Supplementary Materials

1. Genotyping & sample filtering

With the exception of three colonies (#NC33, NC71, & NC94 in the online supplemental data file [OSDF]), all were genotyped using the mitochondrial open reading frame assay of Flot et al. [48], with results described previously [12]. Of the 101 colonies genotyped, 80 and 21 were *Pocillopora damicornis* and *Pocillopora acuta*, respectively. Since the *P. acuta* sample set was small, and no night dive colonies were genotyped as *P. acuta*, only *P. damicornis* data were analyzed herein. Of the 80 uniquely sampled *P. damicornis* colonies (associated with 99 biopsies), 2 were sampled between 14:00 and 18:00 and were excluded due to low sample size in this time bin. A multivariate outlier analysis based on the Mahalanobis distance [12] identified eight corals displaying aberrant behavior; these were also removed from the dataset.

2. Response variable (RV) filtering & details

Fifteen RV were analyzed in each of the remaining 89 *P. damicornis* biopsies, though only ten were included in the statistical analyses discussed in the main text. Two RV, colony color and Symbiodiniaceae assemblage, were actually considered environmental parameters (EP; Table 1) in the statistical analyses since they were hypothesized to influence the remaining coral RV. Two size parameters (maximum colony length [cm] & surface area [SA; cm^2]) were assessed *in situ* but not considered in the statistical analysis since size was not hypothesized to be a useful estimate of health. Therefore, only 10 of the 15 parameters measured in each colony (the final excluded being host genotype) were considered in the statistical analyses (Table 1).

Expression levels of the Symbiodiniaceae stress response genes ubiquitin ligase (*ubiq-lig*) and heat shock protein 90 (*hsp90*), as well as the carbon fixation gene ribulose-1,5-bisphosphate carboxylase/oxygenase (*rbcL*) and the presumed osmoregulation-associated gene zinc-induced facilitator-like 1-like (*zifl1l*), were measured. The host coral genes included 1) green fluorescent protein-like chromoprotein (*gfp-cp*), which encodes a protein potentially involved in light regulation [25], 2) the reactive oxygen species (ROS) detoxification gene copper-zinc superoxide dismutase (*cu-zn-sod*), 3) the cell adhesion gene *lectin*, and 4) the CO_2 metabolism gene carbonic anhydrase (*ca*). All such RV, as well as the associated real-time PCR primers and protocols, are described in detail in prior works [24-26]. All RV data have been overlaid onto images of the sampled colonies on the open-access coral database coralreefdiagnostics.com. The same web page features protocols, dive site maps, DNA sequences used for genotyping (see above.), and both whole-colony and "macro" (polyp-scale; 1-mm) images of the sampled *P. damicornis* specimens described herein.

3. Multivariate statistical analyses

Both principal components analysis (PCA; on correlations) and discriminant analysis (DCA; on standardized data) were undertaken with JMP® Pro (ver. 15) with the 1) 10 RV, 2) host genes only (n=4), and 3) Symbiodiniaceae genes only (n=4) with the 89-sample dataset. For DCA, all RV were considered, and Wilks' lambda was calculated to depict multivariate mean differences over time (i.e., multivariate ANOVA [MANOVA]; alpha=0.045). Given the typically skewed distributions of the individual RV, as well as their high degree of multicollinearity, the MANOVA findings are mainly discussed in the Supplementary Materials only. As a comparison, permutational ANOVA (PERMANOVA) was undertaken with PRIMER (ver. 6) after creating a Euclidean-distance matrix based on the standardized data across all 10 RV (unrestricted permutation of raw data, type III model). Unlike MANOVA, PERMANOVA was only carried out with all 10 RV (not with host- or Symbiodiniaceae-only subsets). PERMANOVAs of other EP were also performed, and an alpha of 0.045 was set *a priori*. In another set of PERMANOVAs, the outliers were included to determine if they influenced the overall effects documented (Tables S1 and S2); this analysis is not addressed in the main text.

