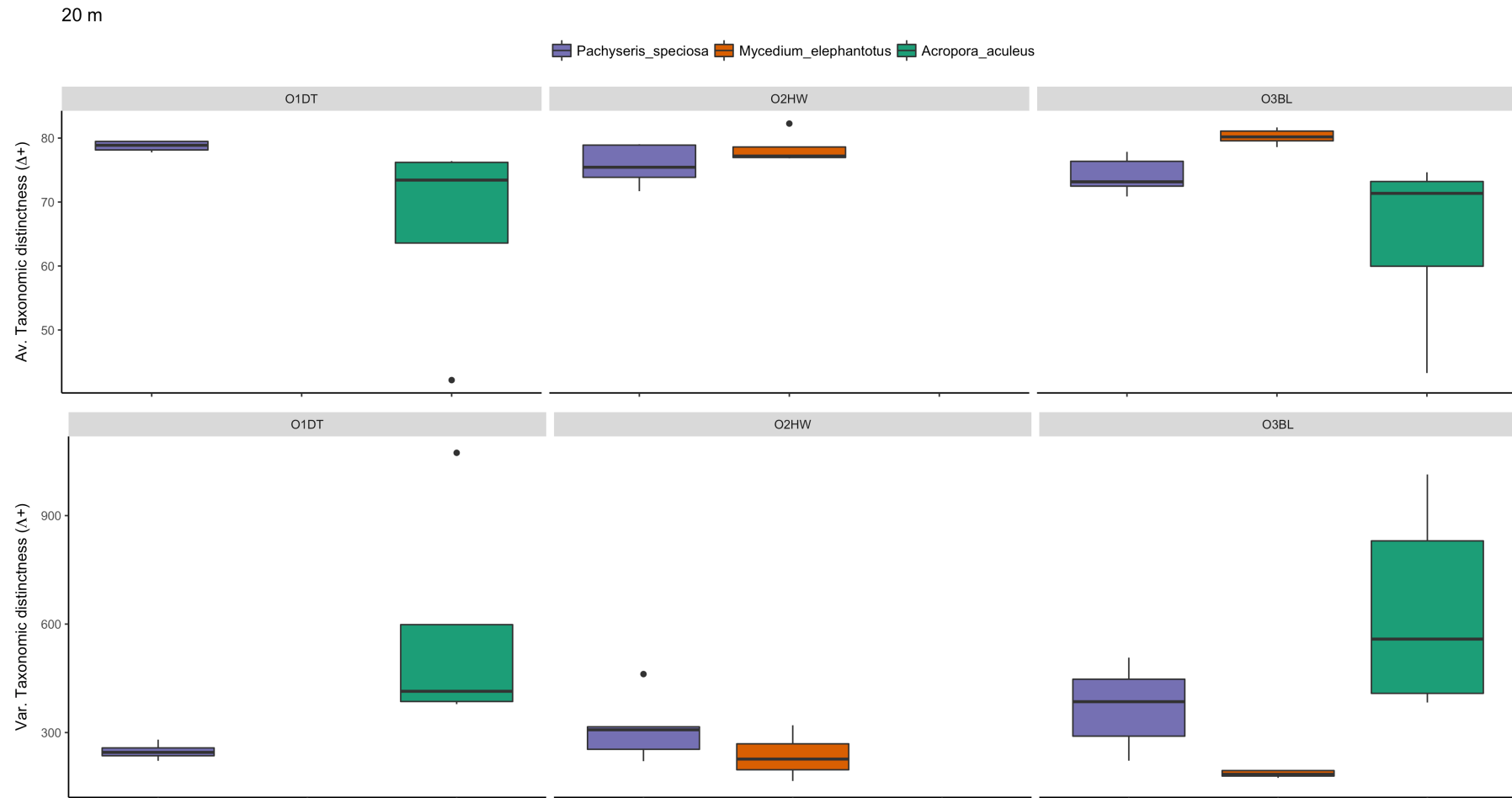


Fig. S4. Average and Variation of Taxonomic distinctness of bacterial assemblages per reef at 20 m depth. *P. speciosa* and *M. elephantotus* show similarity in the average and variation of Taxonomic distinctness of their bacterial assemblages across 20 m reefs. As observed at 10 m, in terms of taxonomy *A. aculeus* has a more variable bacterial assemblage. O1DT: Dutch Towers (Osprey), O2HW: Halfway Wall (Osprey), O3BL: Bigeye Ledge (Osprey).

40 m

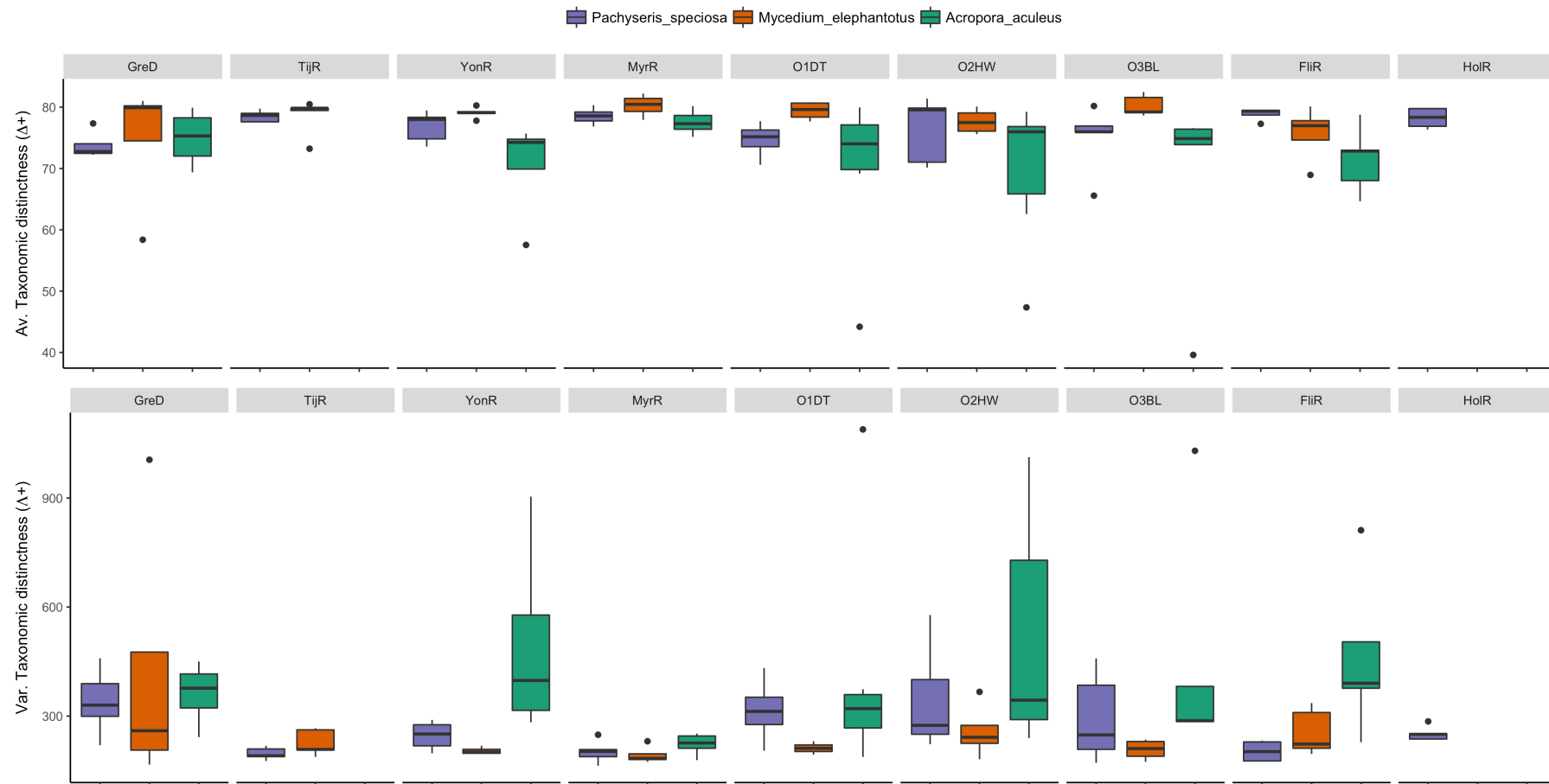


Fig. S5. Average and Variation of Taxonomic distinctness of bacterial assemblages per reef at 40 m depth. As observed in reefs at 10 m (Fig. S3), the average of Taxonomic distinctness shows bacterial assemblages with similar taxonomic breadth among coral species and between reefs. However, high variability in the shape of the taxonomic trees (bottom graph, the variation of Taxonomic distinctness) is observed. GreD: Great Detached, TijR: Tjou Reef, YonR: Yonge Reef, MyrR: Myrmidon Reef, O1DT: Dutch Towers (Osprey), O2HW: Halfway Wall (Osprey), O3BL: Bigeye Ledge (Osprey), FliR: Flinders Reef, HolR: Holmes Reef.

