Supplementary Tables

Supplementary Table S1
A list of geographic coordinates for all the sampling sites and which depth zones were targeted at each site; the number of samples collected at each depth zone from each site; the number of samples with successfully sequenced *ITS2* libraries that were included in the Symbiodiniaceae community analysis; the number of samples with successfully sequenced 2bRAD libraries; and the number of samples that were identified as unique multilocus genotypes (i.e. clones removed, n_g) that were retained in the coral host population genetics analysis.

Reef Populations	Latitude	Longitude	Samples Collected	*ITS2* Sequenced	2bRAD Sequenced	*ng*
Alacranes						
	22.3962	-89.7058	5	5	4	4
10 m	22.5113	-89.7974	5	5	5	5
	22.5458	-89.6601	8	8	7	7
	22.3962	-89.7058	3	3	3	3
15 m	22.5113	-89.7974	5	5	4	4
	22.5458	-89.6601	8	8	4	4
	22.3962	-89.7058	7	7	6	6
25 m	22.5093	-89.62780	3	3	3	3
	22.5867	-89.7521	6	6	6	6
35 m	22.3959	-89.7056	9	9	8	8
	22.5867	-89.7521	7	7	7	7
Bajos del Norte						
10 m	23.2474	-88.7078	15	15	10	10
15 m	23.2474	-88.7078	15	15	12	12
25 m	23.2837	-88.7116	19	18	8	7
35 m	23.3071	-88.7162	11	10	11	11

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Reef Populations	Latitude	Longitude	Samples Collected	*ITS2* Sequenced	2bRAD Sequenced	*ng*
Alacranes						
	22.3962	-89.7058	5	5	4	4
10 m	22.5113	-89.7974	5	5	5	5
	22.5458	-89.6601	8	8	7	7
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Supplementary Table S2

Mean heterozygosity calculated for each sample population across all sites (variant and invariant) and across variant sites (SNP loci) only. n_g indicates the number of unique genotypic individuals within each sample population

Reef	Depth Zone (m)	H_O (Variant and Invariant Sites)	H_O (Variant Sites Only)	n_g
Alacranes	10	0.0030	0.2599	16
	15	0.0028	0.2500	11
	25	0.0029	0.2548	15
	35	0.0030	0.2566	15
Bajos del Norte	10	0.0032	0.2759	10
	15	0.0030	0.2701	12
	25	0.0031	0.2696	7
	35	0.0030	0.2647	11

Supplementary Table S3
List of outlier SNP loci identified by BAYESCAN within ±2 kb of *Montastraea cavernosa* annotated gene regions. The Clusters of Orthologous Groups (COG) functional category notations are as follows: **A** RNA processing and modification; **B** chromatin structure and dynamics; **C** energy production and conversion; **D** cell cycle control and mitosis; **E** amino acid metabolism and transport; **F** nucleotide metabolism and transport; **G** carbohydrate metabolism and transport; **H** coenzyme metabolism; **I** lipid metabolism; **J** translation; **K** transcription; **L** replication and repair; **M** cell wall/membrane/envelop biogenesis; **N** cell motility; **O** post-translational modification, protein turnover, chaperone functions; **P** inorganic ion transport and metabolism; **Q** secondary structure; **T** signal transduction; **U** intracellular trafficking and secretion; **Y** nuclear structure; **Z** cytoskeleton; **R** general functional prediction only; **S** function unknown. Significance level is indicated by the number of asterisks, * <0.1, ** <0.05, *** <0.01.

Locus	Gene ID	COG Functional Category	Gene Annotation	Significance Level
2390	Mcavernosa02795	K	Cell division cycle 73, Paf1 RNA polymerase II complex component, homolog (*S. cerevisiae*)	*
2802	Mcavernosa04395	S	Coiled-coil domain containing 6	***
3780	Mcavernosa13861	G	Solute carrier family 16, member	*
3818	Mcavernosa13785	T	Receptor	**
6256	Mcavernosa15490	T, Z	Dishevelled Associated Activator of Morphogenesis	*
7435	Mcavernosa20088	K	Zinc finger CCCH-type containing	*
7801	Mcavernosa17690	I	Phospholipase C	***
9798	Mcavernosa12028	S	Responsible for the deiodination of T4 (3,5,3,5- tetraiodothyronine, by similarity)	**

Supplementary Table S4

Results from pairwise permutational multivariate analysis of variance (PERMANOVA; 9,999 permutations) of Symbiodiniaceae communities based on *ITS2* type profile composition between all depth zones with significant comparisons bolded (FDR-corrected *p*-values).

Depth Zone Comparison	Pseudo-*F*	*p*-value
10 m vs. 15 m	1.107	0.3450
10 m vs. 25 m	9.163	**0.0001**
10 m vs. 35 m	6.901	**0.0001**
15 m vs. 25 m	5.707	**0.0001**
15 m vs. 25 m	4.853	**0.0001**
25 m vs. 35 m	2.343	**0.0403**