Partial least squares (PLS) and stepwise regression (SRA) were used to develop models for the coral light vs. dark response. Specifically, SRA was used to determine the RV (or suites of RV) that best modeled the differences across time (n=3 bins) and light (photosynthetically active radiation [PAR]=0 vs. PAR>0). For PLS, a misclassification rate was calculated based on the model's predictions, and for SRA, models were built in reverse fashion until the Bayesian information criterion was minimized. Readers are referred to Mazerolle [49] for a treatise on why such information criteria-based analyses should see more widespread adoption by ecologists. EP were assessed in terms of their strength of effect on multivariate coral physiology (all 10 RV); this was based on 1) PERMANOVA (lower *p*-values signifying stronger effect), 2) the percent variation explained in the multivariate trait space (the first four coordinates from a multi-dimensional scaling analysis of standardized data from the 10 RV) by each EP in isolation via PLS (NIPALS fit with kfold validation of 7; higher percent variation explained indicative of stronger effect size), and 3) the PLS misclassification rate from the DCA (lower misclassification rate=better predictor of the coral response; see Table 2.).

4. Supplemental tables

Table S1. Comparison of statistical methods on the *Pocillopora damicornis* multivariate response (10 response variables). This table bears similarity to Table 2, except that an additional column has been added to show the PERMANOVA (permutational ANOVA (similarity [Euclidean distances] among standardized data) results when all outliers were

included. MANOV=multivariate ANOVA (standardized data), NS=not statistically significant (p>0.045), and Sym=Symbiodiniaceae.

EP	**MAN-OVA**	**PERMANOVA without 8 outliers (n=89)**	**PERMANOVA with outliers (n=97)**	**Conclusion(s)**
light	p<0.01	p<0.001	NS[a]	All tests gave same result unless outliers were included.
coral cover	p<0.01	p<0.01	p<0.001	All tests gave same result.
time	p<0.01	p<0.01	NS[a]	All tests gave same result unless outliers were included.
region	p<0.001	p=0.01	p<0.045	All tests gave same result.
reef type	p<0.001	p<0.05	p<0.01	All tests gave same result.
colony color	p<0.001	p<0.01[a]	p<0.045[a]	All tests gave same result. No significant effect when both species were analyzed together.
depth	p<0.01	p<0.05	p<0.045	All tests gave same result.
island	p=0.001	p<0.05	NS	All tests gave same result unless outliers were included.
temperature	p<0.045	p<0.01	NS[a]	All tests gave same result unless outliers were included.
exposure	p<0.045	p<0.045	NS[a]	All tests gave same result unless outliers were included.
salinity	NS	p<0.045	NS	No significant effect on coral physiology.
reef zone	NS	NS	NS	No effect on coral physiology.
Sym assemblage	NS	NS	NS	No effect on coral physiology.

[a]Finding differs from when both species (*P. damicornis* & *P. acuta*) were analyzed together.

Table S2. Effects of light: univariate statistics. Please note the differences between this table and Table 4; only data from *Pocillopora damicornis* (Pdam) colonies that were *not* considered multivariate outliers have been included in Table 4. Rank-based tests were used for all response variables due to lack of normality. In general, Symbiodiniaceae density (i.e., GCP) and *zifl1l* mRNA expression were 1.5-fold higher during the day, whereas *hsp90* (1.5-fold), *rbcL* (2-fold), and *ubiq-lig* (1.5-fold) and host coral *lectin* (1.5-fold) and *cu-zn-sod* (1.5-fold) mRNA expression levels were higher at night. Please note that, in the main text, we excluded the late afternoon (14:00-18:00) sampling time data due to low sample sizes; in this table, however, all four time periods were considered in the columns that include "time" as a model term. Unlike the main text, both species were included in certain models, and, for certain comparisons, outliers have been left in the analysis. NS=not statistically significant.

Response variable	**Both species-time (n=119)**	**Both species-light vs. dark (n=119)**	**Pdam-matched pairs (light vs. dark; n=26)**[a]	**Pdam only-time (n=99)**	**Pdam-only light-vs. dark (n=99)**	**Pdam only-no outliers-time (n=91)**	**Pdam only-no outliers-light vs. dark (n=91)**
RNA/DNA	NS	NS	NS	NS	NS	No *post-hoc* differences	Dark>light
Sym GCP	Night<all other	Light>dark	NS[b]	NS	NS	NS	Light>dark
Sym *hsp90*	Night>morning	Dark>light	NS	Night>morning	Dark>light	Night>morning Night>midday	Dark>light
Sym *ubiq-lig*	Night>morning	Dark>light	NS	Night>morning	Dark>light	Night>morning	Dark>light
Sym *zifl1l*	Morning>afternoon Morning>night	Light>dark	Light>dark	Morning>night	Light>dark	NS	NS
Sym *rbcL*	Night>morning	Dark>light	NS	Night>morning	Dark>light	Night>morning	Dark>light

Host *ca*	NS	NS	Light>dark	NS	NS	NS	NS
Host *lectin*	Night>morning	Dark>light	NS	Night>morning	Dark>light	Night>morning	Dark>light
Host *cu-zn-sod*	Night>morning	Dark>light	NS	Night>morning	Dark>light	Night>morning	Dark>light
Host *gfp-cp*	NS	NS	Light>dark	NS	NS	NS	NS

[a]Identical to the respective column in **Table 4**. [b]Light>dark when testing one-way light/dark ratio>1 (signed-rank test, $p<0.05$).