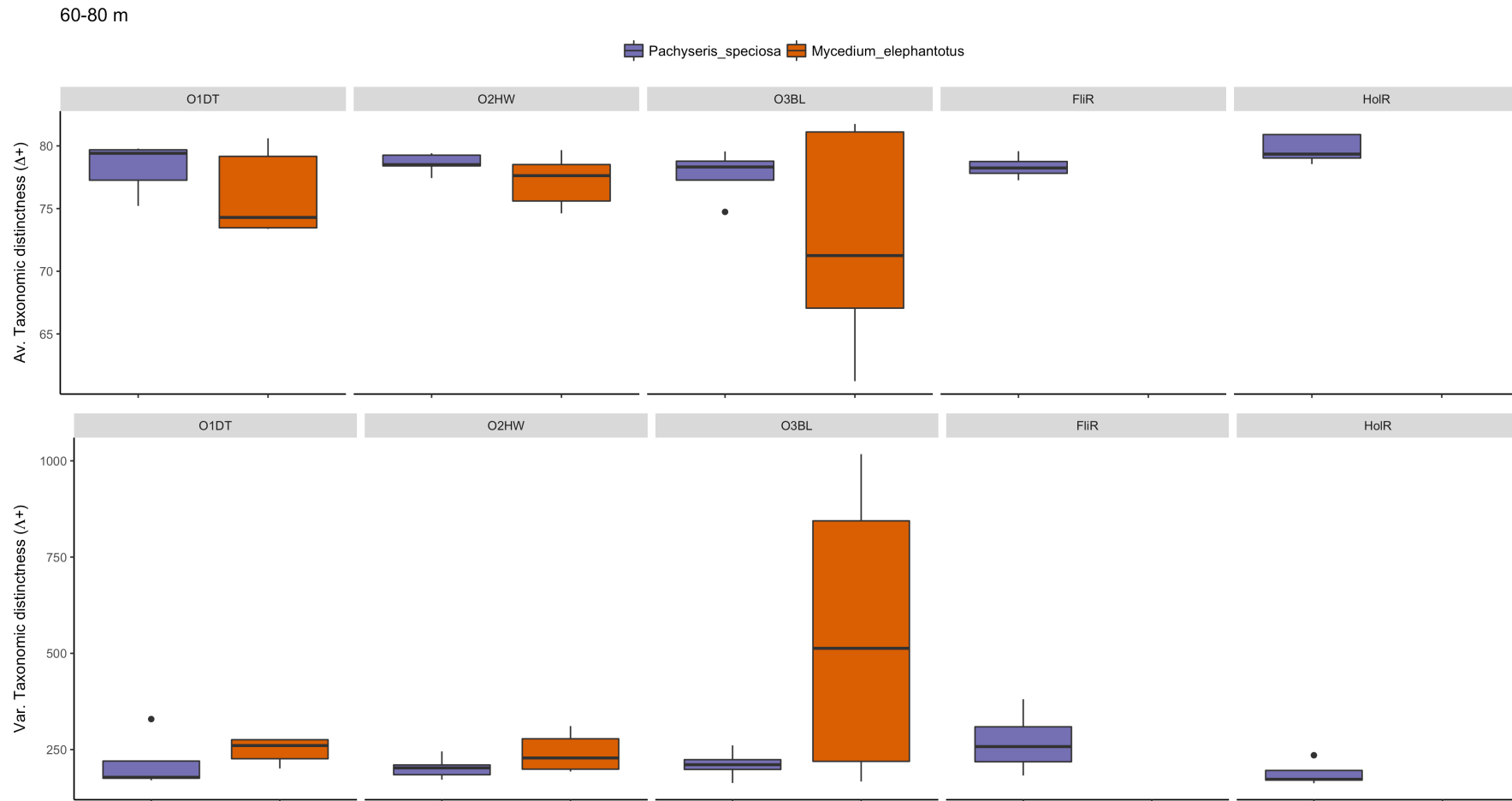


Fig. S6. Average and Variation of Taxonomic distinctness of bacterial assemblages per reef at 60-80 m depth. Across mesophotic reefs (60-80 m), as observed in other depths (previous figures), the average of Taxonomic distinctness indicates similarity in the taxonomic breadth of bacterial assemblages in *P. speciosa* and *M. elephantotus*. The exception to this observation occurs for *M. elephantotus* at Bigeye Ledge (O3BL, Osprey reef), where both the average and variation of Taxonomic distinctness describe a more variable assemblage. This variability is also observed in the microbial assemblages of *M. elephantotus* in the same reef at 10 m. GrED: Great Detached, TijR: Tijou Reef, DayR: Day Reef, YonR: Yonge Reef, MyrR: Myrmidon Reef, O1DT: Dutch Towers (Osprey), O2HW: Halfway Wall (Osprey), O3BL: Bigeye Ledge (Osprey), FliR: Flinders Reef, HolR: Holmes Reef.

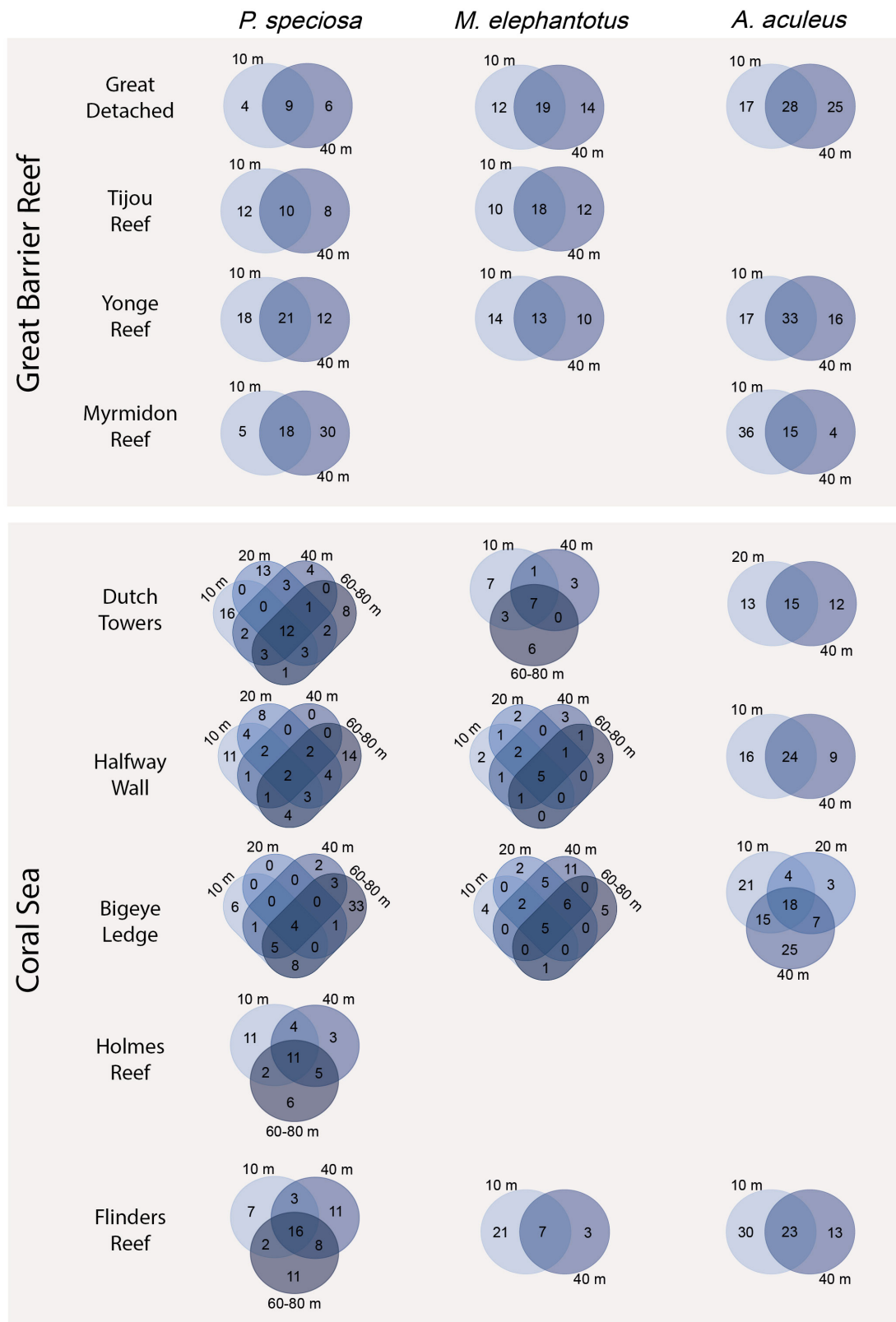


Fig. S7. Core microbiome of the lowest level of the design (reef x depth) showed bacteria phylotypes in common between the depths (intersection of the Venn diagrams).

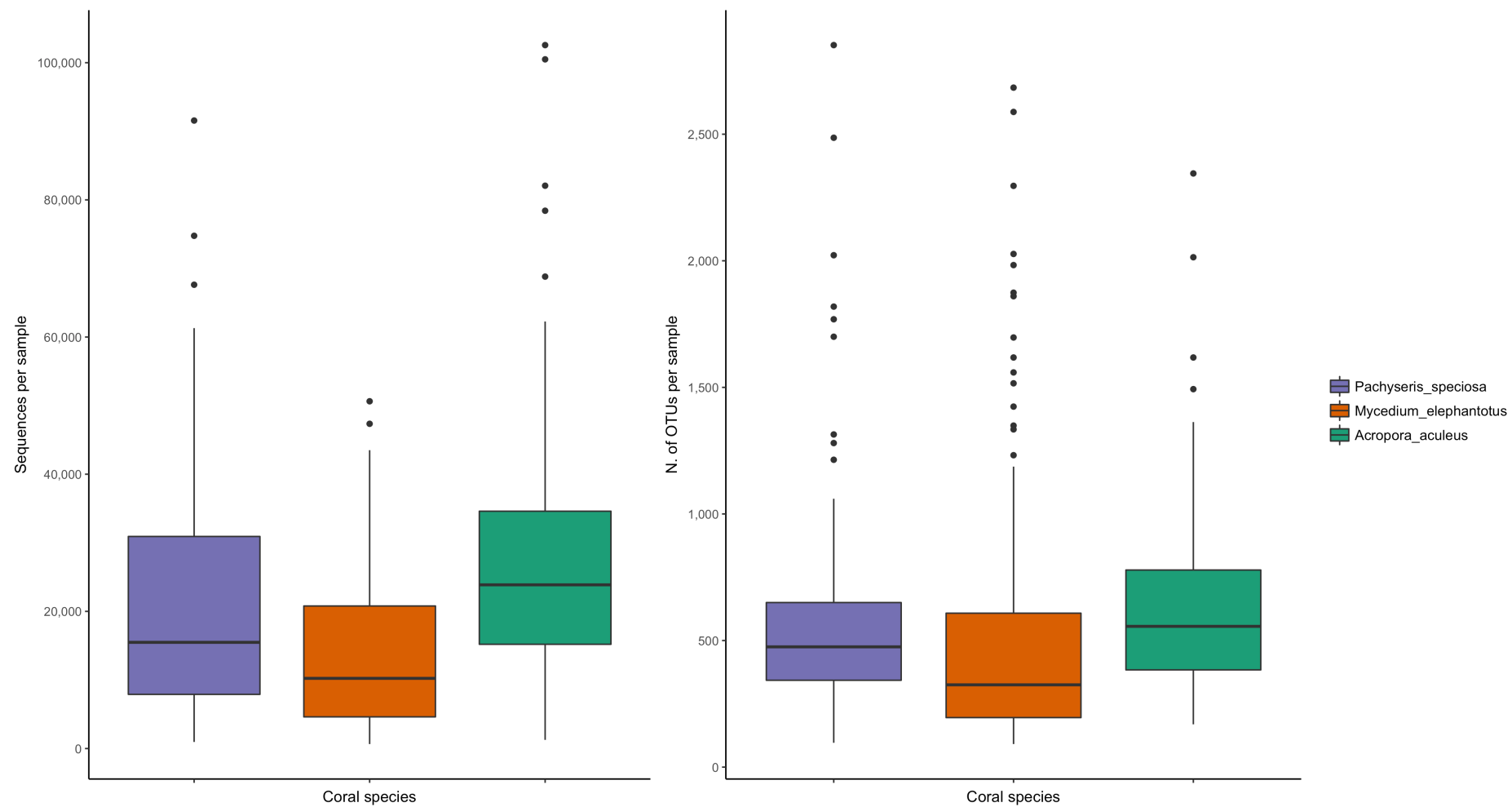


Fig. S8. Distribution of sequences and number of OTUs per sample per species. Boxplots are constructed with raw data after the elimination of chloroplast, non identified and unassigned sequences (6.4 millions of sequences, 49 thousands of OTUs, Table S1).

