

**Supplementary information for:**

**Intrapopulation adaptive variance supports selective breeding in a reef-building coral**

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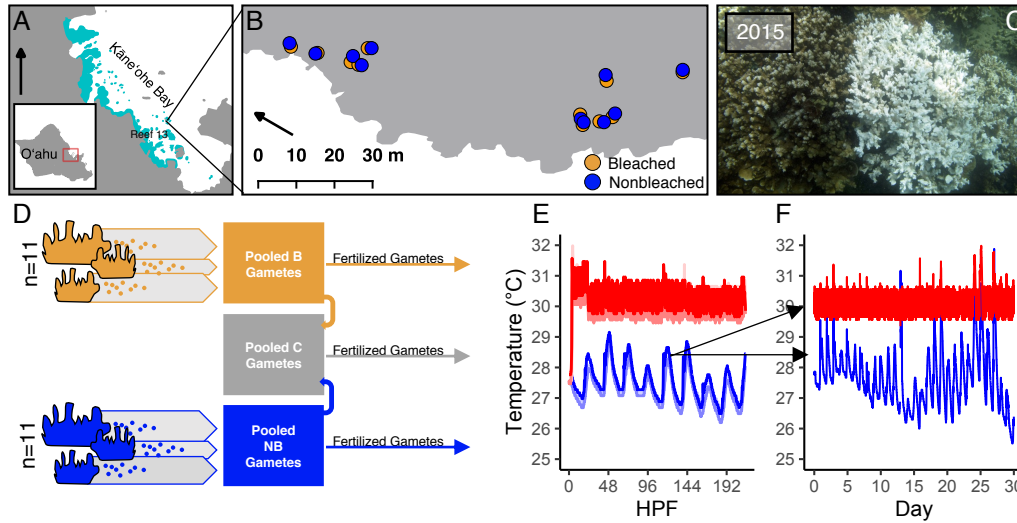
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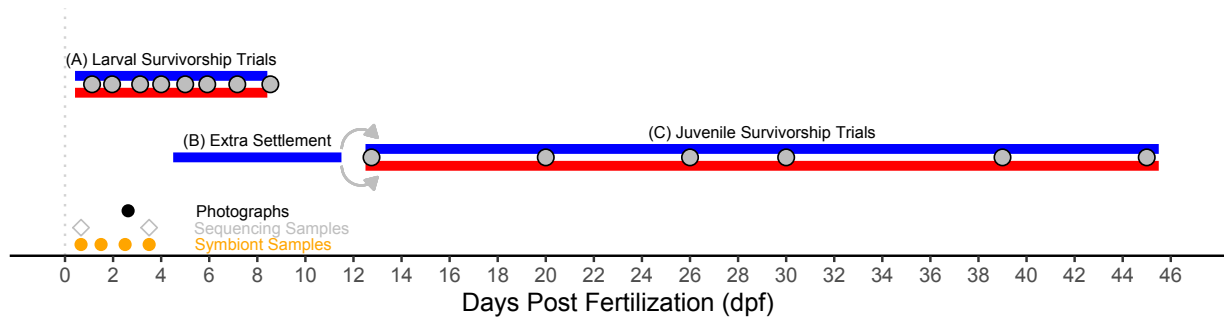
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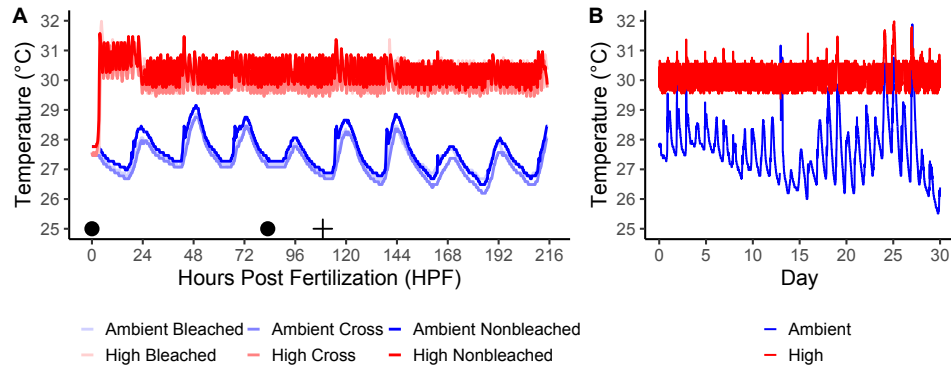
### Supplemental Figure 1 – Site and Experimental Framework

