Code S1. Text to be copied into R in order to compute standard error (SE) for broad-sense heritability, R code developed by Fei Heng

```
## R code for estimating H2 and SE of H2
library(VCA)
library(openxlsx)
#column1 = genotypes of samples (string), column2 = phenotypic data of samples (numeric)
heritability <- read.xlsx("Heritability.xlsx", sheet = 1, startRow = 1, colNames = TRUE)
heritability$genotype <- factor(heritability$genotype)
# rptR under LMM
library(rptR)
set.seed(123)
rpt.1000 <- rpt(lifespan_diff ~ (1|genotype), grname="genotype",
          data=heritability, nboot=1000, npermut=0, datatype = "Gaussian")
# reml for gaussian
summary(rpt.1000)
```

Table S1. Original collection information for the Tavernier Nursery Coral Restoration Foundation (CRF) *Acropora cervicornis* colonies used in this study. Collection information provided by Amelia Moura, CRF. Depth was not measured at the collection site but was approximated from the latitude and longitude coordinates using the NOAA Bathymetric Data Viewer (https://maps.ngdc.noaa.gov/viewers/bathymetry/)

Genotype	Region	Collection Site	Latitude	Longitude	Approximate Depth	Collection Date
M3	Middle Keys	East Turtle Shoal off Grassy Key	24° 42.801' N	80° 56.687' W	5.83 m	4/24/2008
M5	Middle Keys	East Turtle Shoal off Grassy Key	24° 42.707' N	80° 56.758' W	6.79 m	4/24/2008
M6	Middle Keys	East Turtle Shoal off Grassy Key	24° 42.649' N	80° 56.880' W	5.03 m	4/24/2008
M7	Middle Keys	East Turtle Shoal off Grassy Key	24° 43.107' N	80° 55.847' W	7.90 m	12/6/2008
U1	Upper Keys	Off Plantation Key, Inside Little Conch	24° 57.542' N	80° 29.447' W	3.94 m	12/10/2009
U7	Upper Keys	Molasses Trench Patch Reef	25° 0.573' N	80° 24.898' W	5.38 m	1/13/2006
U12	Upper Keys	Patch Reef off Plantation Key	24° 57.096' N	80°29.322' W	5.28 m	4/1/2010
U15	Upper Keys	Patch Reef off Tavernier, inside nursery	24° 59.261' N	80° 26.085' W	7.13 m	2/18/2006
U19	Upper Keys	Patch Reef off Tavernier	24° 59.272' N	80° 28.070' W	5.01 m	5/6/2008
U23	Upper Keys	Reef edge off Lower Matecumbe	24° 49.526' N	80° 39.066' W	14.37 m	5/13/2008
U30	Upper Keys	Patch Reef just off Tavernier	24° 59.312' N	80° 28.008' W	4.87 m	5/13/2008
U33	Upper Keys	Patch Reef just off Tavernier	25° 0.215' N	80° 27.055' W	5.33 m	9/20/2008
U37	Upper Keys	Pickles Rubble Zone	24° 59.316' N	80° 24.154' W	25.82 m	10/2/2009
U40	Upper Keys	Conch Rubble Zone/Little Conch outer ledge	24° 57.114' N/ 24° 56.107' N	80° 27.068' W/ 80° 28.054' W	7.36 – 57.4 m	5/5/2010
U44	Upper Keys	Inside Conch, Patch Reef off Tavernier	24° 59.287' N	80° 27.823' W	4.79 m	5/7/2010
U46	Upper Keys	Patch Reef inshore from Molasses Trench area	25° 0.823' N	80° 24.900' W	4.01 m	10/17/2010
U56	Upper Keys	Lower Matecumbe	24° 49.931' N	80° 38.446' W	15.67 m	10/17/2010
U58	Upper Keys	Lower Matecumbe	24° 49.832' N	80° 38.626' W	12.77 m	1/25/2006
U70	Upper Keys	Patch Reef inshore from Molasses Trench area	25° 0.127' N	80° 24.068' W	9.11 m	9/26/2010
U76	Upper Keys	Lower Matecumbe	24° 49.298' N	80° 39.365' W	14.07 m	6/14/2011

Table S2. Allele frequencies and mean heterozygosity of the 15 microsatellite markers used for genotyping the coral colonies used in the present study. Primers for the loci were developed by Baums et al. 2005, 2009