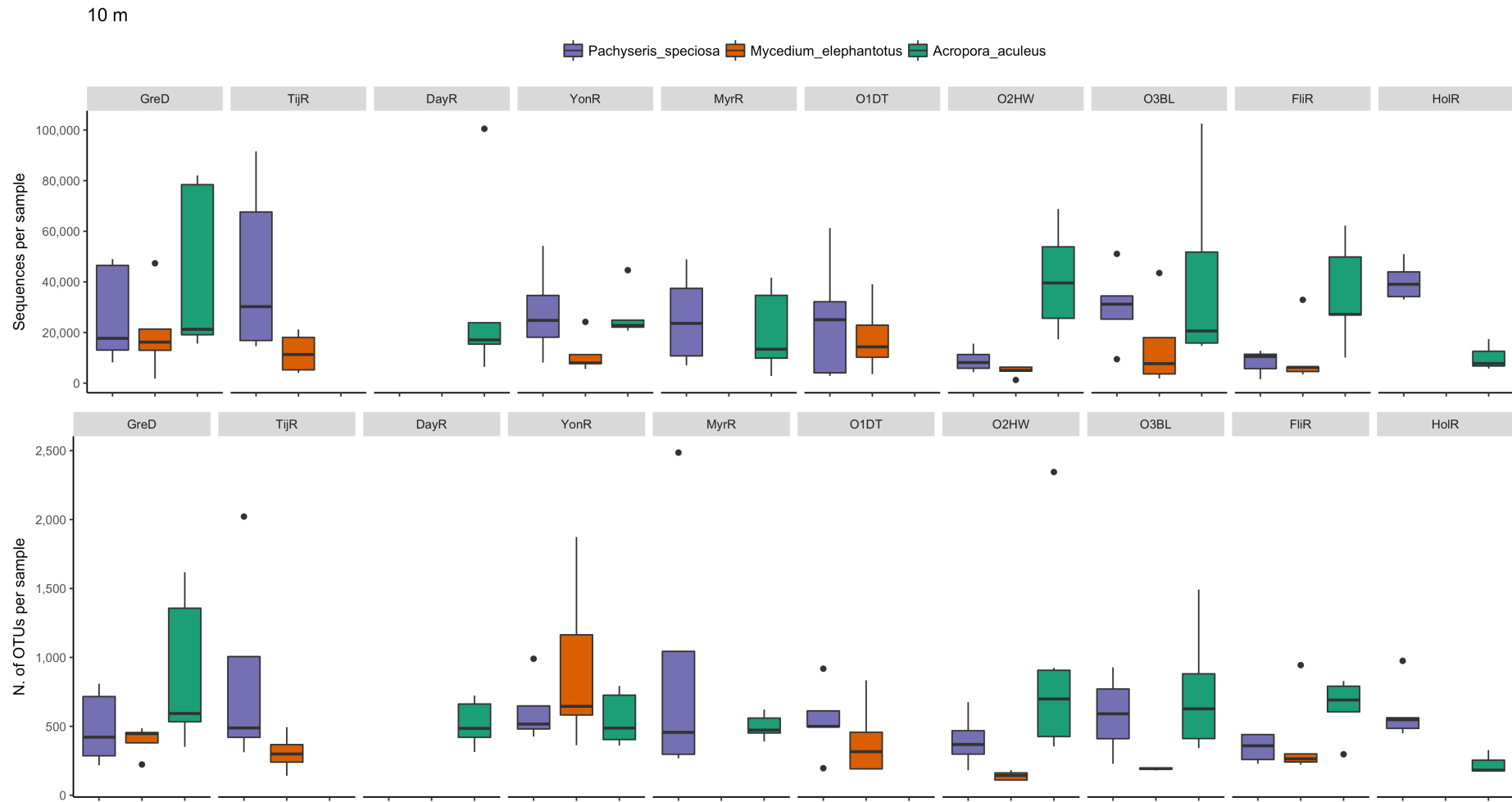


Fig. S9. Distribution of sequences and number of OTUs per sample per reef at 10 m. Patterns in the number of sequences and number of OTUs per sample are similar. Few exceptions are in *M. elephantotus* and *A. aculeus* at Yonge Reef, *A. aculeus* at Myrmidon Reef and *P. speciosa* at Dutch Towers. Note the difference in scale and median between this graph and the other depths. GreD: Great Detached, TijR: Tijou Reef, DayR: Day Reef, YonR: Yonge Reef, MyrR: Myrmidon Reef, O1DT: Dutch Towers (Osprey), O2HW: Halfway Wall (Osprey), O3BL: Bigeye Ledge (Osprey), FliR: Flinders Reef, HolR: Holmes Reef.

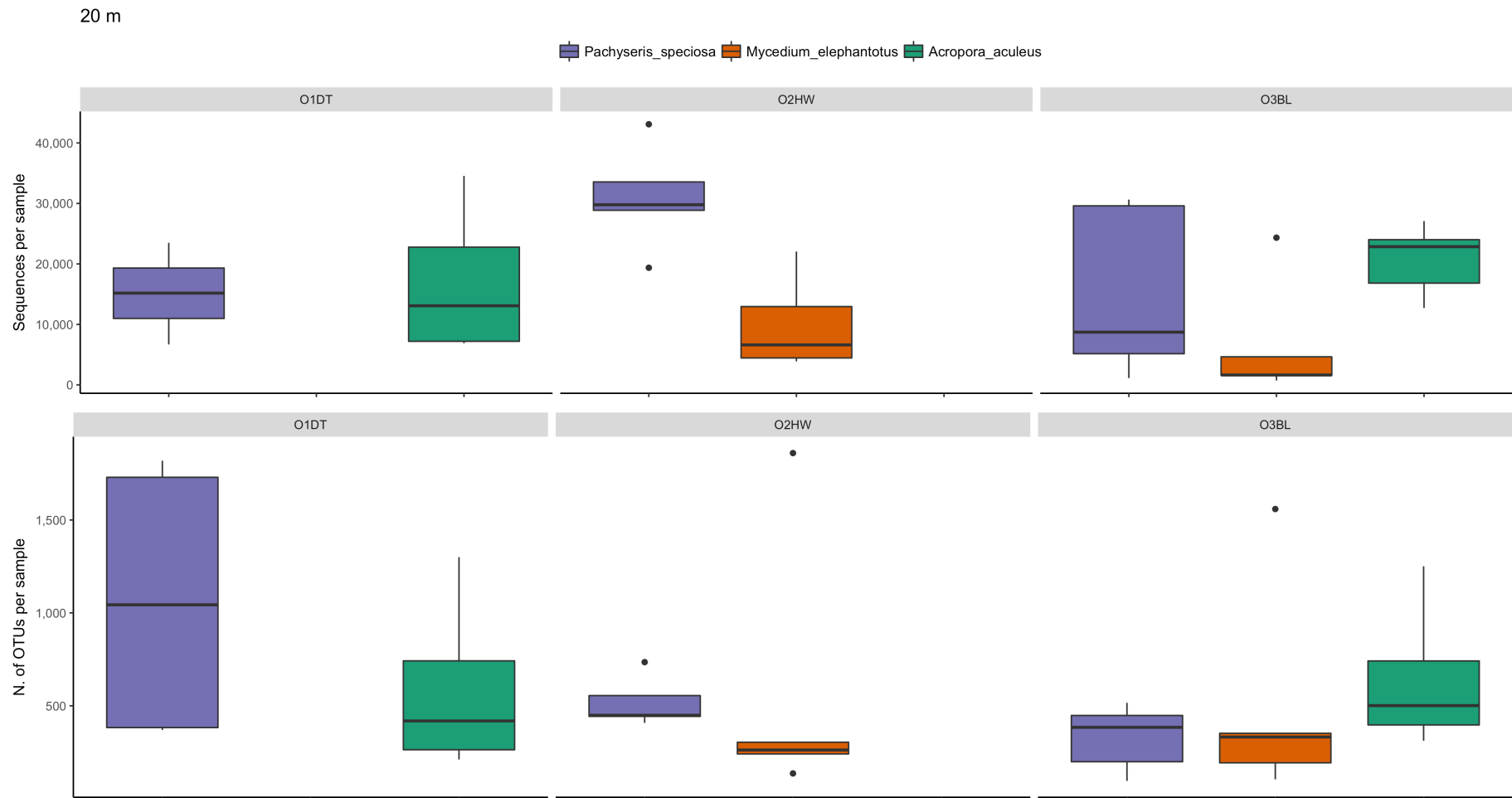


Fig. S10. Distribution of sequences and number of OTUs per sample per reef at 20 m. As seen in previous figures, patterns observed in sequences number are reflective of the trend in the number of OTUs. Exceptions are observed in the variability of *P. speciosa* Dutch Towers and Bigeye Ledge. Note the difference in scale in regards to other depths. O1DT: Dutch Towers (Osprey), O2HW: Halfway Wall (Osprey), O3BL: Bigeye Ledge (Osprey).

40 m

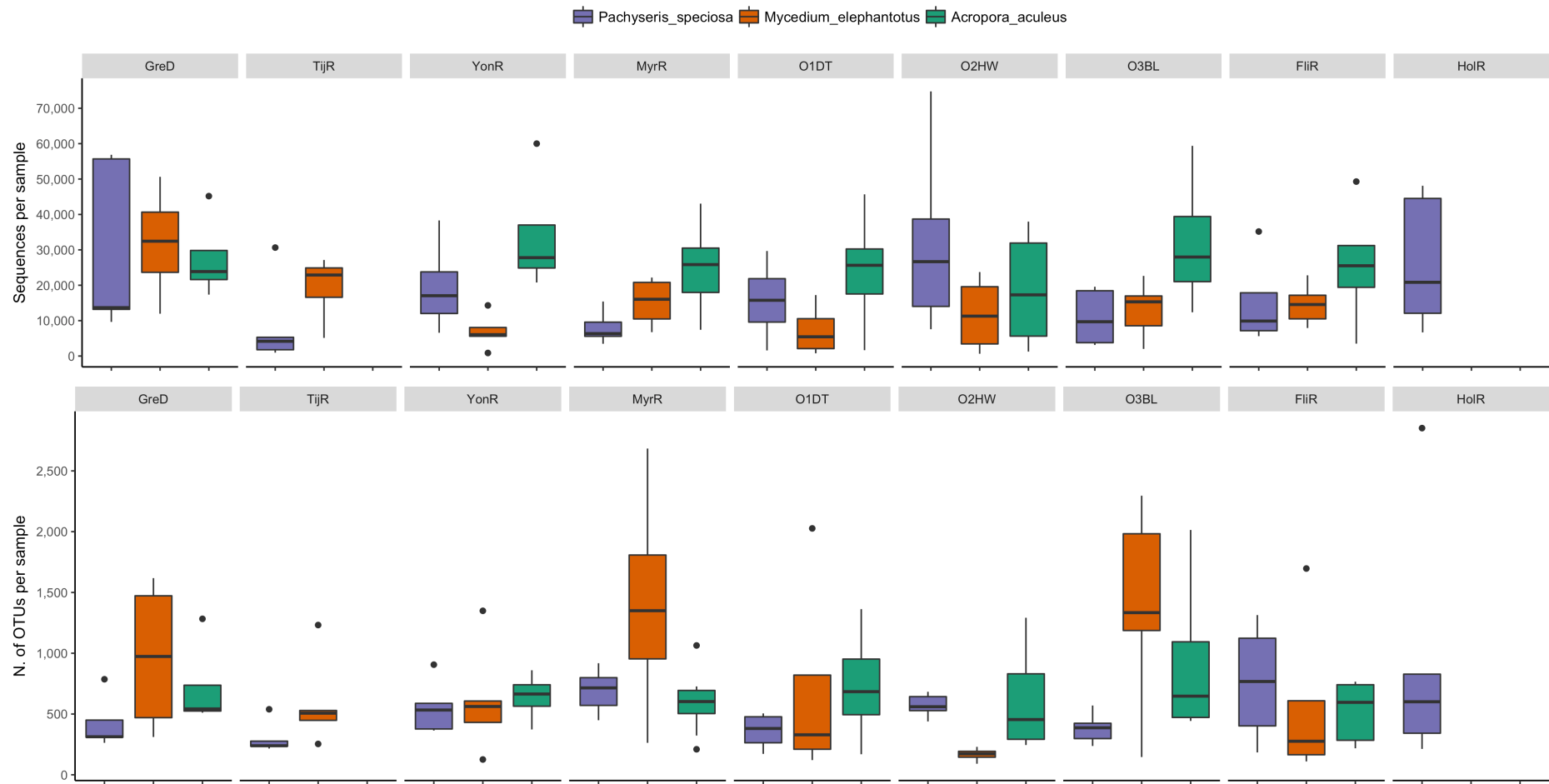


Fig. S11. Distribution of sequences and number of OTUs per sample per reef at 40 m. The pattern in the number of sequences per samples is also observed in the number of OTUs per sample. *M. elephantotus* at Myrmidon Reef and Bigeye Ledge and *P. speciosa* Halfway Wall are exceptions to this observation. Note the difference in the scales among depths. GreD: Great Detached, TijR: Tjijou Reef, YonR: Yonge Reef, MyrR: Myrmidon Reef, O1DT: Dutch Towers (Osprey), O2HW: Halfway Wall (Osprey), O3BL: Bigeye Ledge (Osprey), FliR: Flinders Reef, HolR: Holmes Reef.