A) Gamete collections were made at Reef 13 in Kāneʻohe Bay, Oʻahu, Hawaiʻi on 13 July 2018. B) Individual colonies were netted for collections using C) pairs identified in the 2015 bleaching event to minimize microhabitat differences and select for parental thermal tolerance. D) Gametes were collected from 11 colonies of each phenotype and used to create pools of all nonbleached gametes and all bleached gametes. The site-wide cross was then created from equal volumes of the bleached and nonbleached pools and all three pools were exposed to E) larval temperature treatments downstream starting 12 hours after fertilization. At 109 hours after fertilization, larvae from all three phenotypes were allowed to settle on preconditioned aragonite plugs for 8 days and then exposed to F) juvenile temperature treatments. See Supplementary Fig. 1-2 for full details. Color scheme maintained in subsequent figures.



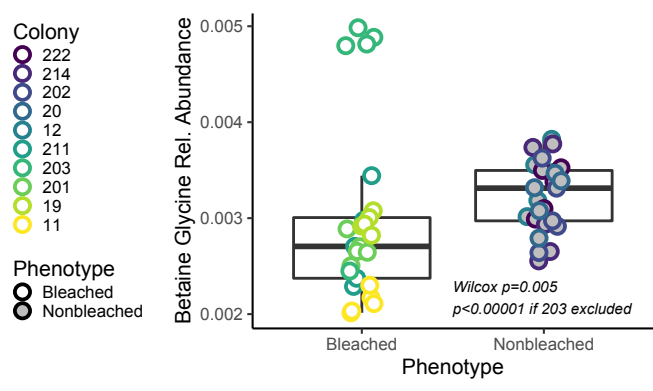
### Supplementary Figure 2 - Experimental Timeline

Timeline in days post fertilization detailing temperature treatments, sequence, and data collection. Blue and red bars represent duration of treatment for larval and juvenile stress tests, with nested gray dots at survivorship survey timepoints. Points correspond to data collection for symbiont samples, larval sequencing and photographs for growth measurements. Briefly, (A) larvae were aliquoted into 50mL tubes for survivorship analysis at two temperatures on 1 dpf. Sequencing samples were collected from larval cultures (not from survivorship aliquots) at 1 and 4 dpf. (B) After final sequencing samples were collected (4 dpf) extra larvae at ambient temperatures were allowed to settle at ambient temperatures without interrupting survivorship aliquots. (C) These settled juveniles were randomly allocated to high and ambient temperatures at 12 dpf and monitored until 45dpf.