Locus	Allele (bp)	Allele frequency	Locus	Allele (bp)	Allele frequency	Mean heterozygosity
166	136	0.075	5047	221	0.075	0.508
	140	0.375		224	0.100	
	143	0.075		227	0.525	
	145	0.075		230	0.075	
	146	0.325		233	0.200	
	149	0.075		236	0.025	
181	156	0.025	0585	154	0.447	
	162	0.175		160	0.211	
	165	0.025		161	0.053	
	168	0.100		164	0.053	
	171	0.300		166	0.026	
	174	0.150		169	0.079	
	177	0.150		170	0.026	
	183	0.050		175	0.079	
	186	0.025		176	0.026	
6212	230	0.306	201	133	0.333	
	233	0.083		134	0.167	
	242	0.167		136	0.583	
	245	0.250		139	0.167	
	248	0.028		141	0.167	
	251	0.111		142	0.167	
	254	0.028		144	0.167	
	260	0.028		147	0.167	
9253	236	0.750	1490	234	0.667	
	238	0.050		246	0.278	
	240	0.200		249	0.056	
1195	200	0.667	187	109	0.179	
	209	0.111		112	0.321	
	212	0.111		115	0.464	
	227	0.111		118	0.036	
207	154	0.125	2637	255	0.125	
	158	0.625		258	0.550	
	161	0.050		261	0.150	
	164	0.075		264	0.025	
	166	0.025		267	0.100	
	167	0.100		269	0.025	
	173	0.025		272	0.025	
182	137	0.025	0007	117	0.025	
	143	0.075		121	0.125	
	152	0.025		129	0.125	
	154	0.050		133	0.025	
	155	0.050		137	0.025	
	157	0.025		141	0.025	
	158	0.025		145	0.050	
	160	0.025		149	0.525	
	161	0.250		153	0.050	
	164	0.075		165	0.025	
	166	0.050	0513	185	0.850	
	167	0.275		191	0.125	
	170	0.025		209	0.025	
	185	0.025				

Table S3. OTUs of the symbionts present within each coral colony tested, as determined by sequencing of the cp23S marker. Numbers correspond to number of reads per exact sequence variant (ESV) ID (arbitrarily assigned by QIIME2). Coral genotypes U23, U30, U37, U40, U44, and U56 are not shown as no cp23S reads were generated for these fragments

	Coral genotype													
Taxonomy	M3	M5	M6	M7	U1	U7	U12	U15	U19	U33	U46	U58	U70	U76
Symbiodinium fitti (nomen novum) A3														
Variant 1	0	4465	0	2702	15343	2006	2932	0	2416	7088	6266	0	2624	3102
Variant 2	0	0	0	0	0	0	0	0	0	0	2922	0	0	0
Variant 3	0	0	0	0	0	0	0	0	0	0	1068	0	0	0
Variant 4	0	0	0	0	560	0	0	0	0	0	0	0	0	0
Variant 5	0	0	0	0	480	0	0	0	0	0	0	0	0	0
Variant 6	0	0	0	27	0	0	0	0	0	0	0	0	0	0
Breviolum	0	0	0	0	0	0	0	2514	0	0	0	282	0	0
Breviolum similar to B1														
Variant 1	6915	0	0	0	0	0	0	0	0	0	0	4165	0	0
Variant 2	0	0	0	0	0	0	0	0	0	0	2112	0	0	0
Variant 3	0	0	0	0	0	0	0	0	0	0	0	4	0	0
Breviolum similar to B2	29	0	0	0	0	0	0	0	0	0	0	0	0	0
Cladocopium	0	0	9	0	7	0	63	0	0	0	0	0	0	0