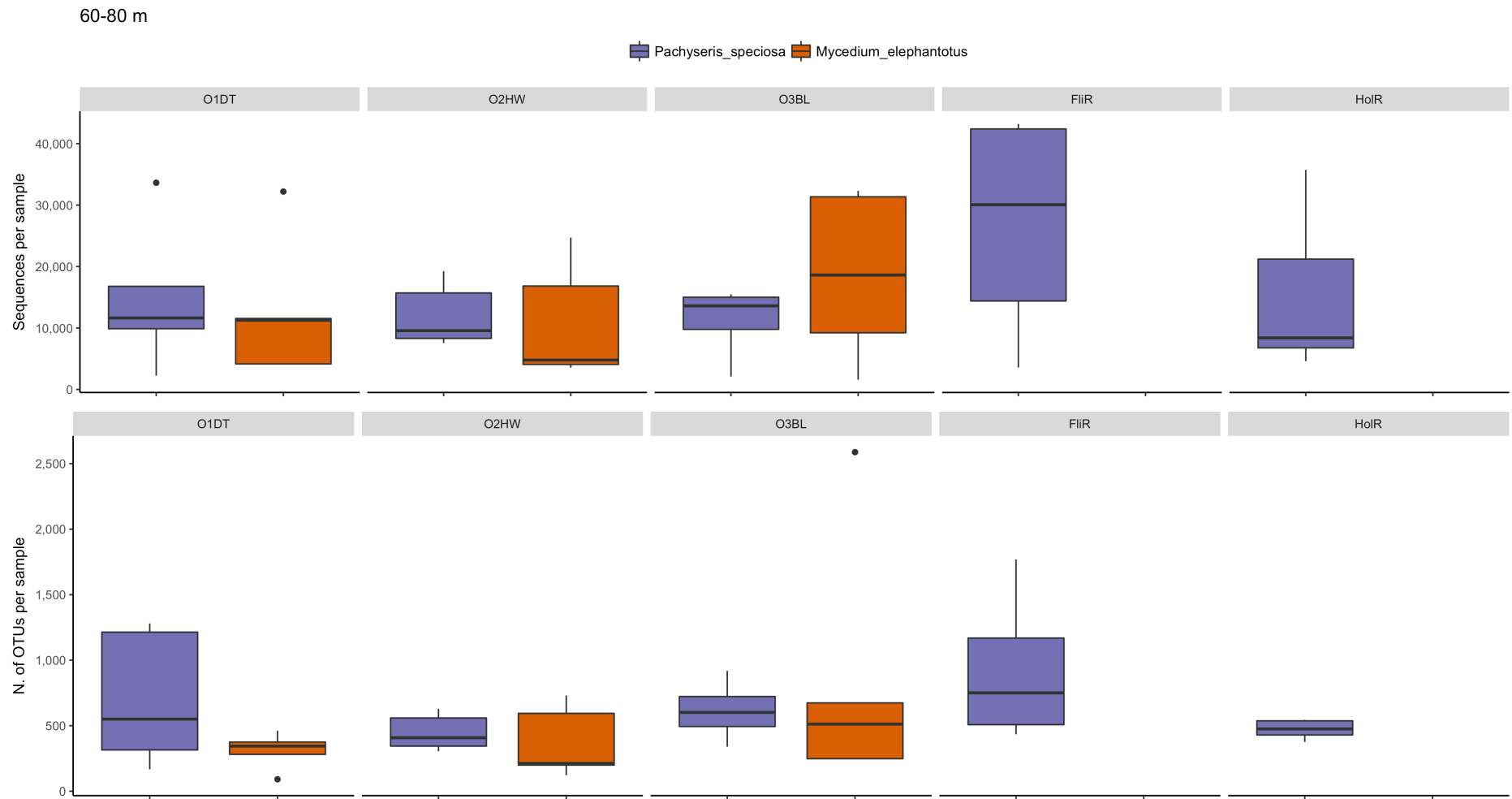


Fig. S12. Distribution of sequences and number of OTUs per sample per reef at 60-80 m. Relative differences observed in the number of sequences were also presented in the number of OTUs per sample. Note the difference in scale in regards to other depths (Fig. S9-11). O1DT: Dutch Towers (Osprey), O2HW: Halfway Wall (Osprey), O3BL: Bigeye Ledge (Osprey), FliR: Flinders Reef, HolR: Holmes Reef.

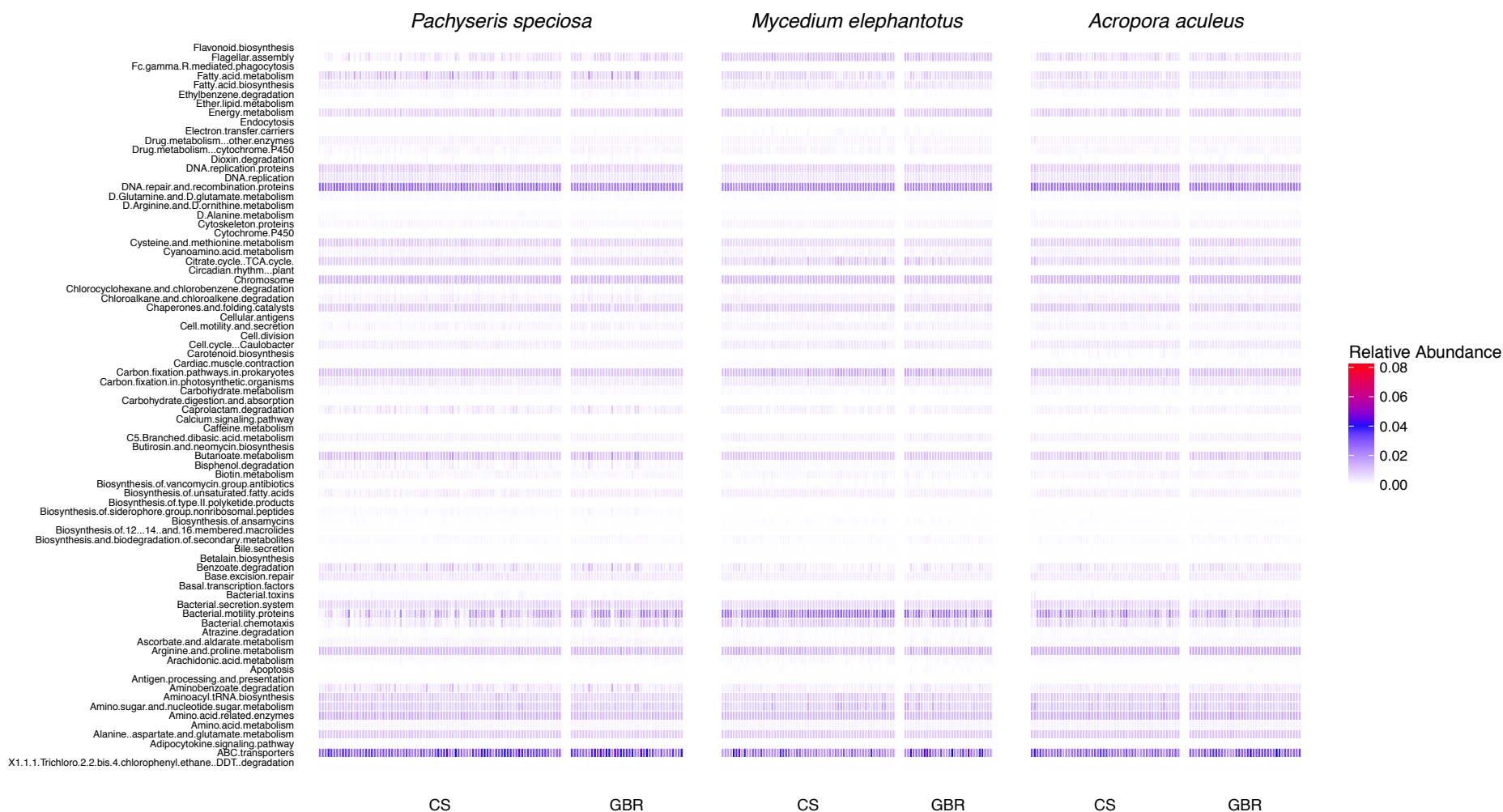


Fig. S13. Functional prediction for content for core microbiome per species – set 1. Functional prediction content generated from the relative abundance of KEGG KO genes, normalized and standardized by sample by total.

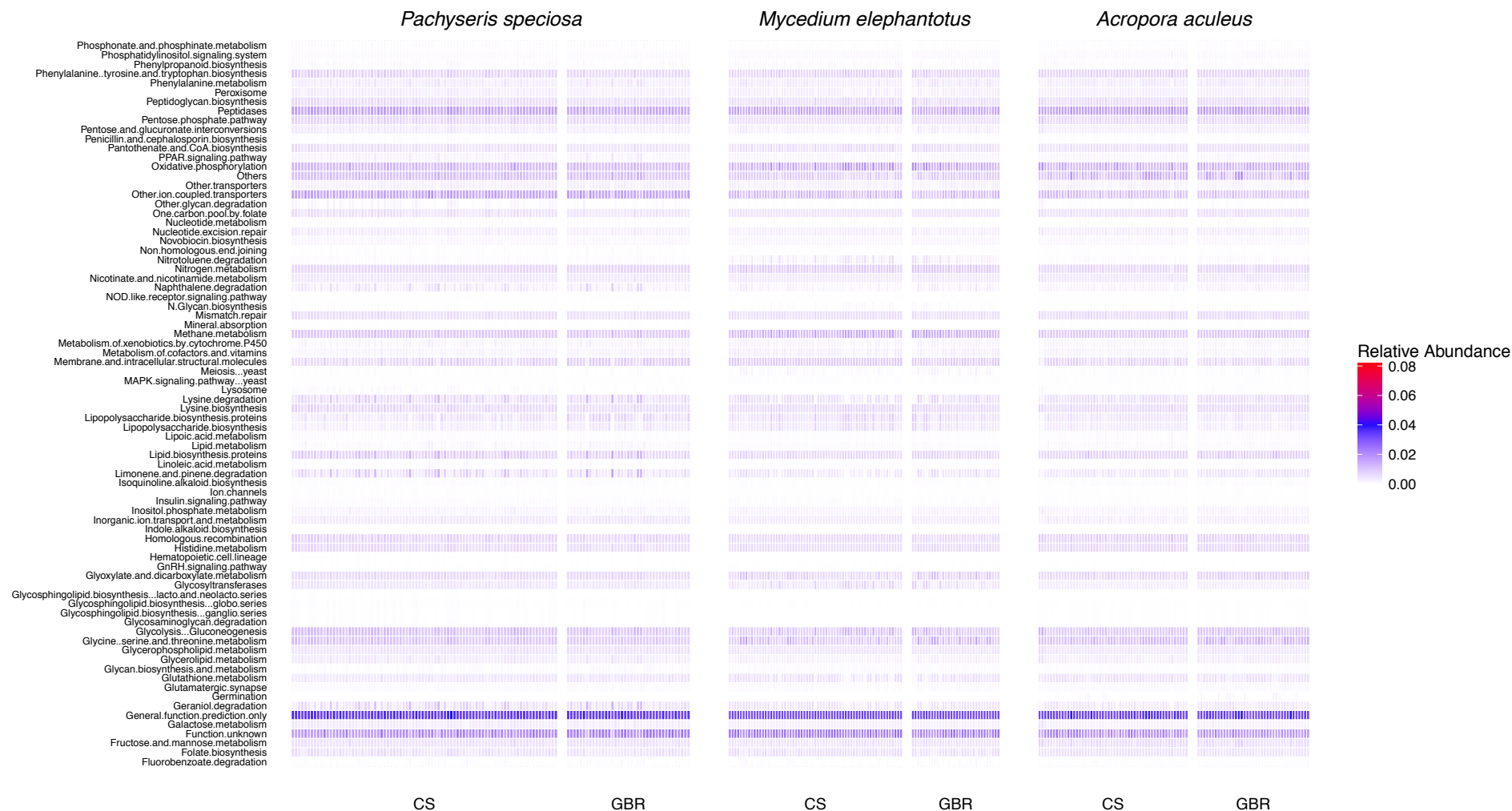


Fig. S14. Functional prediction for content for core microbiome per species – set 2. Functional prediction content generated from the relative abundance of KEGG KO genes, normalized and standardized by sample by total.