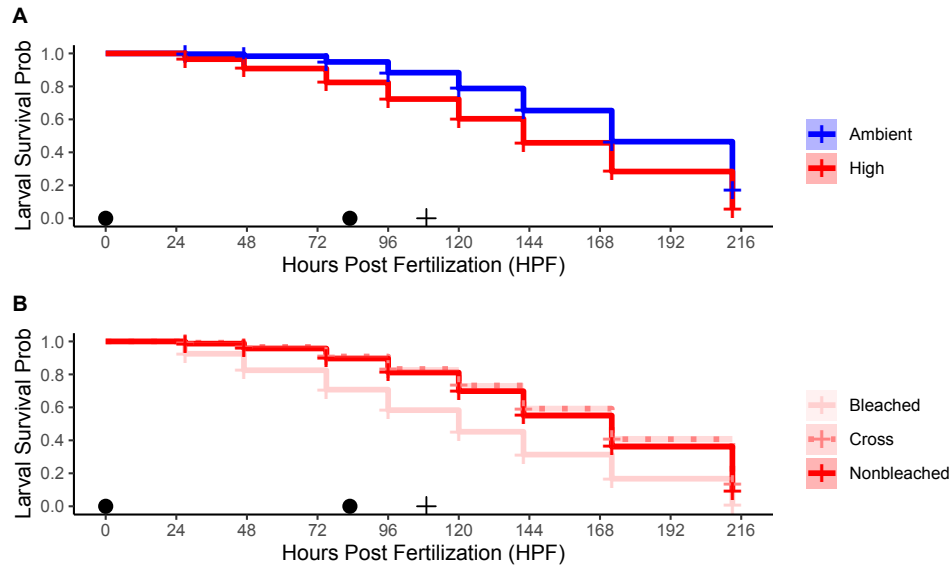
### Supplementary Figure 3 – Temperature Profiles

A) Temperature profiles from each conical during the larval phase. Black circles denote timing of genetics sampling. Cross denotes timing of transfer of remnant ambient larvae to settlement chambers. B) Temperature profiles from each conical during the juvenile phase. Colors correspond to temperature treatment (blue=Ambient, red=High).



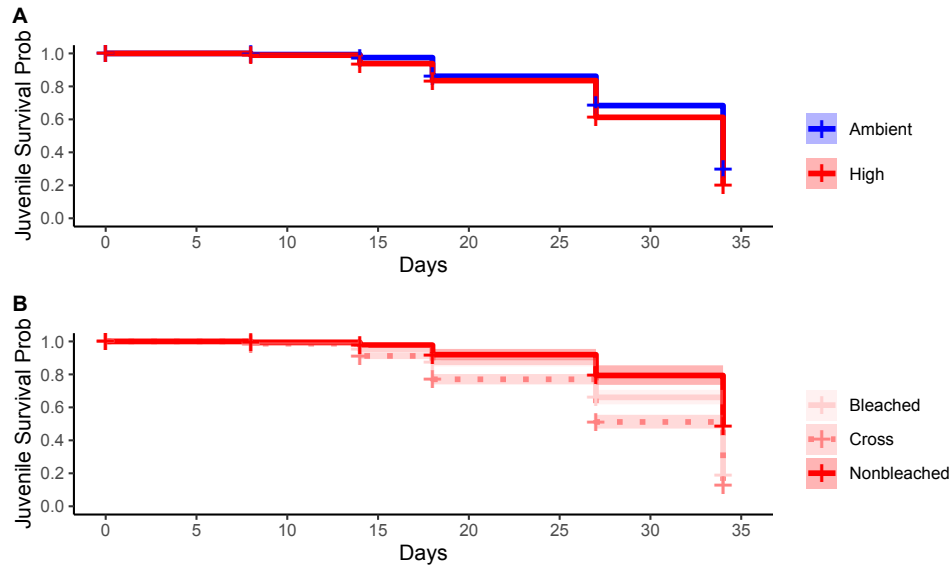
**Supplemental Figure 4 – Betaine Glycine Abundances**

Betaine Glycine abundances from parent colonies in this study.



