Supplementary Materials: Methods and supplements

Selecting Colonies & Transplant site

We selected 80 coral colonies (henceforth called parent colonies) representing four species that were identified based on morphology: *Acropora gemmifera*, *Acropora hyacinthus* (cryptic species HE in Ladner & Palumbi 2012 [1]), *Pocillopora damicornis*, and *Porites cylindrica*. Colonies were within the National Park of American Samoa (14˚11'S, 169˚36'W) and ten of each species were selected from the Highly Variable Pool or the HVP (Pool 300 in [2]) while the remaining ten for each species were selected from the Moderately Variable Pool or the MVP (Pool 400 in [2]). Colonies spanned an area of 0.2 square kilometers in the HVP and 0.3 square kilometers in the MVP and spread from crest to near shore at depths ranging from less than 0.3m at low tide to 2-3m. In addition to spatial distribution, colonies were selected based on size such that sampling never exceeded 10% of the colony. Colonies of *Acropora* ranged in size from 35cm to 120cm diameter, colonies of *Pocillopora* ranged in size from 30cm to 80cm, and colonies of *Porites* ranged in size from 45cm to 200cm. All colonies were tagged, photographed, measured, and recorded at their latitude and longitude to the fifth decimal place. A subset of colonies (~50) had long-term temperature loggers collecting data every ten minutes to half hour.

The transplant site was selected within the proposed Sili region based on its depth (>3' at low tide) and accessibility. Since no suitable substrate was available to tie down the crates, a local construction crew helped create cement pallets to hold crates in the transplant site. Ten pallets were set up in pairs from shore to crest spanning less than 0.1 square kilometer. Pallets were designed to hold one replicate of all 80 colonies with a temperature logger collecting data every ten minutes.

Creating nubbins & transplanting

We cut ten small fragments (~3cm in length, all 4g±1g), hereafter nubbins, from each of the 80 parent colonies in their native environments. The nubbins were glued underwater to nylon bolts using two-part underwater epoxy. Nubbins recovered in their native environment for up to 1 week and were then redistributed so all colonies from a single species were represented on one crate (20 colonies per crate x 4 species x 10 replicates = 800 nubbins across 40 crates). Each nubbin was photographed and buoyant weighed for baseline growth data.

Once the 40 crates had recovered in their native environments, crates were relocated to our selected transplant site. Crates were moved across the island in 40-gallon bins of seawater and were zip-tied down onto the ten replicate pallets at the transplant site.

We tested multi-locus-genotypes for the three species that bleached and found all parents to be different genotypes in *Acropora hyacinthus*. For *Acropora gemmifera* there were 18 genets among 20 parent colonies. And for *Pocillopora damicornis*, there were 11 genets among 20 parent colonies. Parent colonies are used in analysis for three reasons: they represented wild colonies experiencing different acclimatization histories, they allowed

us to test the tolerance of a nursery established without genotyping, and in the case of *Pocillopora damicornis*, they represented different combinations of coral clone and dominant symbiont type.

Remote & field monitoring

Photographs were taken of the transplanted corals approximately every week to assess survival, predation, and physiological responses to environment. From these photos, coral nubbins were categorized into four classes: alive (any pigmented and unwounded tissue); predated (visible wound); dead (complete algae cover over skeleton); missing (removed from crate via predation event).

Predation was most extensive on *Pocillopora damicornis* however also present in *Acropora hyacinthus*. Predation was nearly absent in *Porites cylindrica* and *Acropora gemmifera*, potentially due to skeletal density and size of branches. Due to the overall faster growth rate and healing of the *Acropora* species, predation had a much stronger impact on survival of *Pocillopora damicornis* than on survival of *Acropora hyatinus*. We were unable to detect a signal of predation by predicted resilience or by genotype (ANOVA $p > 0.05$) indicating an overall average impact on predation for growth rates and performance during the bleaching event.

We also included three additional field seasons (Dec 2014, April 2015, and August 2015) to measure growth via buoyant weight, assess experimental stress tolerance, and exchange temperature loggers. Data are included in Dataset S2.

Characterizing proxies of resilience

Three simple environmental and physiological proxies of bleaching tolerance were measured at the nursery's establishment. One proxy was habitat of origin: the Highly Variable Pool (or the HVP) experiences more frequent heat extremes above 34°C whereas the Moderately Variable Pool (or the MVP) rarely experiences temperatures above 33°C (Figure 1a and Figure 3a) [2]. The second proxy was based on the time spent above 31˚C for each parent colony, measured directly by thermo-logger or interpolated from nearby loggers over one austral summer (see *Interpolating temperature data for microclimate characterization*). The third proxy was derived from specific tests of heat tolerance for each colony assessing physiological response from a standard lab-induced heat stress administered by a portable tank (see *characterizing experimental stress performance*). The tank is inexpensive and is deployable in remote locations. In addition to these three proxies, we also assessed the symbiont clade in each colony because clade D symbionts are thought to be much more thermally tolerant than co-occurring clade C symbionts [3]. Finally we assessed biomarkers for thermal tolerance, based on genotypes at multiple loci identified as candidate heat-tolerance alleles by Bay and Palumbi 2014 [4] and a single SNP marker developed by Jin et al. 2016 [5] (see *Determining biomarkers*).

Interpolating temperature data for microclimate characterization

Temperature loggers collecting data at ten-minute intervals were placed to cover the extent of the microhabitats for parent colonies. For colonies that did not have temperature

loggers, temperature was interpolated using an Inverse Distance Weighting algorithm and temperature was sampled for each colony from the raster surface. For the duration of the austral summer (December 2014-April 2015), we counted each observation above 31˚C (the nominal bleaching temperature for the region [4] as well as the 95th percentile of the temperature distribution) and ranked each colony within species from hottest (most time points above 31˚C) to coolest. We selected time points spent above 31˚C, though the integral of time above 31˚C had a high correlation (cor = 0.99, $p < 2e\text{-}16$) to time spent above 31˚C. Two colonies in the MVP (SU09 and SU10) did not have temperature data during the summer evaluated and were not near other loggers (>0.1 km). They were excluded from the temperature analysis. Data of time spent above 31˚C for each parent colony are included in Dataset S1.

Characterizing experimental stress performance

For each species, we first determined the T50 or the temperature at which 50% of the bleaching response occurred after a three-hour ramp from control temperatures (29˚C) to the high temperature and a three hour hold at the high temperature. The established T50 temperature for *Acropora hyacinthus* for this region is 34˚C. We established the T50 for the other three species by testing four fragments at control temperatures of 29˚C and two to four fragments across multiple ramps with high temperatures ranging from 33˚C to 37˚C. The T50 temperatures were established as 34˚C for *Acropora hyacinthus*, 35˚C for *Acropora gemmifera* and *Pocillopora damicornis*, and 36˚C for *Porites cylindrica*.