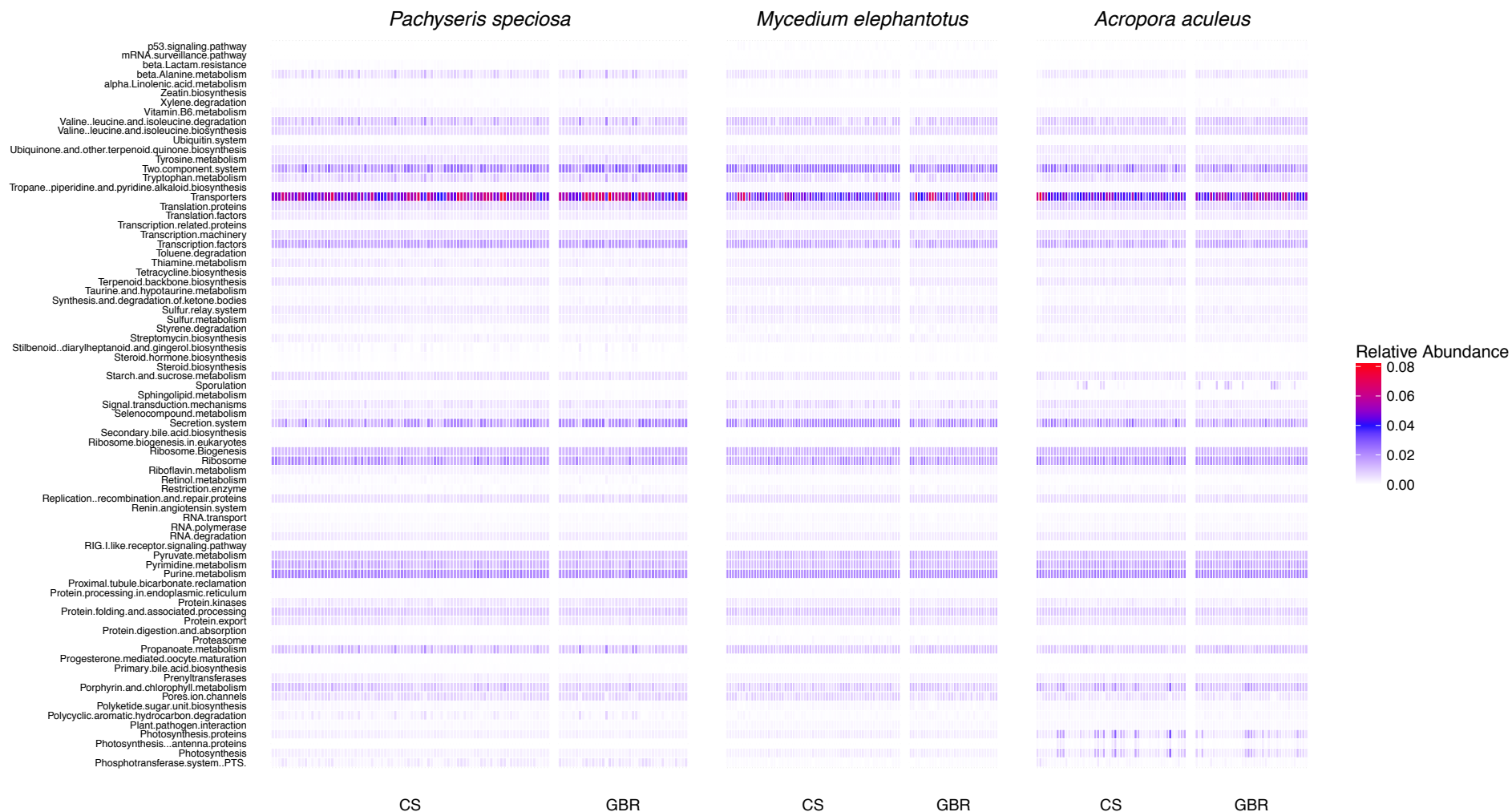


Fig. S15. Functional prediction for content for core microbiome per species – set 3. Functional prediction content generated from the relative abundance of KEGG KO genes, normalized and standardized by sample by total.

variable	028H05.PBN.P5	Brachyspirae	Gemm.1	OD1.class	SHA.26
	3BR.5F	Brevinematae	Gemm.2	ODP123	SHAB590
	4C0d.2	Brocadiae	Gemm.4	OM190	SJA.4
	A712011	BS119	Gemm.5	OP8_2	SM2F11
	AB16	C6	Gemmatimonadetes	OPB56	Soilbacteres
	ABY1	Chlamydia	Gitt.GS.136	Opitutae	Spartobacteria
	Acidimicrobiia	Chloracidobacteria	GKS2.174	Oscillatoriothricaceae	Sphingobacteriia
	Acidobacteria.class	Chlorobia	Gloeobacterophycideae	PAUC34f.class	Spirochaetes
	Acidobacteria.5	Chloroflexi	GN02.class	PAUC37f	Sva0725
	Acidobacteria.6	Clostridia	GN07	PBS.25	Synechococcophycideae
	Acidobacteriia	Coriobacteriia	GN10	Pedosphaerae	Synergistia
	Actinobacteria	Cyanobacteria.class	GN15	Phycisphaerae	TA18
	Alphaproteobacteria	Cytophagia	Holophagae	Pla3	Thermoleophilia
	Anaerolineae	Deferribacteres	Ignavibacteria	Pla4	Thermomicrobia
	AncK6.class	Deinococci	iii1.8	Planctomycetes.class	TK17
	AT.s2.57	Deltaproteobacteria	koll11	Planctomycetia	TM7.class
	AT.s54	EC1113	KSB1	Poribacteria.class	TM7.1
	Bacilli	EC214	KSB3.class	Proteobacteria.class	TM7.3
	Bacteria.class	Ellin6529	Ktedonobacteria	PRR.11	TSBW08
	Bacteroidetes.class	Elusimicrobia	Lentisphaeria	PRR.12	vadinHA49
	Bacteroidia	Epsilonproteobacteria	Leptospirae	RB25	Verruco.5
	BB34	Erysipelotrichi	MB.A2.108	Rhodothermi	Verrucomicrobiae
	BD1.5	FBP.class	Methylacidiphilae	Rubrobacteria	VHS.B5.50
	BD7.11	Fibrobacteria	ML635J.21	S085	wb1.A12
	Betaproteobacteria	Fimbrimonadia	Mollicutes	Saprospirae	WPS.2.class
	BHI80.139.class	Flavobacteriia	Nitrospira	SAR202	ZB2
	BME43	Fusobacteriia	NKB19.class	SBRH58	
	BPC102	Gammaproteobacteria	Nostocophycideae	SHA.109	

Fig. S16. Legend of all taxonomic classes considered in Figure 3 and 5.

1.2 Supplementary Tables

Table S1. Raw data depuration and division between the three coral species. *Excluding* column reflects groups eliminated in the data of the previous row. The first row represents raw data after the elimination of ambiguous base calls, homopolymer, barcodes, and primers. Unassigned: not assigned to Kingdom Bacteria.

Coral species	Excluding	N. samples	N. sequences (total)	N. sequences (av. by samples)	N. OTUs
3 coral species	-	311	17,210,426	55,338.99	79,724
	Chloroplast and None	311	10,449,737	33,600.441	70,932
	Low count samples	309	10,376,444	33,580.725	70,932
	Unassigned	309	6,425,024	20,792.958	49,044
<i>P. speciosa</i>	-	123	2,606,830	21,193.74	25,124
<i>M. elephantotus</i>	-	95	1,274,202	13,412.653	19,964
<i>A. aculeus</i>	-	91	2,543,992	27,955.956	19,875

Table S2. Bacterial phylotypes comprising the core microbiome. Rel. abundance: Relative abundance, Per. Occurrence: percentage of occurrence, Taxonomical ID: lower taxonomical level of identification. NROTU: New Reference OTU, NCROTU: New Clean up Reference OTU.

P. speciosa

OTU	Rel. Abundance	Per. Occurrence	Taxonomical ID.
580295	1.59	99.19	Genus <i>Gluconacetobacter</i>
439036	5.11	98.37	Genus <i>Corynebacterium</i>
806717	1.59	97.56	Family Alteromonadaceae
NROTU1421	2.01	96.75	Order Campylobacterales
NROTU839	1.97	96.75	Genus <i>Rhodobacter</i>
4331183	0.93	95.12	Genus <i>Gluconacetobacter</i>
NROTU2242	2.32	93.50	Family Hyphomicrobiaceae
555495	0.57	87.80	Genus <i>Mycobacterium</i>
396109	3.00	86.18	Genus <i>Cloacibacterium</i>
NROTU491	0.90	86.18	Family Rhodobacteraceae
613414	0.59	86.18	<i>Acinetobacter rhizosphaerae</i>
1088265	0.44	86.18	<i>Propionibacterium acnes</i>
NROTU352	2.49	84.55	Family Weeksellaceae
543864	0.71	84.55	Genus <i>Pseudomonas</i>
170405	0.44	84.55	Genus <i>Pseudomonas</i>
309489	0.72	83.74	Genus <i>Pseudoalteromonas</i>
NROTU1103	1.37	82.93	Order Campylobacterales

M. elephantotus

OTU	Rel. Abundance	Per. Occurrence	Taxonomical ID.
NROTU1987	16.85	100.00	Order EC94
NROTU377	11.83	98.95	Order Kiloniellales
NROTU681	9.03	98.95	Family Ellin6075
251481	1.02	97.89	Family Rhodobacteraceae
806717	0.78	97.89	Family Alteromonadaceae
NROTU839	3.44	95.79	Genus <i>Rhodobacter</i>
NROTU1950	2.26	95.79	Order Kiloniellales
NROTU703	1.16	95.79	Class Alphaproteobacteria
549595	1.22	86.32	Family Nitrospiraceae
NROTU1261	3.19	83.16	Order EC94
NROTU2624	1.47	81.05	Order Kiloniellales

A. aculeus

OTU	Rel. Abundance	Per. Occurrence	Taxonomical ID.
806717	3.83	100.00	Family Alteromonadaceae
4435279	3.31	100.00	Family Flavobacteriaceae
NROTU998	4.82	98.90	Family Endozoicomonadaceae
221108	1.74	98.90	Family Endozoicomonadaceae
4314827	1.37	97.80	Family Flavobacteriaceae
562126	1.21	97.80	Family Rhodobacteraceae
543999	0.38	97.80	Family Alteromonadaceae
309489	0.69	96.70	Genus <i>Pseudoalteromonas</i>
318171	0.19	96.70	Family Alteromonadaceae
NROTU235	1.65	95.60	Family Flavobacteriaceae
2999126	0.71	95.60	Family Rhodobacteraceae
557211	0.46	95.60	Genus <i>Synechococcus</i>
3991527	2.89	93.41	Genus <i>Alicyclobacillus</i>
355538	0.68	92.31	Genus <i>Prochlorococcus</i>
NROTU1152	0.86	91.21	Family Endozoicomonadaceae
NCROTU817811	0.69	91.21	Family Endozoicomonadaceae
1106960	0.60	91.21	Family Alteromonadaceae
1088265	0.31	90.11	<i>Propionibacterium acnes</i>
4302976	0.47	87.91	Family Flavobacteriaceae
250136	1.30	86.81	Family Rhodobacteraceae
276493	0.36	86.81	Family Pseudoalteromonadaceae
NROTU2323	0.45	85.71	Family Endozoicomonadaceae
550168	0.15	85.71	Genus <i>Synechococcus</i>
NROTU1528	0.84	84.62	Family Endozoicomonadaceae
91492	0.37	84.62	Genus <i>Alteromonas</i>
NROTU1465	0.95	83.52	Family Endozoicomonadaceae
169836	0.43	83.52	<i>Vibrio fortis</i>
634455	0.24	83.52	Genus <i>Synechococcus</i>
145419	1.20	82.42	Family Flavobacteriaceae
NROTU1322	0.57	82.42	Family Rhodobacteraceae
543864	0.22	82.42	Genus <i>Pseudomonas</i>
NROTU2362	0.34	81.32	Family Endozoicomonadaceae
1784974	0.30	81.32	Genus <i>Oleibacter</i>
251481	0.40	80.22	Family Rhodobacteraceae

Table S3. Top 20 significant alignments with OTU 806717 (Family Alteromonadaceae). Sequence ID: Accession number.