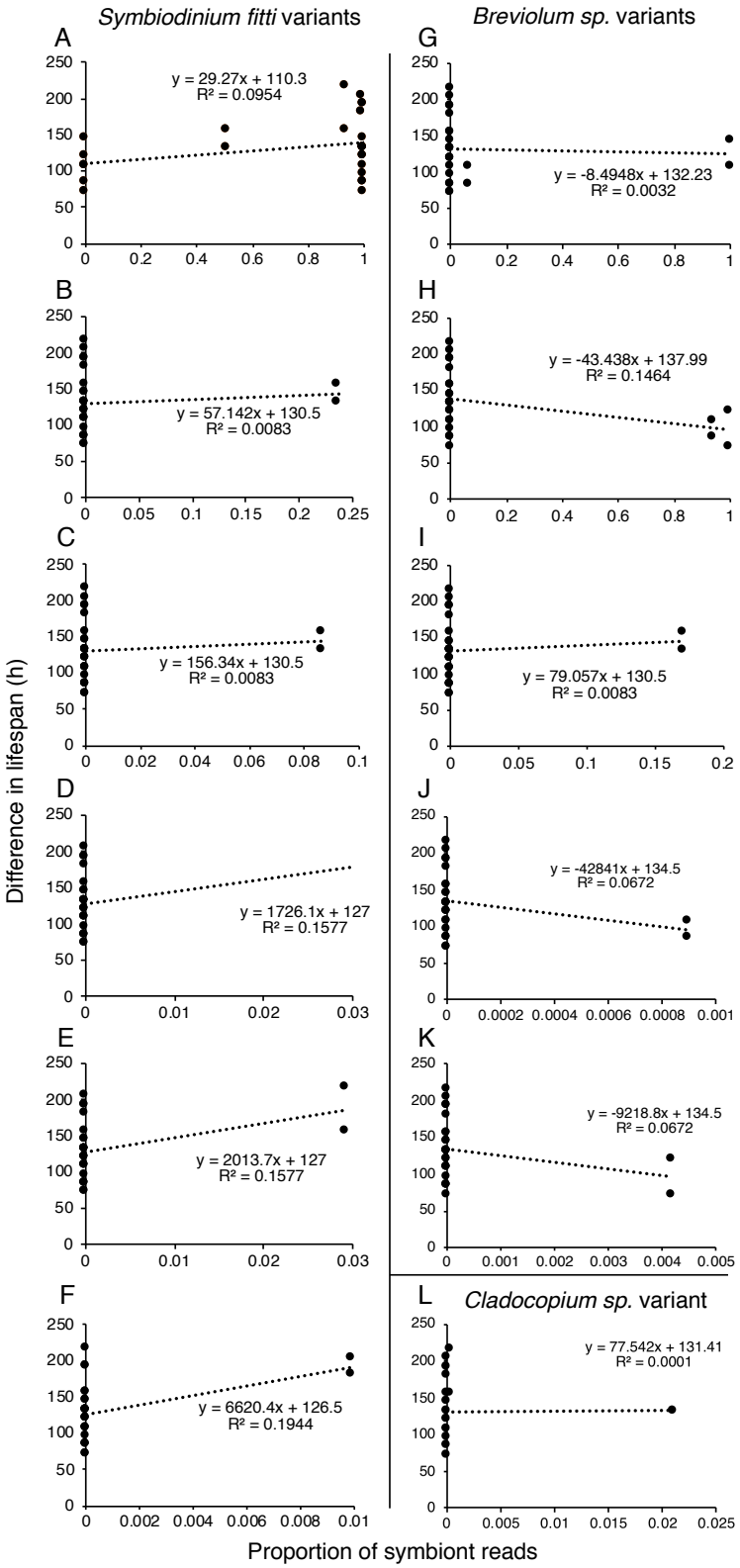

Fig. S1. Linear regressions for different symbiont proportions compared to difference in lifespan (h) for the 13 colonies (2 fragments each, n = 26) for which cp23S reads were able to be amplified. (A - F) *Symbiodinium fitti* variants 1 – 6. (G) *Breviolum*. (H – J) *Breviolum* similar to B1 variants 1 – 3. (K) *Breviolum* similar to B2. (L) *Cladocopium* sp