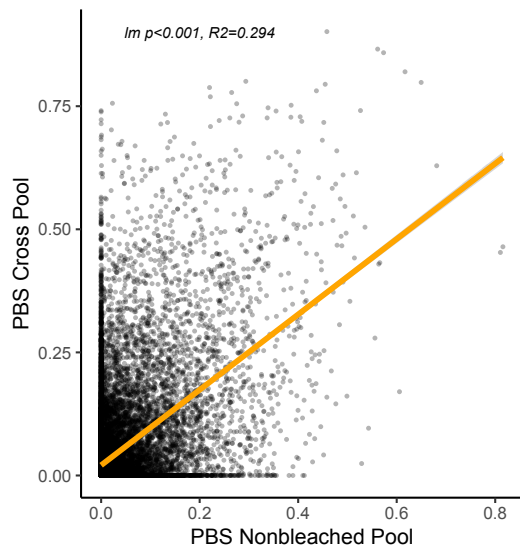
**Supplementary Figure 5 – Survivorship Dynamics of Larval *M. capitata***

A) Probability estimates from Kaplan-Meier larval survivorship fits for each temperature over hours in temperature treatment, line shown with 95% confidence interval shading. B) Probability estimates from Kaplan-Meier larval survivorship fits for each phenotype in high temperature treatment, line is shown with 95% confidence interval shading. Black circles denote timing of genetics sampling. Plus denotes timing of transfer of remnant ambient larvae to settlement chambers. Colors correspond to temperature treatment (blue=Ambient, red=High), transparency corresponds to phenotype.



**Supplementary Figure 6 – Survivorship Dynamics of Juvenile *M. capitata***

A) Probability estimates from Kaplan-Meier juvenile survivorship fits for each temperature over hours in temperature treatment, line shown with 95% confidence interval shading. B) Probability estimates from Kaplan-Meier larval survivorship fits for each phenotype in high temperature treatment, line is shown with 95% confidence interval shading. Black circles denote timing of genetics sampling. Plus denotes timing of transfer of remnant ambient larvae to settlement chambers. Colors correspond to temperature treatment (blue=Ambient, red=High), transparency corresponds to phenotype.



**Supplemental Figure 7**

Correlation of Population Branch Statistic (PBS) for the Cross and Nonbleached pool. PBS represents selection pressure under heat stress at each loci (n=31,794).



**Supplemental Table 1**

PBS calculation framework, comparing heat-selected larval pools of each phenotype to initial and parental pools.  $T = -\log(1-F_{ST})$ , where pairwise  $F_{ST}$  was calculated on a per-site basis for each variant (i.e.,  $T_{FA} = T$  based on pairwise  $F_{ST}$ )

Phenotype	(F) Focal Group	(A) Outgroup A	(B) Outgroup B	Formula
NB	Final Pool (n=250)	Initial Pool (n=250)	Nonbleached Parents (n=11)	$PBS = (T_{FA} + T_{FB} - T_{AB})/2$
B	Final Pool (n=250)	Initial Pool (n=250)	Bleached Parents (n=10)	$PBS = (T_{FA} + T_{FB} - T_{AB})/2$
Cross	Final Pool (n=250)	Initial Pool (n=250)	All Parents (n=21)	$PBS = (T_{FA} + T_{FB} - T_{AB})/2$

**Supplemental Table 2**

SIRIUS 4 parameters used for the *in silico* molecular formula annotations of the mass spectrometry data generated from MZmine 2. Mascot graphical format file (mgf) was imported and processed as follows:

Module	Parameters	
Sirius	Instrument	Orbitrap
	MS <sup>2</sup> isotope scorer:	Score
	MS <sup>2</sup> mass deviation	5 ppm
	Candidates	5
	Databases	Bio database, GNPS, Natural Products
ZODIAC	Default	
CSI: FingerID	Databases	Bio database, GNPS, Natural Products
	Adducts	M+H] <sup>+</sup> , [M+Na] <sup>+</sup> and [M+K] <sup>+</sup>
	Enforce	True
CANOPUS	True	

### Supplemental Table 3

Annotations from individual genes significantly ( $p < 0.01$ ) associated with bleaching phenotype in adults. Black text denotes annotations from megablast, blue text denotes annotations from discontinuous megablast.