Once we established the T50, we collected eight ~3cm pieces of live coral fragment from each parent colony and placed them in our stress assay tanks. Tanks had constant flow-through at 1 ml/s, had no more than 12 fragments of coral per test, and had standardized light conditions of 700uE set on a 12-hour light/dark cycle. We kept four samples per colony at a constant 29˚C as a control and exposed four samples per colony to a three-hour ramp from 29˚C to the species-specific T50 followed by a three-hour hold at the species-specific T50 followed by a return to baseline 29˚C. We allowed fragments to recover in tanks overnight.

All samples were assessed for visual bleaching the following morning and were placed into 95% ethanol to extract chlorophyll. Chlorophyll was measured using spectrophotometric analysis [6] and was standardized based by the surface area of each sample measured using the wax-dip method [7]. Resilience was calculated by measuring the chlorophyll retained by dividing the average chlorophyll of heat-stressed samples by the average chlorophyll of control samples.

This established our baseline experimental stress tolerance in August of 2015 (end of the austral winter) and foundation for predicted resilience from the experimental stress assay. Coral were then ranked within species from highest chlorophyll retention (most tolerant) to lowest. Data chlorophyll retained and standard deviation for each parent colony is included in Dataset S1.

***Determining unique genotypes for* Acropora *and* Pocillopora**

Genetic samples were collected for parent colonies, all 20 *Acropora gemmifera,* all 20 *Pocillopora damicornis,* and 3 *Acropora hyacinthus* in August of 2014 or April of 2015. The remaining 17 colonies of *Acropora hyacinthus* had previously been identified and classified as unique in Bay & Palumbi 2014 and Palumbi et al. 2014. RNA libraries were created for the 43 parent colonies and were sequenced on two Illumina HiSeq lanes and subsequently mapped to de novo transcriptomes for each respective species. High quality SNPs (called in all individuals, MAF > 0.05, and overall QUAL > 30, genotype quality GQ > 20) were called using FreeBayes and 23,721 SNPs for *Acropora gemmifera* and 22,481 SNPs for *Pocillopora damicornis* were analyzed using separate principle components analysis. A threshold of 0.1 of relatedness across SNPs for each species was used to call clonal or highly similar genotypes. Most of the clones existed among *Pocillopora damicornis* with 20 colonies collapsing to 11 genotypes. In *Acropora gemmifera*, 20 colonies collapsed to 17 colonies. There were no identical parents in *Acropora hyacinthus*. The identification of unique genotypes allowed us to test the relative contributions of the host to bleaching and recovery during the bleaching event. VCF files will be available on the SRA.

To determine the proportion of bleaching explained by host, origin, species, crate, and symbiont, we utilized the genotype identity to group replicates. To determine the correlation between bleaching severity in the nursery and in the native lagoons, we averaged bleaching severity across all clonal replicates. Finally, to determine effects of predation, bleaching severity, and host identity on survival, we used the genotype identity to group replicates.

Determining biomarkers

Biomarker SNPs were tested using RNA-Seq transcriptome data for *Acropora hyacinthus* and *Acropora gemmifera*. For *Acropora hyacinthus*, 14 transcriptome libraries were previously part of the characterization of biomarker environmental correlates of thermal tolerance (Bay & Palumbi 2014 [4], available through NCBI with BioProject accession PRJNA379450). The additional 3 transcriptomes for AH150, AH151, and AH152, and the 20 parent transcriptomes of *Acropora gemmifera* used for determining unique genotypes (previous section) were used for testing biomarkers. Each colony was treated independently (not aggregated into clonal group) since biomarkers may be tested blind of the underlying host genotype.

For the 114 SNPs across 92 contigs established by Bay & Palumbi 2014 [4], libraries from *Acropora hyacinthus* and *Acropora gemmifera* were mapped directly onto the 92 *Acropora hyacinthus* contigs with BowTie2 (-very-sensitive, bSq > 10). SNPs were called using FreeBayes (--use-best-n-alleles 3) and filtered with vcffilter (-f "TYPE = snp & QUAL > 30" –g "GQ > 20"). In *Acropora hyacinthus*, for each library, we calculated the fraction of candidate loci (22 of 114 SNPs where all individuals were called at that loci) where the individual has at least one minor allele (comparable calculations for other *Acropora hyacinthus* individuals are located in supplementary table S2 of Bay & Palumbi 2014 [4]). All new calculations were generated for *Acropora gemmifera* for the 23 of 114 SNPs called in all 20 individuals. Minor Allele Frequencies are included in Dataset S3.

We then ranked parent colonies by species and then by their Minor Allele Frequencies. We took the top half with the highest proportion of the minor allele (predicted resilient) and compared a nursery constructed with best performers from the biomarker assay to a nursery with best performers from our three proxies (Supplemental figure 5).

For the Jin et al. 2016 genotype [5], we mapped *Acropora hyacinthus* and *Acropora gemmifera* directly onto the EZ013402.1 *Acropora millepora* sequence with BowTie2 (--very-sensitive, bSq > 10). SNPs were called with FreeBayes and filtered with vcffilter (--use-best-n-alleles 3 | -f "TYPE = snp & QUAL > 30" –g "GQ > 20"). The genotype was called at position 1054 (biomarker C70S236 with probe 5' GTACTTTTATGACGcGCTAAATGCATGACTT 3') [8]. Genotypes are included in Dataset S3.

Determining symbiont genus

Symbiont genus was characterized in three ways in this study: 1) gel-based identification of the cp23s region for genus-level characterization of parent colonies across multiple time-points, 2) mapping of transcriptome sequences to a ~260 bp region of the ITS2 marker for species characterization, and 3) *de novo* analysis of 579 SNPs across the entire symbiont transcriptome for variant characterization within species.

Transcriptomes were generated for 17 *Acropora hyacinthus* colonies, 20 *Acropora gemmifera* colonies, 20 *Pocillopora damicornis* colonies, and 3 *Porites cylindrica* colonies. To map to the ITS2 region, 176 Genbank accessions of ITS2 were taken for known symbiont species from Correa and Baker 2009 [9]. Sequences were downloaded, aligned, and trimmed to an approximately ~260bp region across all subclades. Duplicate sequences were removed and the first accession of a unique haplotypes as established by Correa and Baker 2009 was used in the final FASTA. This left 107 sequences, 100 belonging to genus *Cladocopium* and 7 belonging to genus *Durusdinium*. Untrimmed and unclipped FASTq libraries for each transcriptome were mapped with bowtie2 (-very-sensitive) to these 107 ITS2 regions with an average of 290 reads mapping at least one time across all libraries and 99% of reads mapping more than once (indicating non-specific mapping to subclades). Reads were then filtered for mapping quality (-q 10) leaving very few reads for each parent colony (average of 16 reads, median of 3 reads). Across all libraries, 96% of reads were predominantly distributed in four symbiont species (*Cladocopium* C3k, C1d, and C15 and *Durusdinium* D1 (= *trenchii*)). Of these, *Cladocopium* C3k mapped only to symbionts in *Acropora* colonies (20 libraries successfully mapped at least one read, all were *Acropora*), *Cladocopium* C1d mapped predominantly to *Pocillopora* (7 libraries successfully mapped at least one read, 6 of these were *Pocillopora*), *Cladocopium* C15 mapped to only *Porites* (5 libraries successfully mapped at least one read, all were *Porites*), and D1 mapped to both *Acropora* and *Pocillopora* (19 libraries successfully mapped at least one read, 9 were *Pocillopora* and 10 were *Acropora*). These preliminary findings indicate that mapping transcriptome libraries to the ITS2 region distinguishes species within genus *Cladocopium,* but may not be as revealing for genus *Durusdinium* [10].