Table S3. Permutational MANOVA of 13 environmental parameters (EP) on multivariate coral colony similarity. A Euclidean distance matrix was built from standardized data from the 10 coral holobiont response variables with the exclusion of eight outliers (n=89 *Pocillopora damicornis* biopsies). The type III model featured unrestricted permutation of raw data. Light was assessed as photosynthetically active radiation (PAR): light (PAR>0) vs. dark (PAR=0). *PERMDISP (multivariate dispersion), $p<0.05$.

EP (source of variation)	***df***	**SS**	**MS**	**Pseu-do *F***	***p***	**Pairwise tests**
REGION*[a]	1	30.942	30.942	3.2	**0.010**	north≠south
residual	89	869.06	9.7647			
total	90	900				
ISLAND[a]	5	77.069	15.414	1.6	**0.044**	Ile des Pins≠Cook Reef (p=0.06)
residual	85	822.93	9.6815			
total	90	900				
REEF TYPE	3	55.995	18.665	1.9	**0.020**	fringing reef≠barrier reef
residual	87	844.01	9.7012			fringing reef≠atoll
total	90	900				
REEF ZONE[a]	3	37.308	12.436	1.3	0.242	
residual	87	862.69	9.916			
total	90	900				

EP (source of variation)	*df*	SS	MS	Pseudo *F*	*p*	Pairwise tests
EXPOSURE	2	41.524	20.762	2.1	**0.027**	
residual	88	858.48	9.7554			protected≠intermediate
total	90	900				
TIME	3	75.594	25.198	2.7	**0.005**	night≠10:00-14:00 (afternoon)
residual	87	824.41	9.4759			night≠before 10:00 (morning)
total	90	900				
LIGHT vs. DARK	1	50.072	50.072	5.2	**0.001**	light≠dark
residual	89	849.93	9.5497			
total	90	900				
DEPTH	5	80.527	16.105	1.7	**0.042**	
residual	85	819.47	9.6409			
total	90	900				
CORAL COVER*	2	56.394	28.197	2.9	**0.005**	5-10≠10-15 m, 5-10≠20-25 m
residual	88	843.61	9.5864			5-10≠25-30 m
total	90	900				PERMDISP: 15-30%>30-45%
TEMPERATURE	4	79.937	19.984	2.1	**0.010**	Driven by null data
residual	86	820.06	9.5356			
total	90	900				
SALINITY	4	67.152	16.788	1.7	0.048	
residual	86	832.85	9.6843			
total	90	900				
COLONY COLOR	4	84.527	21.132	2.2	**0.008**	green≠pale, normal, very pale, or
residual	86	815.47	9.4822			purple
total	90	900				
SYM ASSEMBLAGE						
	2	21.649	10.824	1.1	0.327	

EP (source of variation)	***df***	**SS**	**MS**	**Pseudo *F***	***p***	**Pairwise tests**
residual	88	878.35	9.9813			
total	90	900				

[a]Same findings as when both species (*P. damicornis* & *P. acuta*) were analyzed together (Tables S1 and S2).