locus	gene name	e-value	organism	function	ref
114:270077-1166526(+)_382645	Ethanolamine phosphotransferase 1-like	2e-64	<i>Acropora digitifera</i>	Sphingolipid biosynthesis	25
1142:22067-267875(+)_240011	Ankyrin repeat and zinc-finger domain-containing protein 1-like	2e-12	<i>Acropora digitifera</i>	Immunity	1,32
135:165149-681565(+)_107553	Monocarboxylate transporter 10-like	1e-124	<i>Acropora millepora</i>	Nitrogen cycling; amino acid metabolism	2
16:103141-1930322(+)_88237	Histamine H2 receptor-like	3e-71	<i>Acropora millepora</i>	Immune response	3
175:84843-855127(+)_390354	PAX-C	4e-114	<i>Montipora sp.</i>	Growth/development; host-algal symbiosis regulation	4,5
23:0-1877333(+)_1275116	Neuropeptide SIFamide receptor	8e-37	<i>Orbicella faveolata</i>	Larval migration, settlement, metamorphosis	6,7
2374_33003	18s rRNA	0.0	<i>Montipora verrucosa</i>	Protein synthesis	28
2644:0-29873(+)_8082	Histamine N-methyltransferase-like	0.0	<i>Acropora millepora</i>	Methylation (humans)	8
316:172135-793760(+)_405758	PAX-C	6e-83	<i>Montipora solanderi</i>	Growth/development, host-algal symbiosis regulation	4,5
32:221614-1703322(+)_986481	Histamine H2 receptor-like	2e-38	<i>Acropora millepora</i>	Immune response	3
362:154151-476426(+)_296306	Unknown	2e-24	<i>Acropora millepora</i>	Unknown	-
416:25677-496747(+)_417623	Mucin-like	2e-31	<i>Acropora digitifera</i>	Mucus generation/secretion; DNA damage repair	9,23
462:90630-579403(+)_429238	Octopamine receptor beta-1R-like	3e-73	<i>Orbicella faveolata</i>	Oocyte development/maturation	10

5:218022-2430108(+)_851904	Adenosine receptor A2a-like	2e-93	<i>Acropora millepora</i>	Immune response; inflammation	1,11
50:672149-1522693(+)_465625	Polyubiquitin-C	0.0	<i>Stylophora pistillata</i>	Oxidative stress resistance; protein catabolism	12,29
<a href="#">553:474523-500157(+)_13812</a>	Ribonuclease Y-like	7e-133	<i>Orbicella faveolata</i>	Unfolded protein response	13
<a href="#">615:456522-469093(+)_1880</a>	Plexin-B-like	1e-47	<i>Acropora millepora</i>	Cytoskeleton dynamics; cell adhesion; axon guidance	14,23
69:44661-1355009(+)_72740	Phosphoinositide 3-kinase regulatory subunit 4-like	2e-58	<i>Acropora digitifera</i>	Host autophagy	15
<a href="#">94:79413-1187499(+)_1064347</a>	kelch-like protein diablo	8e-113	<i>Acropora millepora</i>	Oxidative stress response; protein ubiquitination	26,30
chr1_RagTag_22018874	Golgi-associated PDZ and coiled-coil motif-containing protein-like	8e-77	<i>Acropora millepora</i>	Protein binding/transport	16
chr1_RagTag_31003888	Dynein assembly factor 3, axonemal-like	2e-32	<i>Actinia tenebrosa</i>	Cytoskeletal construction; autophagy	17,31
chr10_RagTag_8284035	Putative ankyrin repeat protein RF_0381	1e-49	<i>Dendronephthya gigantea</i>	Immunity	1
chr11_RagTag_4203672	Neurexin	2e-68	<i>Acropora digitifera</i>	Biom mineralization	18
<a href="#">chr11_RagTag_4215008</a>	TFIID subunit 5-like	1e-46	<i>Acropora digitifera</i>	Cell signaling; transcription factor activity; protein binding	21
<a href="#">chr12_RagTag_25257908</a>	Phosphoinositide 3-kinase regulatory subunit 4-like	5e-65	<i>Acropora digitifera</i>	Host autophagy	15
chr2_RagTag_20154540	Tetratricopeptide repeat protein 28	2e-108	<i>Orbicella faveolata</i>	Apoptotic signaling	27
<a href="#">chr4_RagTag_11047240</a>	kelch-like protein diablo	6e-45	<i>Acropora digitifera</i>	Oxidative stress response; protein ubiquitination	26,30