To further elucidate patterns of sub-clade differences in symbionts within and between species of coral, transcriptomes were mapped with bowtie2 (very-sensitive-local) to the *S. microadriaticum* [11] reference transcriptome on ReefGenomics.org. Symbiont transcripts in this study represent the entire population of symbionts in the homogenized tissue. As such, a Single Nucleotide Polymorphism or "SNP" defined in this analysis actually represents the population level polymorphism for a given colony. SNPs were called on high quality reads (-q 10) using FreeBayes (--genotype-qualities --use-best-n-alleles 3) and SNPs were filtered for high quality SNPs with a MAF of 0.05 ("TYPE = snp & QUAL > 30 & AF > 0.05 & AF < 0.95 & NUMALT = 1") called in all coral individuals. This left 579 SNPs called across all colonies. These 579 SNPs were then plotted in a Principal Component Analysis to determine clustering of groups of colonies based on their symbionts.

The first Principal Component axis (Supplemental Figure 6) explained 75.6% of the total variance and separated the colonies with predominately genus *Durusdinium* from predominately genus *Cladocopium* colonies with mixed populations in the center. The second Principal Component axis explained 5.1% of the variance and separated by coral genera for both the genus *Cladocopium* and genus *Durusdinium* symbionts. This indicates sub-clade specialization of symbiont type by genera in not only genus *Cladocopium* but additionally genus *Durusdinium* symbionts. The first two Principal Component axes were significantly correlated to the bleaching outcome in the common gardened nursery (the first axis Pearson's correlation of 0.57 and p-value of 2.4e-6, the second axis Pearson's correlation of 0.38 and p-value of 2.7e-3) though this was mostly representative of the correlation between symbiont genus (axis one) and coral genera (axis two). After the first two axes, none of the axes explaining more than 1% of the variance significantly correlated with bleaching outcome in the common gardened nursery.

We also tested symbiont type throughout the experiment using the cp23 marker and a gel-based assay to determine the relative proportions of symbiont genera. Baseline *Symbiodinium* types were used based on samples collected from parent colonies in August of 2014. Genomic DNA was extracted from skeleton fragments used in chlorophyll analysis for one replicate of each genotype. The 23s ribosome in the chloroplast (cp23s, 23S4F: 5'– GACGGCTGTAACTATAACGG–3'; 23S7R: 5'– CCATCGTATTGAACCCAGC–3') was amplified for the two main genera of symbionts present in American Samoa. A 99 base pair insertion in the genus *Durusdinium* sequence allowed for gel-based classification symbionts. If bands for only genus *Cladocopium* were present, the fragment was categorized as C (1). If bands for only genus *Durusdinium* were present, the fragment was categorized as D (5). If both bands were present, the colony was characterized by C-dom (2), mixed (3), or D-dom (4) based on visual densitometry. Data are included in Dataset S1.

Symbiont type was calculated for all parent colonies at the start of the experiment. Symbiont type was also recorded for the parent colonies of *Pocillopora damicornis* and *Acropora gemmifera* in April of 2015, while corals were visually bleached. There was

insufficient sample of *Acropora hyacinthus* to record symbiont type for all individuals at that time point. Thus, symbiont type was recorded for parent colonies in August 2015. Parent colonies were considered 'switchers' if they moved two or more categories (i.e. from C to mixed or from D-dom to C-dom) between the baseline time point and the time point after warming stress.

Because we had symbiont type characterized by the gel assay and transcriptomes for colonies at a given time point, we were able to validate gel-based genus-level symbiont classifications with transcriptome data. For *Acropora gemmifera*, we had all twenty transcriptomes collected during April of 2015. From separate samples collected in the same field season, we characterized the cp23s gel-based genus-level symbiont classifications. We took the untrimmed and unclipped *Acropora gemmifera* libraries and mapped them with bowtie2 (--very-sensitive) to two ITS2 regions and the cp23s region for genus C and genus D (fasta included in supplement). We took high-quality mapped reads (-q 10) and then averaged the portion of mapping to genus D across the three markers. We correlated the portion of genus D with the numeric classification (1 as C, 2 as C-dom, 3 as mixed, 4 as D-dom, 5 as D) from the gel assay. The resulting correlation (Supplementary Figure 7) shows a highly significant 0.98 correlation ($p = 7.7e-15$). This finding demonstrates that the transcriptome symbiont classification and gel-based classifications are highly correlated.

Calculating maximum bleaching in the nursery

From weekly photos of the transplants, we were able to assess the severity of bleaching through visual categorization of each nubbin into eight classes: 100% pigmented, 80% pigmented, 60% pigmented, 40% pigmented, 20% pigmented, 0% pigmented, dead, or not evaluated. Categories represent average bleaching integrated across the entire colony. In 2015, eleven time points spanning 200 days were included in this analysis to cover the extent of the bleaching event. For each crate at each time point, each nubbin was evaluated blind of its location. This analysis was repeated three times. Across the triplicate assessment, the median category was chosen for each time point (bleaching scores for a single nubbin never ranged more than three bleaching categories). A final 'maximum' score was calculated for each nubbin across the 11 time points, representing the most severe bleaching observed, prior to mortality if mortality occurred. Data are included in Dataset S2.

For the 2017 bleaching event, one set of photographs was collected on March 8, 2017 by collaborators at the Department of Marine and Wildlife Resources. Nubbins were scored for bleaching severity three independent times and the median category was chosen for each nubbin (bleaching scores for a single nubbin never ranged more than two bleaching categories). Since we did not have a time series, we compared the 2015 event by selecting a single time point from the eleven recorded assessments across the 200 days of bleaching in 2015. We calculated average bleaching scores for each species at each time point and selected the time point with the most similar bleaching profile (May 9, 2015). Data for bleaching on May 9, 2015 and March 8, 2017 are included in Dataset S1.

Calculating bleaching scores for parent colonies

During the April 2015 field season, photographs and field visual bleaching data were collected. The same classifications of bleaching used in the nursery were used for the parent colonies. Visual bleaching was a consensus between two independent observations of bleaching severity and was integrated across an entire colony head. Data are included in Datase1.

Calculating survival

Survival was evaluated as the final binary state of the 800 nubbins after the one-year project – alive or dead (no live tissue, algae covered). Dead nubbins were categorized into dead or dead after bleaching where the latter was observed to have a lowest bleached score of 40% or greater prior to its death. Data are included in Dataset S2.