Sequence ID	% Identity	Evalue	Bit score	Taxonomy	Isolated source - Host	Citation
MF598548.1	99.799	0	915	uncultured bacterium	algae culture, <i>Symbiodinium</i> clade F core 4	(1)
MF598505.1	99.799	0	915	uncultured bacterium	algae culture, <i>Symbiodinium</i> clade C core 4	(1)
MF598493.1	99.799	0	915	uncultured bacterium	algae culture, <i>Symbiodinium</i> clade B core 2	(1)
KM018569.1	99.6	0	913	uncultured proteobacterium	Red Sea; Upper convective layer of Atlantis II Deep brine pool	(2)
MH169313.1	99.598	0	909	<i>Alteromonas macleodii</i> - Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; <i>Alteromonas</i> <i>macleodii</i>	Red incrusting sponge 4	Unpublished - Bacterial isolates from sponges of the coast of South Brazil. Abraham, W.R.
CP018321.1	99.598	0	909	<i>Alteromonas macleodii</i> - Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; <i>Alteromonas</i> <i>macleodii</i>	<i>Trichodesmium erythraeum</i> IMS101 (in water)	(3)
KX987581.1	99.598	0	909	Uncultured <i>Alteromonas</i> sp. - Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; <i>Alteromonas</i> ; environmental samples.	Sea water from Arabian Sea	Unpublished - Bacterial diversity in west coast of India. Gomes, J.
KX987543.1	99.598	0	909	Uncultured <i>Alteromonas</i> sp. - Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; <i>Alteromonas</i> ; environmental samples.	Sea water from Arabian Sea	Unpublished - Bacterial diversity in west coast of India. Gomes, J.
KX987542.1	99.598	0	909	Uncultured <i>Alteromonas</i> sp. - Bacteria; Proteobacteria;	Sea water from Arabian Sea	Unpublished - Bacterial diversity in west coast of

Sequence ID	% Identity	Evalue	Bit score	Taxonomy	Isolated source - Host	Citation
				Gammaproteobacteria; Alteromonadales; Alteromonadaceae; Alteromonas; environmental samples.		India. Gomes,J.
MF975633.1	99.598	0	909	<i>Alteromonas</i> sp.; Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; Alteromonas; environmental samples.	-	Direct submission – Chen, X.-L., Dong, S., Yang, J.-Y., Zhang, X.-Y. and Zhang, Y.-Z.
MF975628.1	99.598	0	909	<i>Alteromonas</i> sp.; Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; Alteromonas; environmental samples.	-	Direct submission – Chen, X.-L., Dong, S., Yang, J.-Y., Zhang, X.-Y. and Zhang, Y.-Z.
MF975613.1	99.598	0	909	<i>Alteromonas</i> sp.; Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; Alteromonas; environmental samples.	-	Direct submission – Chen, X.-L., Dong, S., Yang, J.-Y., Zhang, X.-Y. and Zhang, Y.-Z.
MF975595.1	99.598	0	909	<i>Alteromonas</i> sp.; Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; Alteromonas; environmental samples.	-	Direct submission – Chen, X.-L., Dong, S., Yang, J.-Y., Zhang, X.-Y. and Zhang, Y.-Z.
MF975571.1	99.598	0	909	<i>Alteromonas</i> sp.; Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; Alteromonas; environmental samples.	-	Direct submission – Chen, X.-L., Dong, S., Yang, J.-Y., Zhang, X.-Y. and Zhang, Y.-Z.
KU578359.1	99.598	0	909	Uncultured bacterium	Ocean water	Unpublished - Temporal analysis of bacterial

Sequence ID	% Identity	Evalue	Bit score	Taxonomy	Isolated source - Host	Citation
						community structure in the north eastern gulf of Mexico Knight, K.T. and Jeffrey, W.H.
KY608081.1	99.598	0	909	<i>Alteromonas macleodii</i> - Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; <i>Alteromonas macleodii</i>	-	Direct submission - Ts, C. and Naval, P.
KX149235.1	99.598	0	909	Uncultured bacterium	Actinia	(4)
KY242369.1	99.598	0	909	<i>Alteromonas macleodii</i> - Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; <i>Alteromonas macleodii</i>	<i>Trichodesmium erythraeum</i> IMS101 (culture)	(3)
CP018023.1	99.401	0	909	<i>Alteromonas</i> sp. – Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; <i>Alteromonas</i> ; environmental samples.	Aquaculture pond	(5)
KU963298.1	99.598	0	909	<i>Alteromonas</i> sp. – Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; <i>Alteromonas</i> ; environmental samples.	Zhangjiang River mangrove sediment	Direct submission – Luo,Y. and Tian,Y.

Table S4. Pairwise comparisons from permutational multivariate analysis of variance (PERMANOVA) for the factor coral species. P/A data represents composition, analyzed based on Sorensen and Unweighted Unifrac; whereas Rel. Abundance stands for relative abundance, evaluated with Bray-Curtis and Weighted Unifrac. P(perm): *P*-value based on permutations, U. perms: Unique permutations, P(MC): Monte Carlo *P*- value.

Data	Distance	Groups	t	P(perm)	Unique perms	P(MC)
P/A	Sorensen	<i>P.spe, M.ele</i>	2.5165	0.0028	9940	0.0001
		<i>P.spe, A.acu</i>	2.5515	0.0009	9944	0.0001
		<i>M.ele, A.acu</i>	2.2811	0.0035	9936	0.0001
	Unweighted Unifrac	<i>P.spe, M.ele</i>	2.9161	0.0018	9937	0.0001
		<i>P.spe, A.acu</i>	2.6282	0.0001	9945	0.0001
		<i>M.ele, A.acu</i>	2.505	0.0026	9955	0.0001
Rel. Abundance	Bray-Curtis	<i>P.spe, M.ele</i>	2.4119	0.0026	9961	0.0001
		<i>P.spe, A.acu</i>	2.4559	0.0007	9937	0.0001
		<i>M.ele, A.acu</i>	2.2091	0.0049	9948	0.0001
Abundance	Weighted Unifrac	<i>P.spe, M.ele</i>	2.1465	0.0114	9947	0.0001
		<i>P.spe, A.acu</i>	2.2804	0.0054	9966	0.0001
		<i>M.ele, A.acu</i>	1.6938	0.0413	9950	0.003

Table S5. Permutational multivariate analysis of variance (PERMANOVA) for the compositional data (Presence/Absence) based on Sorensen distance for the three coral species. Note the similarity between the three coral species in the percentage of estimated components of variation. Test performed using 9,999 permutations. P(perm): *P*-value based on permutations, U. perms: Unique permutations, P(MC): Monte Carlo *P*-value, ECV(%): Estimated components of variation.

P. speciosa

Source	df	SS	MS	Pseudo-F	P(perm)	Unique perms	P(MC)	ECV(%)
Region	1	15066	15066	3.0665	0.0238	8378	0.0001	15.24
Depth	3	12077	4025.7	1.0495	0.3783	9825	0.3059	2.64
Reef(Region)	7	38552	5507.4	1.5915	0.0001	9381	0.0001	12.15
RegionxDepth**	1	4081.5	4081.5	1.0609	0.4107	9903	0.3317	3.29
Reef(Region)xDepth**	13	49906	3838.9	1.1093	0.0006	9125	0.0118	8.83
Residual	97	3.36E+05	3460.5					57.85
Total	122	4.56E+05						

M. elephantotus

Source	df	SS	MS	Pseudo-F	P(perm)	Unique perms	P(MC)	ECV(%)
Region	1	11814	11814	2.605	0.0061	8720	0.0001	14.74
Depth	3	14548	4849.5	1.1565	0.2307	9855	0.1359	5.70
Reef(Region)	6	29905	4984.2	1.4357	0.0001	9569	0.0002	11.27
RegionxDepth**	1	3891.3	3891.3	0.93495	0.5425	9925	0.5809	0.00
Reef(Region)xDepth**	8	33430	4178.7	1.2037	0.0012	9522	0.0084	11.70
Residual	75	2.60E+05	3471.6					56.59
Total	94	3.56E+05						

A. aculeus

Source	df	SS	MS	Pseudo-F	P(perm)	Unique perms	P(MC)	ECV(%)
Region	1	12103	12103	2.5908	0.0084	9637	0.0001	14.48
Depth	2	7930.6	3965.3	1.0642	0.4174	9917	0.3278	3.17
Reef(Region)	7	35513	5073.3	1.5974	0.0001	9485	0.0001	13.69
RegionxDepth**	1	4414	4414	1.1869	0.3482	9938	0.1881	6.17
Reef(Region)xDepth**	5	18638	3727.6	1.1737	0.0054	9525	0.0351	9.55
Residual	74	2.35E+05	3176					52.94
Total	90	3.18E+05						

Table S6. Permutational multivariate analysis of variance (PERMANOVA) for the compositional data (Presence/Absence) based on Unweighted UniFrac distance on data for the three coral species. Note the similarity between the three coral species in the percentage of estimated components of variation. Test performed using 9,999 permutations. P(perm): *P*-value based on permutations, U. perms: Unique permutations, P(MC): Monte Carlo *P*-value, ECV(%): Estimated components of variation.