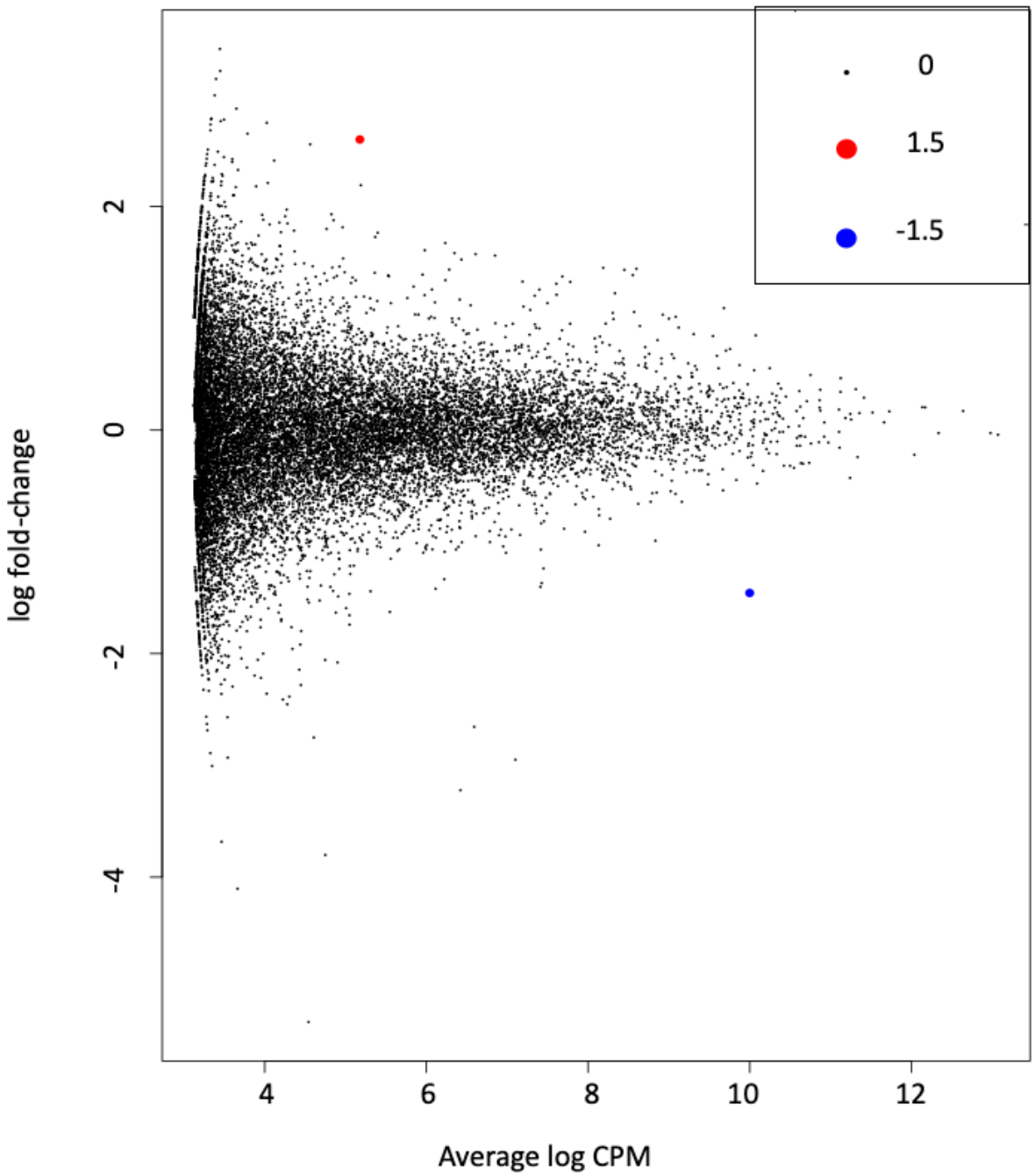

Fig. S2. Fitted model MD plot showing expression changes between heated treatment and ambient temperature samples (n = 18 per group). The $\log_2$ FC for each gene is plotted against the average abundance in $\log_2$ CPM. Red points show genes that are significantly upregulated in heated samples relative to ambient temperature samples, and blue points show genes that are significantly downregulated in heated samples. Significant DE genes were determined using the glmTreat function in R to specify both a $\log_2$ FC cut-off of 1.5 as well as a FDR of 5%

Fig. S3. Heat map across all samples using the 89 significant DE genes between tolerant and susceptible genotypes (n = 18 per group) that were not entirely consistent among genotypes within tolerant and susceptible groupings. Colors range from pink (significantly upregulated in tolerant colonies relative to susceptible colonies) to blue (significantly downregulated in tolerant colonies) and are based on the log CPM. Significant DE genes were determined using the glmTreat function in R to specify both a $\log_2$ FC cut-off of 1.5 as well as a FDR of 5%. Consistent genes were determined by taking each DE and comparing the average control and heated RPKM for each genotype to the average RPKM for that gene for tolerant or susceptible colonies and seeing whether it matched expectations (based on the glmTreat results) for either upregulation or downregulation. Genes are ordered from top to bottom by ascending p-value (3.53e-08 – 1.97e-01)