Calculating growth

Nubbin size was roughly standardized to 3.8±0.5g in buoyant weight including epoxy and bolt. To account for variability in starting weight, we scaled all subsequent measures to starting weight. Baseline weight was measured in August of 2014. Additional weight was measured in December of 2014, April of 2015, and August of 2015. A pre-bleaching growth period was calculated using the difference in scaled weight between December 2014 and August 2014 (5 months). A post-bleaching growth period was calculated using the difference in scaled weight between August 2015 and April 2015 (5 months). Fragments from DA03 were removed from growth analysis due to its outlier growth effects.

Comparing bleaching temperatures in Sili to average temperatures in the HVP and the MVP

The National Park Service provided data for temperature from 1999-2015. Temperature loggers recorded by the National Park Service were constitutively 0.33±0.14˚C lower than average temperature recorded by our loggers in the same lagoons for the same period (12,239 points for the HVP and the MVP recorded every half hour over eight and a half months). This constitutive difference is likely due to differences in temperature sensors. Temperatures in Sili were shifted 0.33˚C to be comparable to long term Park data.

Supplemental material references

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2. Craig, P., C. Birkeland, and S. Belliveau, *High temperatures tolerated by a diverse assemblage of shallow-water corals in American Samoa.* Coral Reefs, 2001. **20**(2): p. 185-189.
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8. LaJeunesse, T.C., et al., *Long-standing environmental conditions, geographic isolation and host-symbiont specificity influence the relative ecological dominance and genetic diversification of coral endosymbionts in the genus Symbiodinium.* Journal of Biogeography, 2010. **37**(5).
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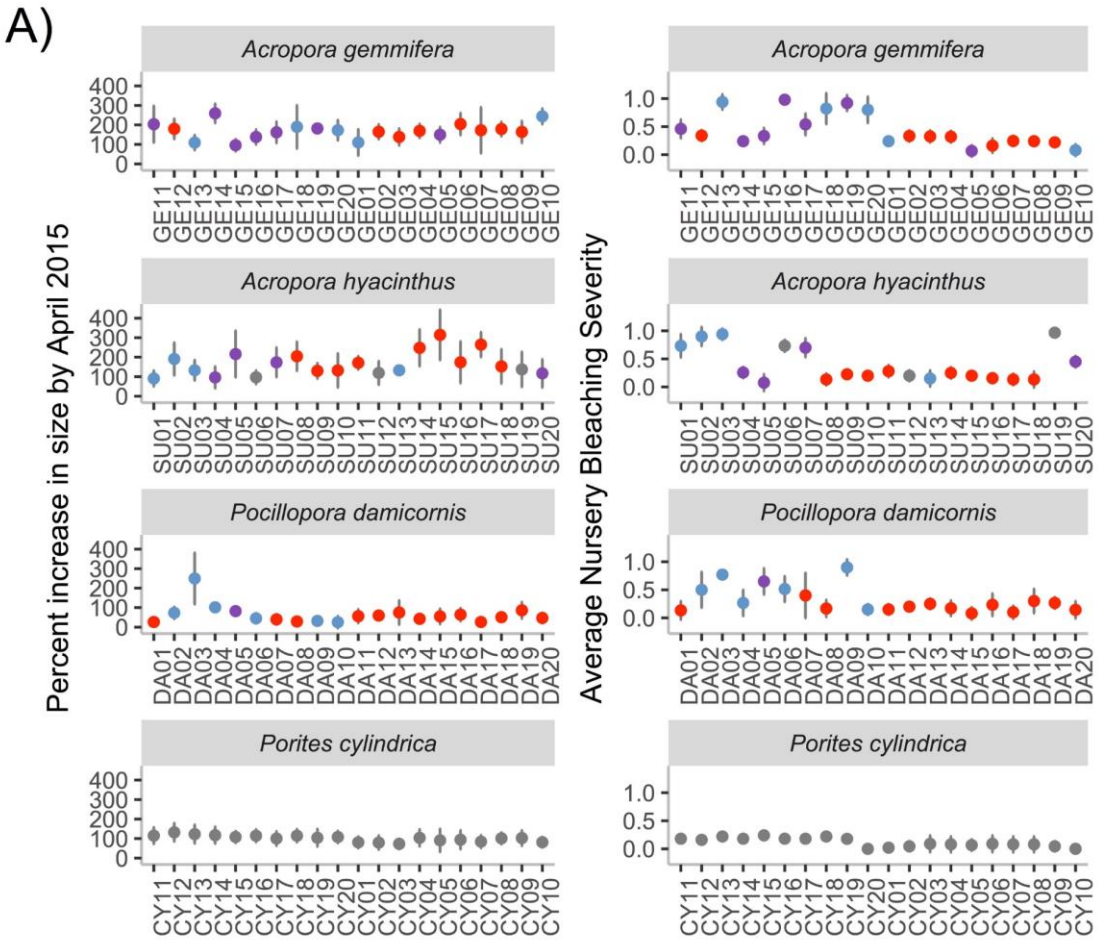
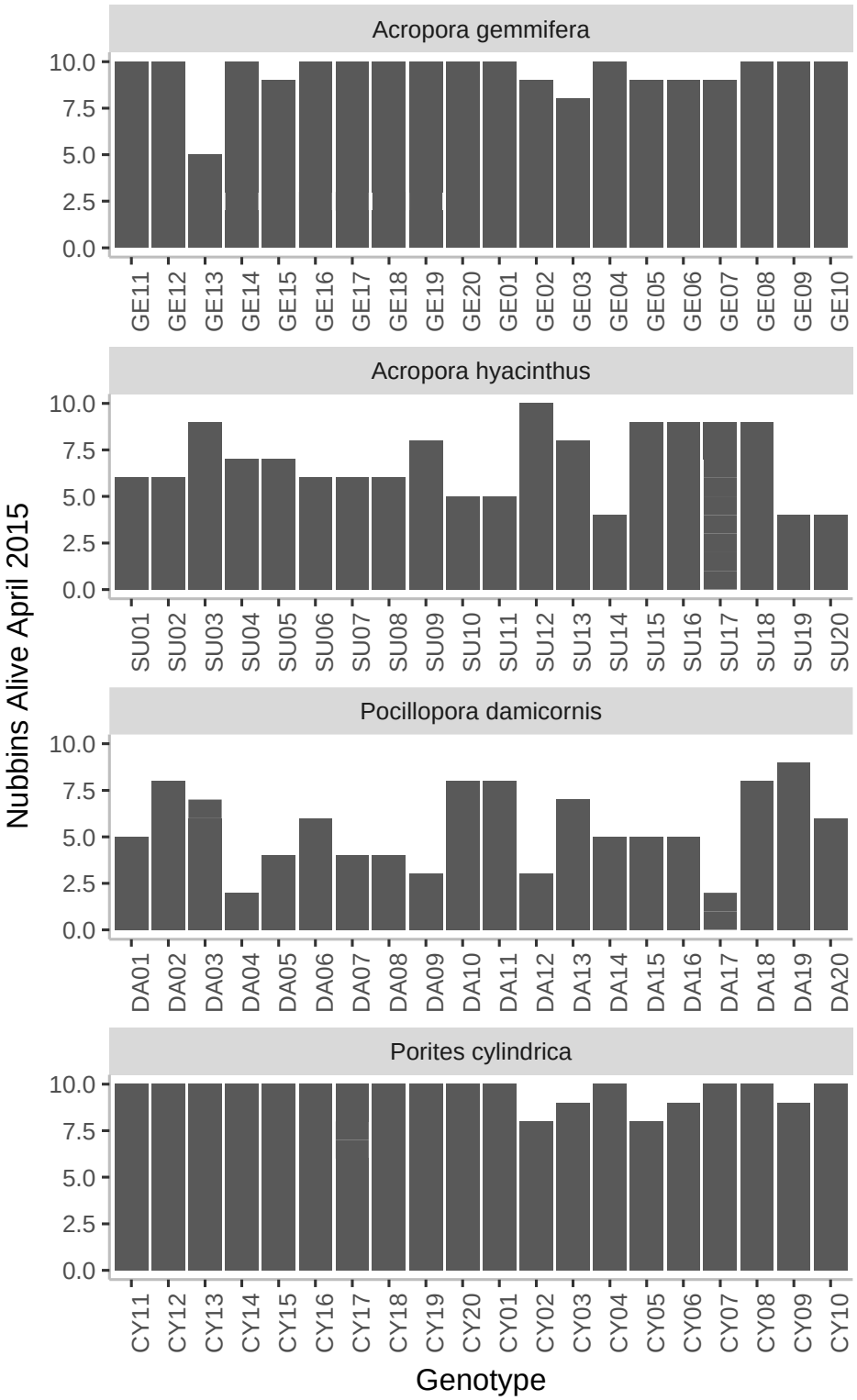
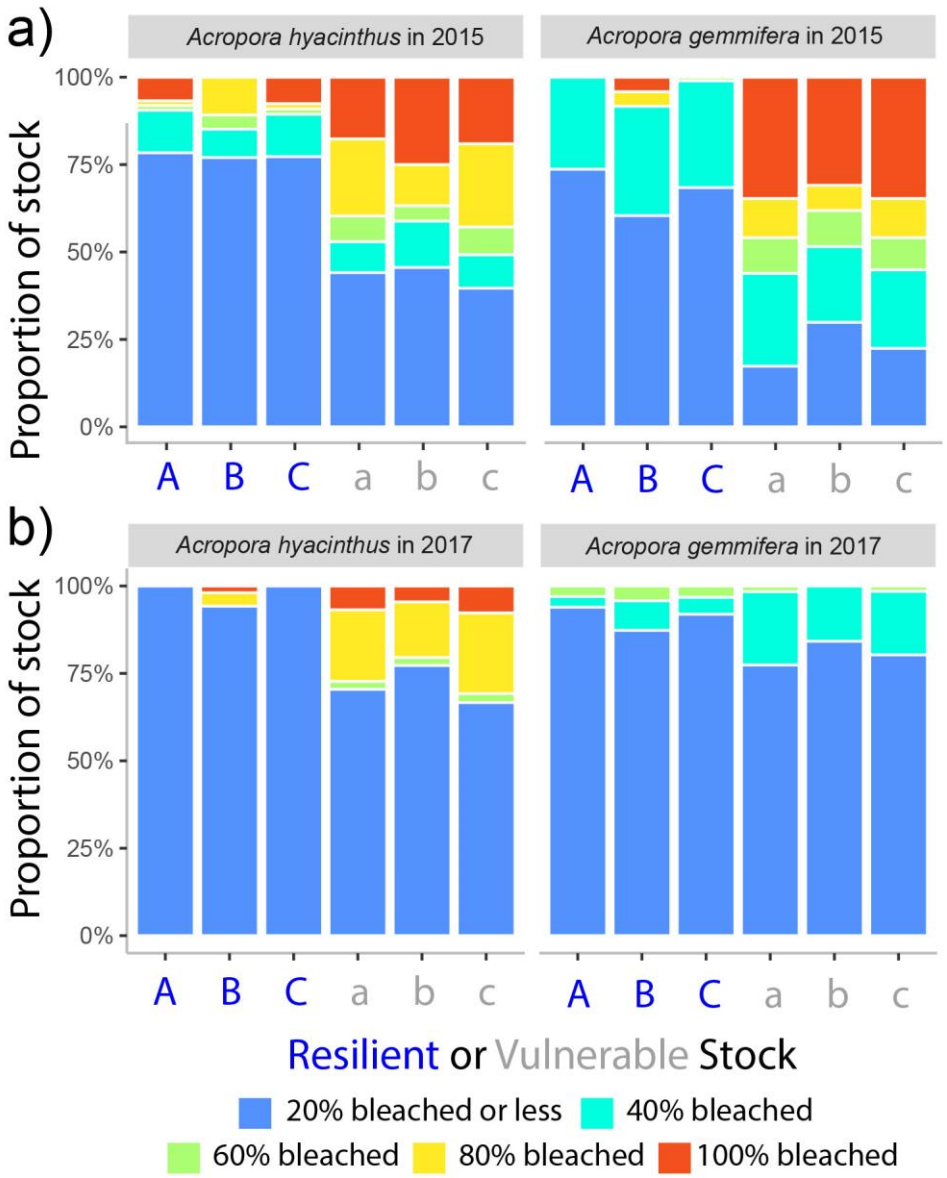