5. Supplemental figure

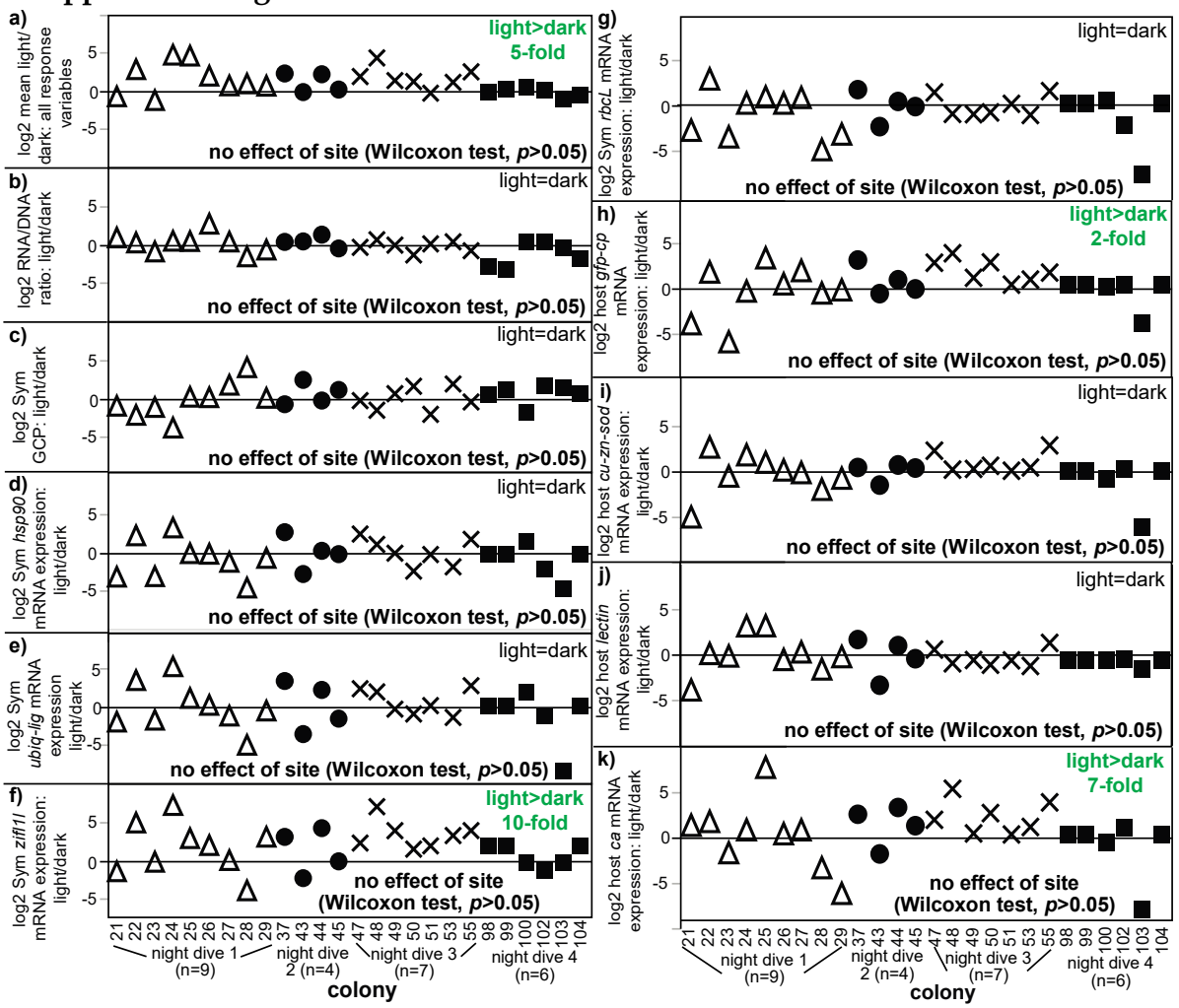

Figure S1. Colony-specific data for the 26 night dive samples. Light/dark ratio data were $\log_2$-transformed prior to plotting, and the effects of both light (upper right corner of each panel; signed-rank test vs. null hypothesis of 0) and site (bottom right of each panel) have been included. When the mean $\log_2$ value across colonies was significantly greater than 0, the difference (as a relative fold change) has been highlighted in green. The triangles, circles, exes, and squares correspond to samples from night dives 1 (south), 2 (south), 3 (south), and 4 (north), respectively. Please note that, when considering *all* data (not only the night dive samples), Symbiodiniaceae (Sym) *hsp90*, *ubiq-lig*, and *rbcL* mRNA expression and host coral *cu-zn-sod* mRNA expression were all found to be significantly up-regulated at night (Table 4).

Supplementary references (not cited in main text)

48. Flot, J.F.; Magalon, H.; Cruaud, C.; Couloux, A.; Tillier, S**.** Patterns of genetic structure among Hawaiian corals of the genus *Pocillopora* yield clusters of individuals that are compatible with morphology. *Comptes Rendus Biol.* **2008**, *331*, 239–247.
49. Mazerolle, M. Improving data analysis in herpetology: Using Akaike's Information Criterion (AIC) to assess the strength of biological hypotheses. *Amphib.-Reptil.* **2006**, *27*, 169–180.