P. speciosa

Source	df	SS	MS	Pseudo-F	P(perm)	Unique perms	P(MC)	ECV(%)
Region	1	0.95417	0.95417	3.2842	0.0134	8411	0.0001	16.12
Depth	3	0.77272	0.25757	1.084	0.3085	9842	0.2431	3.54
Reef(Region)	7	2.2547	0.3221	1.5097	0.0001	9549	0.0001	11.59
RegionxDepth**	1	0.21717	0.21717	0.91295	0.5858	9914	0.6464	0.00
Reef(Region)xDepth**	13	3.0916	0.23782	1.1147	0.0099	9418	0.0336	9.29
Residual	97	20.696	0.21336					59.45
Total	122	28.025						

M. elephantotus

Source	df	SS	MS	Pseudo-F	P(perm)	Unique perms	P(MC)	ECV(%)
Region	1	0.93476	0.93476	3.1297	0.005	8777	0.0002	16.86
Depth	3	0.92826	0.30942	1.149	0.2584	9891	0.1915	5.45
Reef(Region)	6	1.9586	0.32644	1.4015	0.0003	9704	0.0016	10.84
RegionxDepth**	1	0.2575	0.2575	0.96213	0.5028	9926	0.4961	0.00
Reef(Region)xDepth**	8	2.1478	0.26848	1.1527	0.0318	9594	0.0623	10.15
Residual	75	17.469	0.23292					56.70
Total	94	23.803						

A. aculeus

Source	df	SS	MS	Pseudo-F	P(perm)	Unique perms	P(MC)	ECV(%)
Region	1	0.85227	0.85227	2.847	0.0079	9631	0.0001	15.28
Depth	2	0.5465	0.27325	1.3071	0.2032	9909	0.0539	6.35
Reef(Region)	7	2.3041	0.32916	1.7462	0.0001	9536	0.0001	14.42
RegionxDepth**	1	0.26683	0.26683	1.278	0.3012	9939	0.1129	6.89
Reef(Region)xDepth**	5	1.0456	0.20911	1.1093	0.0434	9570	0.1243	7.14
Residual	74	13.949	0.1885					49.90
Total	90	19.15						

Table S7. Permutational multivariate analysis of variance (PERMANOVA) for relative abundance based on Bray-Curtis distance for the three coral species. The similarity in the response of the three species is evident in the percentage of estimated components of variation. Test performed using 9,999 permutations. P(perm): *P*-value based on permutations, U. perms: Unique permutations, P(MC): Monte Carlo *P*-value, ECV(%): Estimated components of variation.

P. speciosa

Source	df	SS	MS	Pseudo-F	P(perm)	Unique perms	P(MC)	ECV(%)
Region	1	13404	13404	2.7065	0.015	8411	0.0001	13.79
Depth	3	12657	4218.9	1.0466	0.3771	9818	0.3072	2.60
Reef(Region)	7	38437	5491	1.51	0.0001	9371	0.0001	11.47
RegionxDepth**	1	4453.4	4453.4	1.101	0.3595	9904	0.2537	4.31
Reef(Region)xDepth**	13	52447	4034.4	1.1094	0.0005	9145	0.0123	8.99
Residual	97	3.53E+05	3636.5					58.83
Total	122	4.74E+05						

M. elephantotus

Source	df	SS	MS	Pseudo-F	P(perm)	Unique perms	P(MC)	ECV(%)
Region	1	11477	11477	2.4973	0.0097	8712	0.0004	14.24
Depth	3	14882	4960.6	1.1271	0.2755	9861	0.1823	5.23
Reef(Region)	6	30186	5031	1.4114	0.0001	9605	0.0002	11.03
RegionxDepth**	1	3851.9	3851.9	0.88209	0.6041	9919	0.6933	0.00
Reef(Region)xDepth**	8	35090	4386.2	1.2305	0.0004	9487	0.0041	12.53
Residual	75	2.67E+05	3564.5					56.97
Total	94	3.64E+05						

A. aculeus

Source	df	SS	MS	Pseudo-F	P(perm)	Unique perms	P(MC)	ECV(%)
Region	1	10627	10627	2.2309	0.0095	9604	0.0001	12.35
Depth	2	8190.6	4095.3	1.0589	0.4308	9915	0.3439	2.97
Reef(Region)	7	36097	5156.7	1.5621	0.0001	9452	0.0001	13.00
RegionxDepth**	1	4463.8	4463.8	1.1563	0.3701	9946	0.2195	5.52
Reef(Region)xDepth**	5	19346	3869.2	1.172	0.0024	9449	0.0322	9.30
Residual	74	2.44E+05	3301.3					51.83
Total	90	3.27E+05						

Table S8. Permutational multivariate analysis of variance (PERMANOVA) for the relative abundance based on Weighted Unifrac for the three coral species. Note the difference in the response concerning the relative abundance with Bray-Curtis (previous table). Test performed using 9,999 permutations. P(perm): *P*-value based on permutations, U. perms: Unique permutations, P(MC): Monte Carlo *P*-value, ECV(%): Estimated components of variation.

P. speciosa

Source	df	SS	MS	Pseudo-F	P(perm)	Unique perms	P(MC)	ECV(%)
Region	1	0.63752	0.63752	3.9452	0.0001	8502	0.001	17.93
Depth	3	0.28221	0.094069	0.75011	0.8125	9906	0.8275	0.00
Reef(Region)	7	1.2561	0.17944	1.5209	0.0063	9843	0.0099	11.45
RegionxDepth**	1	0.15036	0.15036	1.1947	0.2927	9927	0.2709	5.79
Reef(Region)xDepth**	13	1.6311	0.12547	1.0635	0.297	9770	0.3038	6.76
Residual	97	11.444	0.11798					58.07
Total	122	15.542						

M. elephantotus

Source	df	SS	MS	Pseudo-F	P(perm)	Unique perms	P(MC)	ECV(%)
Region	1	0.18042	0.18042	1.0497	0.2743	8739	0.3829	2.97
Depth	3	0.46222	0.15407	1.247	0.2151	9913	0.2072	7.24
Reef(Region)	6	1.1669	0.19448	1.6431	0.0025	9837	0.0032	14.90
RegionxDepth**	1	0.15205	0.15205	1.2352	0.2877	9945	0.2633	7.62
Reef(Region)xDepth**	8	0.98569	0.12321	1.041	0.3732	9812	0.3831	5.71
Residual	75	8.877	0.11836					61.56
Total	94	11.98						

A. aculeus

Source	df	SS	MS	Pseudo-F	P(perm)	Unique perms	P(MC)	ECV(%)
Region	1	0.1533	0.1533	0.8003	0.5574	9632	0.6225	0.00
Depth	2	0.25473	0.12736	0.66143	0.6848	9947	0.8443	0.00
Reef(Region)	7	1.5262	0.21803	2.3429	0.0001	9847	0.0001	19.84
RegionxDepth**	1	0.21249	0.21249	1.1109	0.3638	9950	0.3435	6.08
Reef(Region)xDepth**	5	0.96424	0.19285	2.0723	0.0002	9825	0.0006	22.93
Residual	74	6.8864	0.09306					51.16
Total	90	10.205						

Table S9. Pairwise comparisons from permutational multivariate analysis of variance (PERMANOVA) for the interaction ReefxDepth: composition data per coral species based on Sorensen distances. P(permutation): *P*-value based on permutations, U. perms: Unique permutations, P(MC): Monte Carlo *P*-value.

P. speciosa

Depth (m)		10 vs. 20				10 vs. 40				10 vs. 60-80				20 vs. 40				20 vs. 60-80				40 vs. 60-80			
Region	Reef	t	P(permutation)	U. perms	P(MC)	t	P(permutation)	U. perms	P(MC)	t	P(permutation)	U. perms	P(MC)	t	P(permutation)	U. perms	P(MC)	t	P(permutation)	U. perms	P(MC)	t	P(permutation)	U. perms	P(MC)
Great Barrier Reef	G. Detached	-				0.98302	0.6353	126	0.4775	-				-				-				-			
	Tijou Reef	-				1.054	0.0809	126	0.3608	-				-				-				-			
	Yonge Reef	-				1.017	0.2808	126	0.4196	-				-				-				-			
	Myrmidon Reef	-				1.0524	0.1316	126	0.3618	-				-				-				-			
Coral Sea	Dutch Towers	1.1078	0.1032	126	0.2978	1.1012	0.0501	126	0.3171	1.0931	0.0803	126	0.3104	1.1145	0.1406	35	0.2961	1.0004	0.3981	126	0.4434	1.0706	0.1728	126	0.3493
	Halfway Wall	1.0027	0.4597	126	0.4359	1.0585	0.0665	126	0.364	1.3243	0.0079	125	0.1076	1.0216	0.3022	126	0.4093	1.3433	0.0089	126	0.091	1.144	0.0251	126	0.2465
	Bigeye Ledge	0.98532	0.5432	126	0.4612	0.9756	0.637	126	0.4842	1.0319	0.19	126	0.4026	0.92741	0.9265	126	0.5612	1.0564	0.0988	126	0.3697	1.0739	0.032	126	0.3422
	Holmes Reef	-				0.96928	0.6103	126	0.4964	1.0285	0.2669	126	0.4027	-				-				1.004	0.3707	126	0.4404
	Flinders Reef	-				1.1706	0.0336	126	0.2359	1.157	0.0163	126	0.2387	-				-				0.96868	0.5152	35	0.4805

M. elephantotus

Depth (m)		10 vs. 20				10 vs. 40				10 vs. 60-80				20 vs. 40				20 vs. 60-80				40 vs. 60-80			
Region	Reef	t	P(perm)	U. perms	P(MC)	t	P(perm)	U. perms	P(MC)	t	P(perm)	U. perms	P(MC)	t	P(perm)	U. perms	P(MC)	t	P(perm)	U. perms	P(MC)	t	P(perm)	U. perms	P(MC)
GBR	G. Detached	-				1.0951	0.0651	125	0.3079	-				-				-				-			
	Tijou Reef	-				1.0352	0.2041	126	0.4013	-				-				-				-			
	Yonge Reef	-				1.023	0.2954	126	0.4076	-				-				-				-			
Coral Sea	Dutch Towers	-				0.94	0.8011	126	0.5307	1.0856	0.0985	126	0.3219	-				-				1.112	0.1198	126	0.2942
	Halfway Wall	1.1194	0.0076	126	0.2785	0.96621	0.7915	126	0.4911	1.1783	0.0075	126	0.2108	1.0291	0.2736	126	0.3907	1.0758	0.1523	126	0.3282	1.0129	0.3489	126	0.4201
	Bigeye Ledge	1.2109	0.0152	126	0.1795	1.4719	0.0227	126	0.0547	1.4099	0.0078	126	0.066	1.1574	0.1463	126	0.2328	1.1415	0.1671	125	0.2549	1.258	0.0856	126	0.1511
	Flinders Reef	-				1.1053	0.1517	126	0.2928	-				-				-				-			

A. aculeus

Depth (m)		10 vs. 20				10 vs. 40				20 vs. 40			
Region	Reef	t	P(perm)	U. perms	P(MC)	t	P(perm)	U. perms	P(MC)	t	P(perm)	U. perms	P(MC)
Great Barrier Reef	G. Detached	-				0.98875	0.5373	126	0.4586	-			
	Yonge Reef	-				1.0552	0.1607	126	0.3649	-			
	Myrmidon Reef	-				1.5791	0.0002	5015	0.0069	-			
Coral Sea	Dutch Towers	-				-				0.932	0.8092	330	0.556
	Halfway Wall	-				0.95913	0.5475	461	0.5075	-			
	Bigeye Ledge	1.2265	0.0103	461	0.1591	1.1813	0.0151	126	0.2099	1.0214	0.2989	462	0.4003
	Flinders Reef	-				1.0518	0.184	126	0.369	-			

Table S10. Pairwise comparisons from permutational multivariate analysis of variance (PERMANOVA) for the interaction ReefxDepth: composition data per coral species based on Unweighted Unifrac distances. P(permutation): *P*-value based on permutations, U. perms: Unique permutations, P(MC): Monte Carlo *P*-value.