Supplemental Figure 1A) | Growth and bleaching (with error bars for 10 replicate nubbins) in April 2015 for all 20 parental colonies of four species. The left 10 parents on all plots are from the MVP, the 10 right from the HVP. Color denotes whether the parents had symbiont genus *Cladocopium* ("C", blue), genus *Durusdinium* ("D", red) or switched symbionts during the course of the experiment.

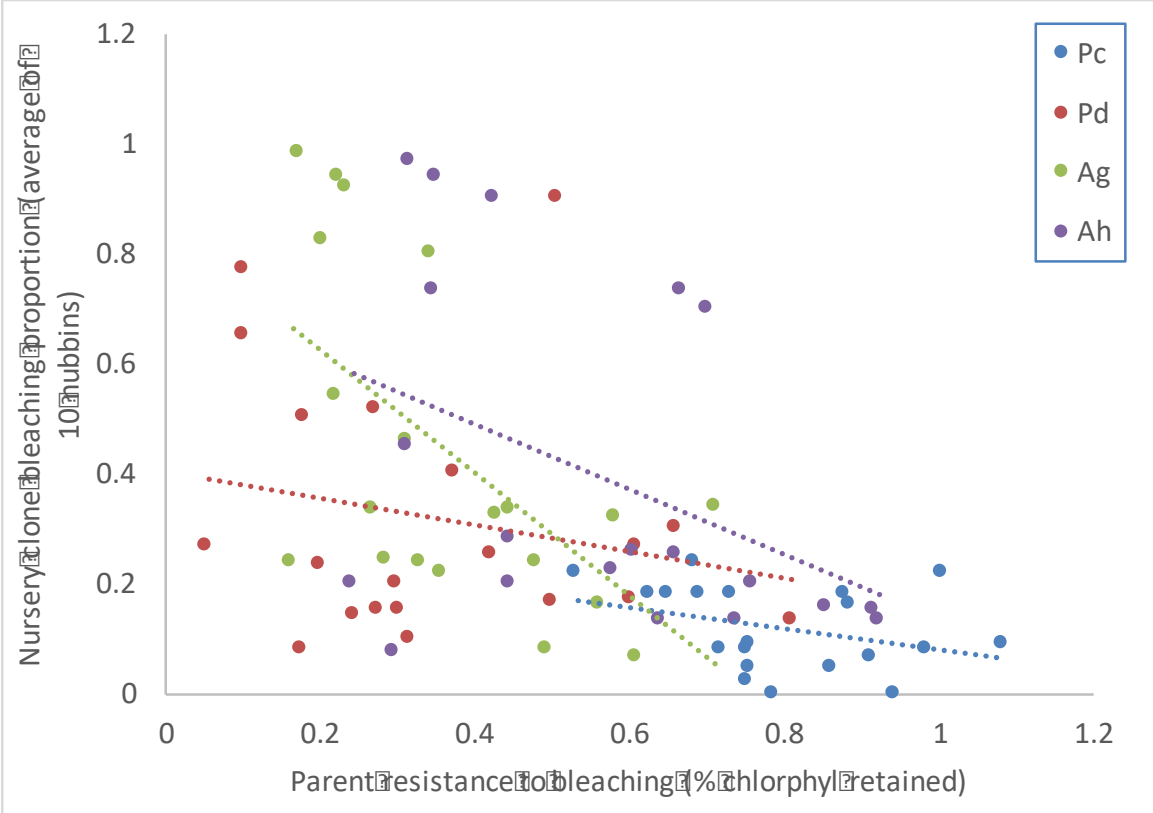


Supplemental Figure 1B) Survival from the period of August 2014 to April 2015 (when bleaching began) of replicate nursery nubbins for each parent colony. Survival was variable across species and was most affected by species specific predation in *Pocillopora damicornis* and *Acropora hyacinthus*.

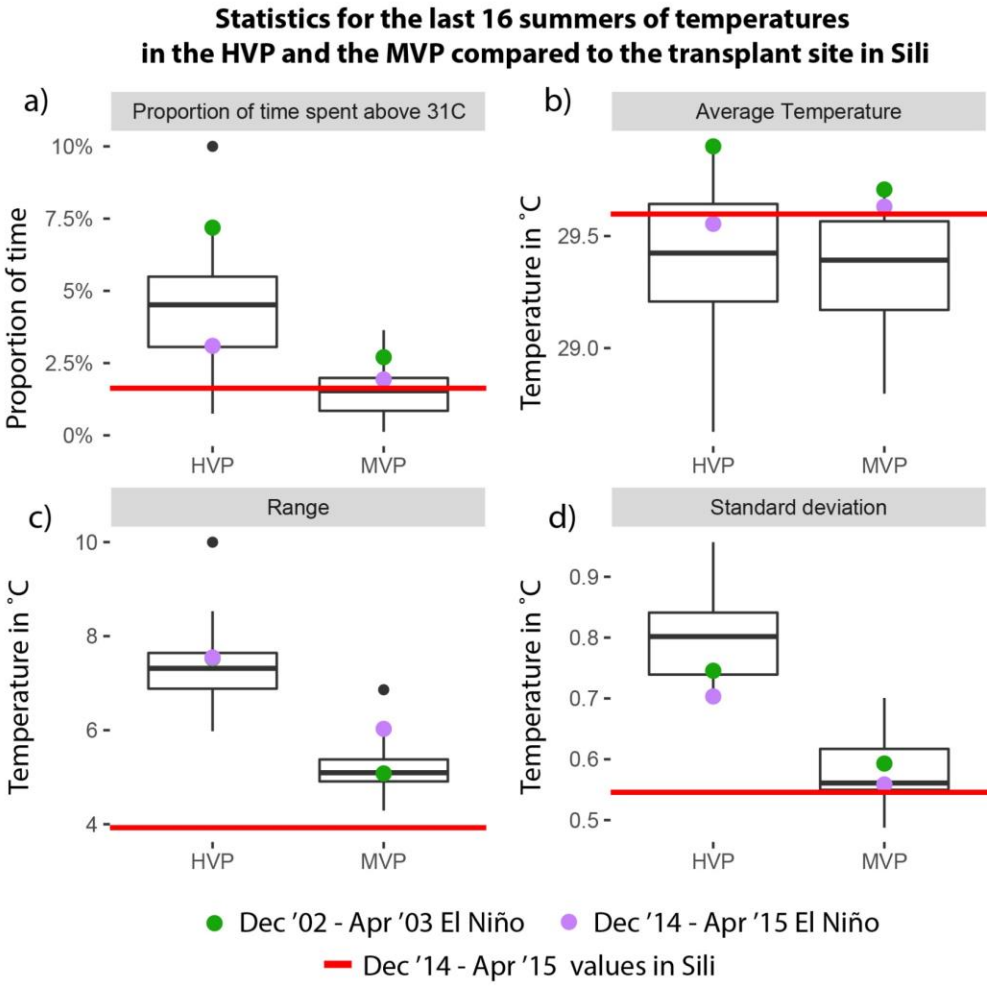


Supplemental Figure 2 | This plot shows the bleaching seen in the nursery by stock type in the a) 2015 and b) 2017 bleaching events in American Samoa. In both seasons, the predicted resilient (A-C) stocks bleached less than the predicted vulnerable (a-c) stocks. The visual bleaching scores in 2015 correspond to May 9, 2015 and the visual bleaching scores in 2017 correspond to March 8, 2017. The two dates were selected to demonstrate comparable severities in bleaching across the two events. In the 2015 bleaching event, both *Acropora hyacinthus* and *Acropora gemmifera* bleached in the vulnerable stock (a-c) to similar extents. However, in 2017, bleaching was less severe for *Acropora gemmifera*. This may indicate multiple bleaching events affect species differently.