chr4_RagTag_5271 861	Unknown	0.0	<i>Acropora millepora</i>	Unknown	-
chr5_RagTag_1120 7344	Unknown	0.0	<i>Acropora millepora</i>	Unknown	-
<a href="#">chr6_RagTag_1341 1819</a>	Arginine/serine-rich protein PNISR-like	8e-145	<i>Acropora digitifera</i>	Protein synthesis	19
<a href="#">chr8_RagTag_1240 9112</a>	Neurexin	6e-70	<i>Acropora digitifera</i>	Biom mineralization	18
<a href="#">chr8_RagTag_4922 595</a>	Ankyrin repeat and zinc-finger domain-containing protein 1-like	2e-12	<i>Acropora millepora</i>	Immunity	1,32
Sc0000015_RagTag_1507093	E3 ubiquitin-protein ligase MARCH5-like	2e-58	<i>Acropora millepora</i>	<i>Symbiodiniaceae</i> stress response; protein degradation	20,21
Sc0000134_RagTag_502413	Somatostatin receptor type 4-like	3e-160	<i>Acropora millepora</i>	Myoregulatory activity; neural pathways; MAP kinase and adenylate cyclase interactions	22
Sc0000201_RagTag_77657	D-inositol 3-phosphate glycosyltransferase-like	4e-50	<i>Acropora digitifera</i>	Host/algal symbiosis regulation	23
Sc0000204_RagTag_980637	Plexin-B-like	1e-64	<i>Acropora millepora</i>	Cytoskeleton dynamics; cell adhesion; axon guidance	14,23
<a href="#">xpSc0000570_RagTag_25400</a>	Cationic amino acid transporter 1-like	2e-58	<i>Stylophora pistillata</i>	Protein/membrane formation	24

**Supplemental Table 4**

Summary of Gene Ontologies enriched in significantly high LRT values, suggesting functions that are significantly different between adult phenotypes and distinguish bleaching tolerance.

<b>Term</b>	<b>Name</b>	<b>P (fdr)</b>	<b>Category</b>
GO:0006412	translation	0.084	BP
GO:0006476; GO:0035601; GO:0098732	protein deacetylation	0.028	BP
GO:0006518	peptide metabolic process	0.046	BP
GO:0006575	cellular modified amino acid metabolic process	0.045	BP
GO:0018200	peptidyl-glutamic acid modification	0.028	BP
GO:0034334; GO:0034332	adherens junction organization	0.045	BP
GO:0043043	peptide biosynthetic process	0.059	BP
GO:0043603	cellular amide metabolic process	0.085	BP
GO:0070373	negative regulation of ERK1 and ERK2 cascade	0.048	BP
GO:0071333; GO:0009749; GO:0071331; GO:0009746; GO:0034284; GO:0009743; GO:0071326; GO:0071322	cellular response to hexose stimulus	0.077	BP
GO:0090630	activation of GTPase activity	0.085	BP
GO:1901565	organonitrogen compound catabolic process	0.077	BP
GO:1902414	protein localization to cell junction	0.024	BP
GO:1903614; GO:1903613; GO:1904894; GO:0018279; GO:0006487; GO:0018196	protein N-linked glycosylation	0.027	BP
GO:0031902	late endosome membrane	0.099	CC
GO:0000287	magnesium ion binding	0.094	MF
GO:0003735	structural constituent of ribosome	0.094	MF
GO:0003887; GO:0004523; GO:0016891	DNA-directed DNA polymerase activity	0.094	MF
GO:0004177; GO:0008238; GO:0070006; GO:0008235	exopeptidase activity	0.094	MF