P. speciosa

Depth (m)		10 vs. 20				10 vs. 40				10 vs. 60-80				20 vs. 40				20 vs. 60-80				40 vs. 60-80			
Region	Reef	t	P(permutation)	U. perms	P(MC)	t	P(permutation)	U. perms	P(MC)	t	P(permutation)	U. perms	P(MC)	t	P(permutation)	U. perms	P(MC)	t	P(permutation)	U. perms	P(MC)	t	P(permutation)	U. perms	P(MC)
Great Barrier Reef	G. Detached	-				0.9836	0.5401	126	0.4695	-				-				-				-			
	Tijou Reef	-				0.93241	0.9012	126	0.5576	-				-				-				-			
	Yonge Reef	-				1.024	0.3418	126	0.4057	-				-				-				-			
	Myrmdon Reef	-				0.96722	0.5981	126	0.4859	-				-				-				-			
Coral Sea	Dutch Towers	1.1064	0.1521	126	0.2985	1.1688	0.0488	126	0.2386	1.0632	0.1604	126	0.3564	1.2278	0.0285	35	0.193	0.99619	0.3706	126	0.4411	1.0439	0.3109	126	0.3777
	Halfway Wall	0.97016	0.6523	126	0.482	0.97206	0.7282	126	0.4816	1.2072	0.0077	126	0.1897	1.1688	0.0262	126	0.224	1.4065	0.0081	125	0.0602	1.0885	0.0743	126	0.328
	Bigeye Ledge	1.0248	0.3409	126	0.4015	0.96295	0.5661	126	0.496	0.99605	0.4835	126	0.4434	0.91289	0.8435	126	0.5809	1.2175	0.0632	125	0.1944	1.2109	0.0438	126	0.1948
	Holmes Reef	-				0.87529	0.9677	126	0.6334	1.0247	0.2958	126	0.4056	-				-				0.95571	0.6728	126	0.5063
	Flinders Reef	-				1.2043	0.0552	126	0.1958	1.208	0.0544	126	0.1958	-				-				0.98864	0.5122	35	0.4615

M. elephantotus

Depth (m)		10 vs. 20				10 vs. 40				10 vs. 60-80				20 vs. 40				20 vs. 60-80				40 vs. 60-80			
Region	Reef	t	P(perm)	U. perms	P(MC)	t	P(perm)	U. perms	P(MC)	t	P(perm)	U. perms	P(MC)	t	P(perm)	U. perms	P(MC)	t	P(perm)	U. perms	P(MC)	t	P(perm)	U. perms	P(MC)
GBR	G. Detached	-				1.0237	0.36	126	0.4082	-				-				-				-			
	Tijou Reef	-				0.98852	0.5119	126	0.4629	-				-				-				-			
	Yonge Reef	-				1.0067	0.373	126	0.4301	-				-				-				-			
Coral Sea	Dutch Towers	-				0.94998	0.6096	126	0.5081	1.0576	0.2455	126	0.3608	-				-				1.1212	0.1621	126	0.2903
	Halfway Wall	1.093	0.1231	126	0.3164	0.92607	0.8446	126	0.5508	1.1101	0.1012	126	0.2944	1.0662	0.1988	126	0.356	1.1794	0.0709	126	0.2146	1.0037	0.39	126	0.4343
	Bigeye Ledge	1.2375	0.0373	126	0.161	1.614	0.0227	126	0.0293	1.2795	0.0082	126	0.1229	1.1178	0.1719	126	0.2782	0.95664	0.5927	126	0.4883	1.1937	0.1556	126	0.1988
	Flinders Reef	-				1.0497	0.2395	126	0.3653	-				-				-				-			

A. aculeus

Depth (m)		10 vs. 20				10 vs. 40				20 vs. 40			
Region	Reef	t	P(perm)	U. perms	P(MC)	t	P(perm)	U. perms	P(MC)	t	P(perm)	U. perms	P(MC)
Great Barrier Reef	G. Detached	-				0.98847	0.5019	126	0.4587	-			
	Yonge Reef	-				1.0543	0.2066	126	0.3543	-			
	Myrmidon Reef	-				1.4702	0.0003	5001	0.017	-			
Coral Sea	Dutch Towers	-				-				0.99057	0.5259	330	0.4561
	Halfway Wall	-				1.0286	0.3083	462	0.4025	-			
	Bigeye Ledge	1.2544	0.016	462	0.1306	1.2595	0.0072	126	0.1447	1.1727	0.0186	460	0.2141
	Flinders Reef	-				0.91964	0.8508	125	0.568	-			

Table S11. Pairwise comparisons from permutational multivariate analysis of variance (PERMANOVA) for the interaction ReefxDepth: relative abundance data per coral species based on Bray-Curtis distances. P(permutation): *P*-value based on permutations, U. perms: Unique permutations, P(MC): Monte Carlo *P*-value.

P. speciosa

Depth (m)		10 vs. 20				10 vs. 40				10 vs. 60-80				20 vs. 40				20 vs. 60-80				40 vs. 60-80			
Region	Reef	t	P(permutation)	U. perms	P(MC)	t	P(permutation)	U. perms	P(MC)	t	P(permutation)	U. perms	P(MC)	t	P(permutation)	U. perms	P(MC)	t	P(permutation)	U. perms	P(MC)	t	P(permutation)	U. perms	P(MC)
Great Barrier Reef	G. Detached	-				0.98407	0.5485	126	0.4751	-				-				-				-			
	Tijou Reef	-				1.053	0.0712	126	0.3655	-				-				-				-			
	Yonge Reef	-				1.0222	0.2968	126	0.4208	-				-				-				-			
	Myrmidon Reef	-				1.0865	0.0531	126	0.3147	-				-				-				-			
Coral Sea	Dutch Towers	1.1328	0.0967	126	0.271	1.1327	0.017	126	1.1327	1.1258	0.0503	126	0.2663	1.162	0.0867	35	0.254	0.99945	0.3668	126	0.4361	1.1039	0.1058	126	0.3061
	Halfway Wall	1.027	0.2885	125	0.405	1.0514	0.1136	126	1.0514	1.2529	0.0072	126	0.1548	1.0266	0.2955	126	0.4035	1.2675	0.0086	126	0.1327	1.076	0.0964	126	0.3393
	Bigeye Ledge	1.0065	0.3469	126	0.4261	0.99589	0.4593	126	0.99589	1.0257	0.2093	126	0.4105	0.96043	0.8077	126	0.5108	1.0588	0.1117	126	0.3507	1.1003	0.039	126	0.3132
	Holmes Reef	-				0.94354	0.767	126	0.5275	1.0017	0.3955	126	0.4447	-				-							
	Flinders Reef	-				1.2013	0.0398	125	0.1988	1.1691	0.0082	126	0.237	-				-							

M. elephantotus

Depth (m)		10 vs. 20				10 vs. 40				10 vs. 60-80				20 vs. 40				20 vs. 60-80				40 vs. 60-80			
Region	Reef	t	P(perm)	U. perms	P(MC)	t	P(perm)	U. perms	P(MC)	t	P(perm)	U. perms	P(MC)	t	P(perm)	U. perms	P(MC)	t	P(perm)	U. perms	P(MC)	t	P(perm)	U. perms	P(MC)
GBR	G. Detached	-				1.1035	0.0558	126	0.3138	-				-				-				-			
	Tijou Reef	-				1.0076	0.3457	126	0.4344	-				-				-				-			
	Yonge Reef	-				1.0113	0.3432	126	0.4308	-				-				-				-			
Coral Sea	Dutch Towers	-				0.94692	0.7816	126	0.5261	1.1029	0.1017	126	0.2931	-				-				1.1273	0.1096	126	0.2792
	Halfway Wall	1.2029	0.0151	126	0.1917	0.99758	0.5317	125	0.4495	1.2264	0.0094	125	0.1709	1.0431	0.2391	125	0.384	1.0821	0.1574	126	0.3139	1.0223	0.2545	126	0.4052
	Bigeye Ledge	1.2032	0.0084	126	0.1929	1.5006	0.0232	126	0.0469	1.4112	0.0096	126	0.0594	1.1491	0.1945	126	0.2458	1.114	0.2153	126	0.2916	1.2424	0.0727	126	0.1629
	Flinders Reef	-				1.1292	0.1068	126	0.2744	-				-				-				-			

A. aculeus

Depth (m)		10 vs. 20				10 vs. 40				20 vs. 40			
Region	Reef	t	P(perm)	U. perms	P(MC)	t	P(perm)	U. perms	P(MC)	t	P(perm)	U. perms	P(MC)
Great Barrier Reef	G. Detached	-				0.99842	0.4106	126	0.4498	-			
	Yonge Reef	-				1.0666	0.1479	126	0.355	-			
	Myrmidon Reef	-				1.5666	0.0002	5005	0.0064	-			
Coral Sea	Dutch Towers	-				-				0.94225	0.7329	330	0.5267
	Halfway Wall	-				0.96824	0.5372	462	0.4974	-			
	Bigeye Ledge	1.1915	0.0216	462	0.1928	1.1571	0.017	126	0.2392	1.0103	0.3677	462	0.4313
	Flinders Reef	-				1.0665	0.1598	126	0.3532	-			

Table S12. Pairwise comparisons from permutational multivariate analysis of variance (PERMANOVA) for the interaction ReefxDepth: relative abundance data per coral species based on Weighted Unifrac distances. P(perm): *P*-value based on permutations, U. perms: Unique permutations, P(MC): Monte Carlo *P*-value

A. aculeus

Depth (m)		10 vs. 20				10 vs. 40				20 vs. 40			
Region	Reef	t	P(perm)	U. perms	P(MC)	t	P(perm)	U. perms	P(MC)	t	P(perm)	U. perms	P(MC)
Great Barrier Reef	G. Detached	-				1.1967	0.0979	126	0.2204	-			
	Yonge Reef	-				0.89674	0.6532	126	0.5127	-			
	Myrmidon Reef	-				3.4194	0.0001	5089	0.0001	-			
Coral Sea	Dutch Towers	-				-				1.2715	0.1373	329	0.1626
	Halfway Wall	-				1.1843	0.1362	462	0.2289	-			
	Bigeye Ledge	0.79435	0.7383	462	0.6413	1.0401	0.3537	126	0.3639	0.77208	0.8822	462	0.72
	Flinders Reef	-				1.0015	0.4558	126	0.4178	-			

Table S13. Indexes Average ($\Delta+$) and variation ($\Delta+$) of taxonomic distinctness for core microbiome of the three species.

Coral species	N. of OTUs	Av. Tax. Distinctness ($\Delta+$)	Var. Tax. Distinctness ($\Delta+$)
<i>P. speciosa</i>	17	76.47	225.32
<i>M. elephantotus</i>	11	71.59	383.26
<i>A. aculeus</i>	34	71.86	528.51

References

1. Lawson CA, Raina J-B, Kahlke T, Seymour JR, Suggett DJ. 2018. Defining the core microbiome of the symbiotic dinoflagellate, *Symbiodinium*. Environ Microbiol Rep 10:7-11.
2. Guan Y, Hikmawan T, Antunes A, Ngugi D, Stingl U. 2015. Diversity of methanogens and sulfate-reducing bacteria in the interfaces of five deep-sea anoxic brines of the Red Sea. Res Microbiol 166:688-699.
3. Hou S, López-Pérez M, Pfreundt U, Belkin N, Stüber K, Huettel B, Reinhardt R, Berman-Frank I, Rodriguez-Valera F, Hess WR. 2018. Benefit from decline: the primary transcriptome of *Alteromonas macleodii* str. Te101 during *Trichodesmium* demise. ISME J 12:981-996.
4. Muller EM, Fine M, Ritchie KB. 2016. The stable microbiome of inter and sub-tidal anemone species under increasing pCO₂. Sci Rep 6:37387.
5. López-Pérez M, Ramon-Marco N, Rodriguez-Valera F. 2017. Networking in microbes: conjugative elements and plasmids in the genus *Alteromonas*. BMC Genomics 18:36.