Categories of stock type are as follows: Predicted resilient: A) Corals from the HVP B) Top experimental stress performers C) Hottest extreme microclimates
Predicted vulnerable: a) Corals from the MVP b) Bottom experimental stress performers c) Coolest extreme microclimates

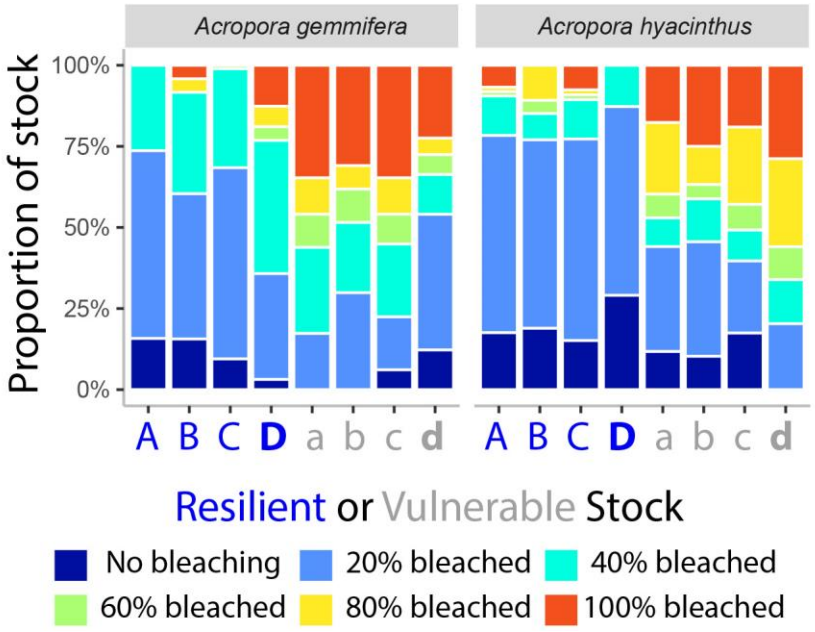


Supplemental Figure 3 | Negative relationship between the resistance of a coral colony of four species to bleaching and the bleaching observed across 10 nubbins from that colony during the April 2015 bleaching event, eight months after transplantation. Dotted lines represent linear regressions for each species.



Supplemental Figure 4 | The graphs depict boxplot distributions of a) proportion of time spent above 31˚C b) the average temperature c) the range in temperature and d) the standard deviation in temperature for the last 16 summers (December to April in the years from 1999-2015) in the HVP and the MVP. The red line depicts the value experienced at the transplant site Sili for the 2014-2015 El Niño. The green dot depicts the values for the 2002-2003 El Niño and the purple dot depicts the same 2014-2015 El Niño in the parks.

Plots indicate that conditions in Sili reached extreme temperatures less frequently (a) and were were less environmentally variable (c & d) than conditions in either the HVP or the MVP over the past 16 years. Yet replicate nubbins in Sili bleached on average 11% more severely than parent colonies did in their home environments. It is possible that in the nursery, other environmental factors or fragment size of nubbins contributed to an increase in the overall bleaching of nubbins. Yet it is also possible that de-acclimatization occurred over the eight-month period prior to the bleaching event. Either way, non-resilient nursery nubbins still bleached, indicating selecting resilient stock may be more important than selecting a nursery site that experiences temperatures that are less extreme.

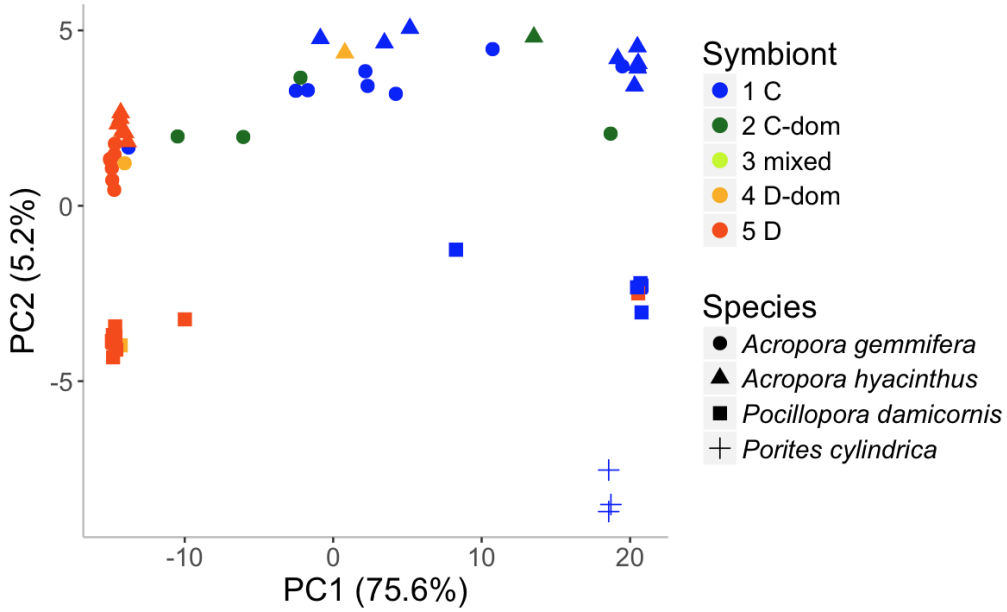


Supplemental Figure 5 | This plot compares the efficacy of the three simple proxies (categories A-C and a-c) to multi-locus biomarkers (category D and d) when partitioning the nursery by stock type. It shows the severity of visual bleaching seen by the stock throughout the 2015 bleaching event. The SNPs, established in *Acropora hyacinthus*, perform best at producing a resilient stock. However, in the closely related congener *Acropora gemmifera*, the same set of SNPs created a nursery that bleached more (D) than a nursery created with simple proxies (A-C).

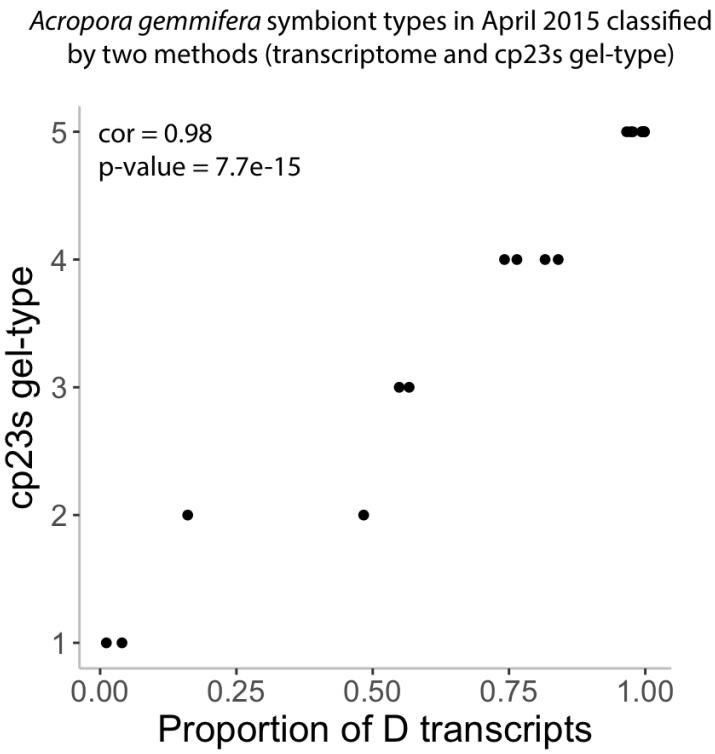
Categories of stock type are as follows:

Predicted resilient: A) Corals from the HVP B) Top experimental stress performers C) Hottest extreme microclimates D) Individuals with the highest proportion of the minor alleles for Bay & Palumbi 2014 [4] SNPs