GO:0004190; GO:0070001	aspartic-type endopeptidase activity	0.094	MF
GO:0008138	protein tyrosine/serine/threonine phosphatase activity	0.093	MF
GO:0008199; GO:0004322; GO:0016724; GO:0016722	ferric iron binding	0.094	MF
GO:0016758; GO:0016757	transferase activity, transferring glycosyl groups	0.093	MF
GO:0017016; GO:0031267	small GTPase binding	0.094	MF
GO:0017048	Rho GTPase binding	0.094	MF
GO:0030144; GO:0140103; GO:0030145; GO:0004864; GO:0019212	protein phosphatase inhibitor activity	0.093	MF
GO:0051020	GTPase binding	0.028	MF
GO:0070851; GO:0005138	growth factor receptor binding	0.094	MF

**Supplemental Table 5**

Summary of Gene Ontologies enriched in significantly low LRT values, suggesting functions that are significantly similar between adult phenotypes and do not distinguish bleaching tolerance.

<b>Term</b>	<b>Name</b>	<b>P (fdr)</b>	<b>Category</b>
GO:0001667	ameboidal-type cell migration	0.048	BP
GO:0001932; GO:0042325	regulation of phosphorylation	0.037	BP
GO:0002252; GO:0051607; GO:0009615	immune effector process	0.045	BP
GO:0002376	immune system process	0.077	BP
GO:0008037	cell recognition	0.077	BP
GO:0008202	steroid metabolic process	0.006	BP
GO:0009605	response to external stimulus	0.077	BP
GO:0009888	tissue development	0.070	BP
GO:0009952	anterior/posterior pattern specification	0.051	BP
GO:0010035	response to inorganic substance	0.045	BP
GO:0010038	response to metal ion	0.084	BP
GO:0010557; GO:0010628; GO:0031328; GO:0009891	positive regulation of gene expression	0.054	BP
GO:0010638	positive regulation of organelle organization	0.048	BP
GO:0016192	vesicle-mediated transport	0.027	BP
GO:0019827; GO:0098727	stem cell population maintenance	0.048	BP
GO:0022604	regulation of cell morphogenesis	0.056	BP
GO:0030278	regulation of ossification	0.077	BP
GO:0030517	negative regulation of axon extension	0.095	BP
GO:0031122	cytoplasmic microtubule organization	0.070	BP
GO:0043207; GO:0009607; GO:0051707	response to biotic stimulus	0.029	BP
GO:0045087	innate immune response	0.045	BP
GO:0045596	negative regulation of cell differentiation	0.044	BP
GO:0045597	positive regulation of cell differentiation	0.092	BP
GO:0045859; GO:0043549; GO:0051338	regulation of transferase activity	0.008	BP
GO:0045926	negative regulation of growth	0.083	BP
GO:0045944	positive regulation of transcription by RNA polymerase II	0.045	BP
GO:0050685	positive regulation of mRNA processing	0.085	BP



GO:0050793	regulation of developmental process	0.056	BP
GO:0051093	negative regulation of developmental process	0.024	BP
GO:0051094	positive regulation of developmental process	0.070	BP
GO:0051128	regulation of cellular component organization	0.020	BP
GO:0051130	positive regulation of cellular component organization	0.028	BP
GO:0051240	positive regulation of multicellular organismal process	0.026	BP
GO:0051241	negative regulation of multicellular organismal process	0.027	BP
GO:0051704	multi-organism process	0.045	BP
GO:0051965; GO:0051963	regulation of synapse assembly	0.085	BP
GO:0070988	demethylation	0.029	BP
GO:0070989	oxidative demethylation	0.006	BP
GO:0071360; GO:0071359; GO:0009597; GO:1900246; GO:0039535; GO:0039531; GO:0032481	cellular response to dsRNA	0.024	BP
GO:0090068; GO:0045787	positive regulation of cell cycle	0.084	BP
GO:0005783	endoplasmic reticulum	0.099	CC
GO:0048786	presynaptic active zone	0.099	CC
GO:1990909; GO:1990851	Wnt signalosome	0.099	CC
GO:0005509	calcium ion binding	0.094	MF
GO:0008395; GO:0070330; GO:0016712; GO:0032451; GO:0101020; GO:0008401; GO:0050649	aromatase activity	0.009	MF
GO:0015026; GO:1904928; GO:0071936; GO:0042813	coreceptor activity	0.094	MF
GO:0020037; GO:0046906	tetrapyrrole binding	0.094	MF
GO:1990837; GO:0003690; GO:0043565	double-stranded DNA binding	0.093	MF