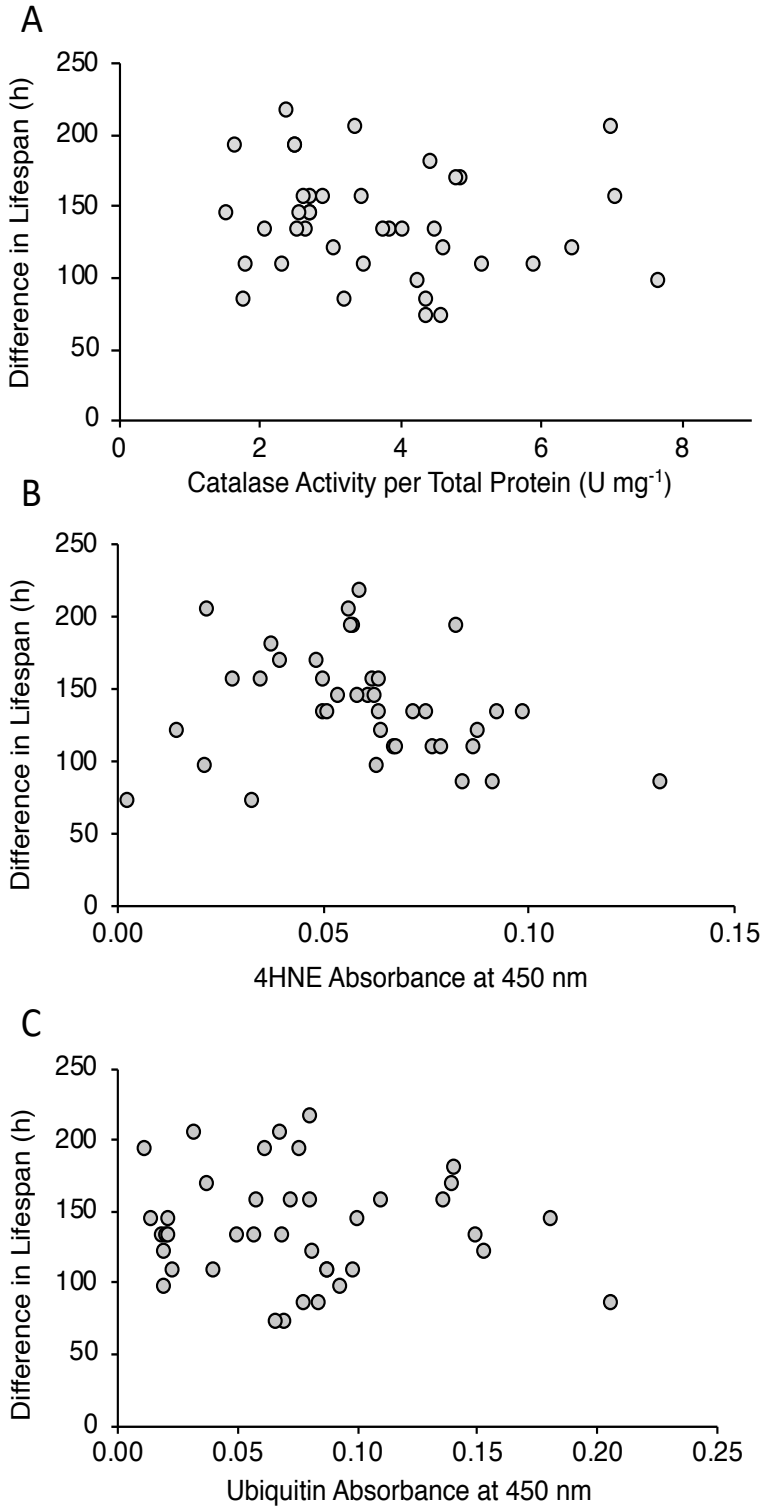

Fig. S4. Correlation analyses showing the association of lifespan differential (control – treatment) of samples from 20 *Acropora cervicornis* genotypes (n = 40) with relative concentration or activity in the heated fragments for the following three stress biomarkers: (A) catalase, (B) ubiquitin, and (C) 4HNE