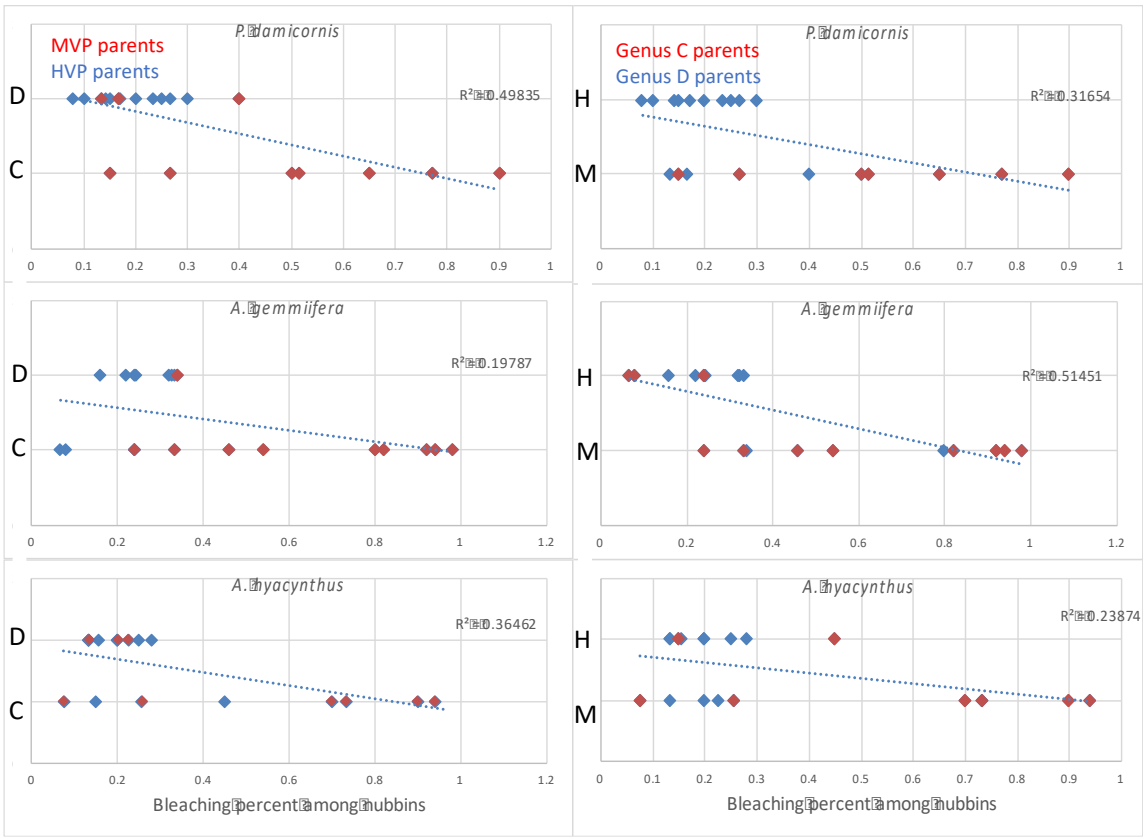
Predicted vulnerable: a) Corals from the MVP b) Bottom experimental stress performers c) Coolest extreme microclimates d) Individuals with the lowest highest proportion of the minor allele across Bay & Palumbi 2014 [4] SNPs



Supplemental Figure 6 | Plot of the first and second Principal Components of the 579 SNPs in the symbiont populations for the 30 parent colonies whose transcriptomes were generated. The first Principal Component corresponds to the differentiation between predominately genus *Cladocopium* and genus *Durusdinium* symbiont populations. The second Principal Component corresponds to differences between genera of coral. The second Principal Component shows genera specialization not only in genus *Cladocopium* symbionts (cooler colors) but also genus *Durusdinium* symbionts (warmer colors).



Supplemental Figure 7 | Classification of symbiont type (D = *Durusdinium*) in *Acropora gemmifera* parent colonies in April of 2015 through two different methods: mapping transcriptomes (x-axis), and gel-based assay (y-axis). The high correlation between the two methods implies strong correlation between gel-based calls and proportions of symbionts classified through symbiont data.



Supplemental Figure 8: Relationship between average nubbin bleaching among nursery replicates at Sili Reef to symbiont genus (*Cladocopium* vs. *Durusdinium*, left) and location of origin (right) for the parental colonies. Both symbiont genus and location correlate with bleaching in all three species. However, symbiont type and location are tightly associated, shown by color coding in each figure, making it unclear which factor controls bleaching rate. For example, colonies with *Cladocopium* symbionts (Genus C) are nearly all found in the MV pool (22 out of 26) whereas the HV pool houses mostly genus *Durusdinium* symbionts (19 of 24). These figures also show the larger range of bleaching results for corals from the MV pool or those with genus *Cladocopium* symbionts. GLM and MLR results show both origin and symbiont type separately are associated with bleaching (see results).

Supplemental Table 1: To test the relationship between bleaching of the nubbins at Sili and the species, origin and symbiont of individual clones, we ran General Linear Models

(using R), with species, origin, and symbiont as binomial variables explaining whether bleaching at Sili was >25%. All three parameters together significantly explained bleaching (P=0.0009), with individual coefficient Origin (p=0.03) being significant, and Symbiont marginally so (p=0.08).

Coefficients:

	Estimate	Std. Error	z value	Pr(>|z|)
(Intercept)	1.0935	1.5285	0.715	0.4743
Species: gemmifera	0.4727	0.7959	0.594	0.5526
Species: hyacinthus	-0.4348	0.7961	-0.546	0.5850
Origin: MVP	1.5287	0.7248	2.109	0.0349 *
Symbiont	-1.2750	0.7236	- 1.762	0.0781 .

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' '

Supplemental Table 2: The same results are obtained from a multiple linear regression of Species, Origin, and Symbiont on the fraction of bleaching at Sili. Origin is again highly significant, but in this analysis, Symbiont is also significant, with a Beta co-efficient that is similar to that for Origin

Here, the multiple r-squared is 0.4343, adjusted R-squared 0.3908. p=0.000005. Accounting for Origin and Symbiont, Species is not significantly associated with bleaching in either model.

Coefficients:

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	0.531427	0.149604	3.552	0.000822 ***
Species:gemmifera	0.065472	0.069522	0.942	0.350673
Species:hyacinthus	0.001947	0.070485	0.028	0.978070
Origin:MVP	0.197792	0.070005	2.825	0.006683 **
Symbiont	-0.189711	0.071660	-2.647	0.010712 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.2124 on 52 degrees of freedom
Multiple R-squared: 0.4343, Adjusted R-squared: 0.3908
F-statistic: 9.981 on 4 and 52 DF, p-value: 4.535e-06

Dataset S1 – Physical, growth, symbiont, bleaching and location data for the 80 colonies and the nubbins derived from them used in this study.

Dataset S2 – Bleaching, growth and mortality data for the 800 nubbins from 80 colonies followed in this study.

Dataset S3 – Genetic biomarkers for bleaching for the 80 colonies used in this study.

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Author Contributions

M.K.M. conceived the study with S.R.P. M.K.M. led field collection and analyses. M.K.M. and S.R.P. wrote the paper.

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