**Supplemental Table 6**

Results from pairwise comparisons of Likelihood Ratio tests between larval Kaplan-Meier survivorship fits for each Phenotype~Temperature combination. A=Ambient, H=High, B=Bleached, C= Site-Wide Cross, NB= Nonbleached.  $p < 0.05^*$ ;  $p < 0.01^{**}$ ;  $p < 0.001^{***}$

	AB	AC	ANB	HB	HC	HNB
Ambient Bleached						
Ambient Cross	***					
Ambient Nonbleached	ns	*				
High Bleached	***	***	***			
High Cross	***	**	***	***		
High Nonbleached	***	***	***	***	***	

**Supplemental Table 7**

Results from pairwise comparisons of Likelihood Ratio tests between juvenile Kaplan-Meier survivorship fits for each Phenotype~Temperature combination. A=Ambient, H=High, B=Bleached, C= Site-Wide Cross, NB= Nonbleached.  $p < 0.05^*$ ;  $p < 0.01^{**}$ ;  $p < 0.001^{***}$

	AB	AC	ANB	HB	HC	HNB
Ambient Bleached						
Ambient Cross	***					
Ambient Nonbleached	ns	***				
High Bleached	***	ns	**			
High Cross	***	**	***	***		
High Nonbleached	ns	***	ns	***	***	

**Supplemental Table 8**

Summary of Gene Ontologies enriched in significantly high differences between PBS in nonbleached and cross corals, isolating functions that are selected significantly more strongly in nonbleached corals and highlighting effects of selective breeding.

<b>Term</b>	<b>Name</b>	<b>P (fdr)</b>	<b>Category</b>
GO:0032230	positive regulation of synaptic transmission, GABAergic	0.035	BP
GO:0032849; GO:0032847	regulation of cellular pH reduction	0.035	BP
GO:0004712	protein serine/threonine/tyrosine kinase activity	0.040	MF
GO:0043812; GO:0034596	phosphatidylinositol phosphate 4-phosphatase activity	0.040	MF
GO:0015491; GO:0015298	cation:cation antiporter activity	0.054	MF
GO:0008307	structural constituent of muscle	0.062	MF
GO:0016209; GO:0004601; GO:0016684	antioxidant activity	0.062	MF
GO:0022821; GO:0008273	potassium ion antiporter activity	0.083	MF
GO:0032160	septin filament array	0.084	CC
GO:0097733	photoreceptor cell cilium	0.084	CC
GO:0150051	postsynaptic Golgi apparatus	0.084	CC
GO:0006900	vesicle budding from membrane	0.090	BP
GO:0032228	regulation of synaptic transmission, GABAergic	0.090	BP
GO:0038083	peptidyl-tyrosine autophosphorylation	0.090	BP
GO:0051453; GO:0030641; GO:0006885; GO:0030004	regulation of pH	0.090	BP
GO:0051592	response to calcium ion	0.090	BP
GO:0060402; GO:0060401; GO:0097553	cytosolic calcium ion transport	0.090	BP
GO:2001225	regulation of chloride transport	0.090	BP

## Supplemental References

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