Electronic Supplementary Material for:

Microbiome signatures in *Acropora cervicornis* are associated with genotypic resilience to elevated nutrients and heat stress

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1. Supplementary methods

Coral collection:

Coral fragments from six genotypes of *A. cervicornis* were donated to the University of Miami (UM) coral nursery by Mote Marine Laboratory in Summerland Key, FL, in July 2017. Replicate single-branched fragments (~ 4 cm in length) were then transported to the Marine Technology and Life Science Seawater (MTLSS) complex at the University of Miami Rosenstiel School in September 2017. Each coral was acclimated to tank conditions (26.2 ºC ± 0.6 with a 12:12 h light:dark cycle) for ~4 months. Within the first month, some fragments experienced rapid tissue loss (RTL) over a 1-2 day period, but no further mortality was observed during the following three months of acclimation. However, this initial mortality resulted in an unbalanced number of fragments tested from each genotype (N=120 fragments, 8-29 fragments per genotype; Table S1).

Coral performance:

Survivorship probabilities and risk of death: Survivorship analyses were performed with the survival 2.38 (Therneau 2015) and survminer 0.4.6 (Kassambara 2018) packages for R. Survival probabilities were calculated with the Kaplan-Meier estimate (Kaplan and Meier 1958). Significant differences among the survival curves were assessed with log-rank tests. Since none of the genotypes experienced mortality in the ambient treatment at any temperature phase, and there were no differences between the survivorship probabilities between the NH_4, and NH_4 + PO_4 treatments (Fig. S1), survivorship data from NH_4 and NH_4 + PO_4 were pooled to test for differences among the six *A. cervicornis* genotypes when exposed to elevated nutrients and further heat stress (Table S2). Additionally, a Cox proportional hazards model was used to estimate the relative risk of death for the different *A. cervicornis* genotypes when exposed to elevated nutrients and heat stress.

Growth rates: Growth rates were estimated using the buoyant weight technique (Davies 1989). Buoyant weight data were transformed to air weight with the formula air weight = 1/(1-water density/coral density) following (Jokiel et al. 1978). Growth rates (mg g^{-1} d^{-1}) were estimated by calculating the difference between the air weight from two consecutive data points (mg), and normalizing this value by the initial weight of the fragment for that interval (g) and by the number of days between the two measurements (d) following previous defined methods (Ezzat et al. 2016). We first tested for the overall effect of nutrients (Ambient, NH_4 and NH_4 + PO_4) on *A. cervicornis* growth with a mixed-effects model that included nutrient treatment and number of days in the experiment as interacting fixed factors, and genotype and fragments as random effects (Tables S3-S4). Since there were no differences between the NH_4 and the NH_4 + PO_4 we pooled these treatments and tested for genotypic differences in ambient and elevated nutrients with a mixed-effects models that included *genotype*, *day*, and *nutrient* treatment (ambient versus elevated nutrients) as fixed factors, as well as coral *fragment* and *replicate* tank as a random factors (Tables S3, S5).

Photochemical efficiency (F_v/F_m): F_v/F_m values were used as a proxy for the algal community function. Declining F_v/F_m indicates dysfunction of the photosystem II, which can be used as an early sign of heat stress that could lead to coral bleaching (Warner, Fitt, and Schmidt 1999). Overall changes in F_v/F_m associated with the nutrient treatments (ambient, NH_4, and NH_4+PO_4) were analyzed with a mixed-effects model that included nutrient *treatment* and number of *days* in the experiment as interacting fixed factors, as well as *genotype*, *fragments* and *replicate* tank as random effects (Table S6). Then ambient values, as well as pooled elevated nutrient values (NH4 and NH4+PO4 treatments), were used to

test for genotypic differences in F_v/F_m among the six genotypes. This mixed-effects model included *genotype*, *day*, and *nutrient* treatment (ambient versus elevated nutrients) as fixed factors, and *fragments* and *replicate* tank as random effects (Table S6, S7) .

Prokaryotic differential abundance:

High-throughput 16S rRNA amplicon sequencing and bioinformatic analysis

Small tissue samples (~3 polyps per fragment) were collected at the end of phase 1 (day 75), and during phase 3 (days 100 and 111) to characterize the microbial communities (Fig. 1). A subset of samples from each day, genotype, and nutrient treatment (N=180) were preserved and extracted using standard organic DNA extraction protocols (Baker and Cunning 2016)16S rRNA gene V4 was amplified and sequenced using previously published primers (Apprill et al. 2015). Briefly, the samples were amplified in a 50 µL reaction using the Platinum Hot Start PCR Master Mix (2X) (ThermoFisher Scientific, Waltham, MA), 2 µL of DNA, and 1 µL of each primer with PCR run at: 1 cycle x 3 min at 94°C, 35 cycles x (45 s at 94°C, 60 s at 50°C, 90 s at 72°C), 1 cycle x 10 min at 72°C. Each PCR product was cleaned with AMPure XP beads (Beckman Coulter, Brea, CA), quantified using a Qubit™ dsDNA HS Assay Kit (TermoFisher Scientific, Waltham, MA), and normalized to 4 nM. Then 5 µL of each sample was combined into a single 1.5 mL tube. The concentration of the pool was quantified with a Qubit™ dsDNA HS Assay Kit and was below the nM threshold and thus was concentrated by using a vacuum centrifuge. The pooled sample was submitted to the Hussman Institute for Human Genomics University of Miami Miller School of Medicine and sequenced on a MiSeq with the PE-300v3 kit. Post-sequencing the data were demultiplexed at the core facility.

Demultiplexed sequences were processed on Qiime2-2018.11 (Bolyen et al. 2019). Upon initial inspection of the sequences, the reverse reads were of poor quality and thus only the forward reads were analyzed. Primers were trimmed from the forward reads with the Cutadapt plugin (Martin 2011) and then processed with the DADA2 plugin (Callahan et al. 2016). The default settings were used for DADA2 and the sequences were trimmed at the 20 and 220 bp positions. The DADA2 program output quality filtered, chimera removed Amplicon Sequence Variants (ASVs). These ASVs were taxonomically classified with a fitted classifier using the function feature-classifier classify-sklearn and a trained Silva-132-99-105-806 database (Bokulich et al. 2018). The sequences that were taxonomically assigned as chloroplast or mitochondria were removed from the analysis. An *Escherichia coli* (ASV) was found across all samples and it was the second most frequent sequence in the dataset. This ASV was removed from the analysis since it was likely a contaminant from the DNA extraction protocol which contained tRNA isolated from *E.coli* (per Millipore Sigma, Burlington, MA). Samples with <100 sequences were removed for downstream analyses (n = 1).

2. Supplementary results

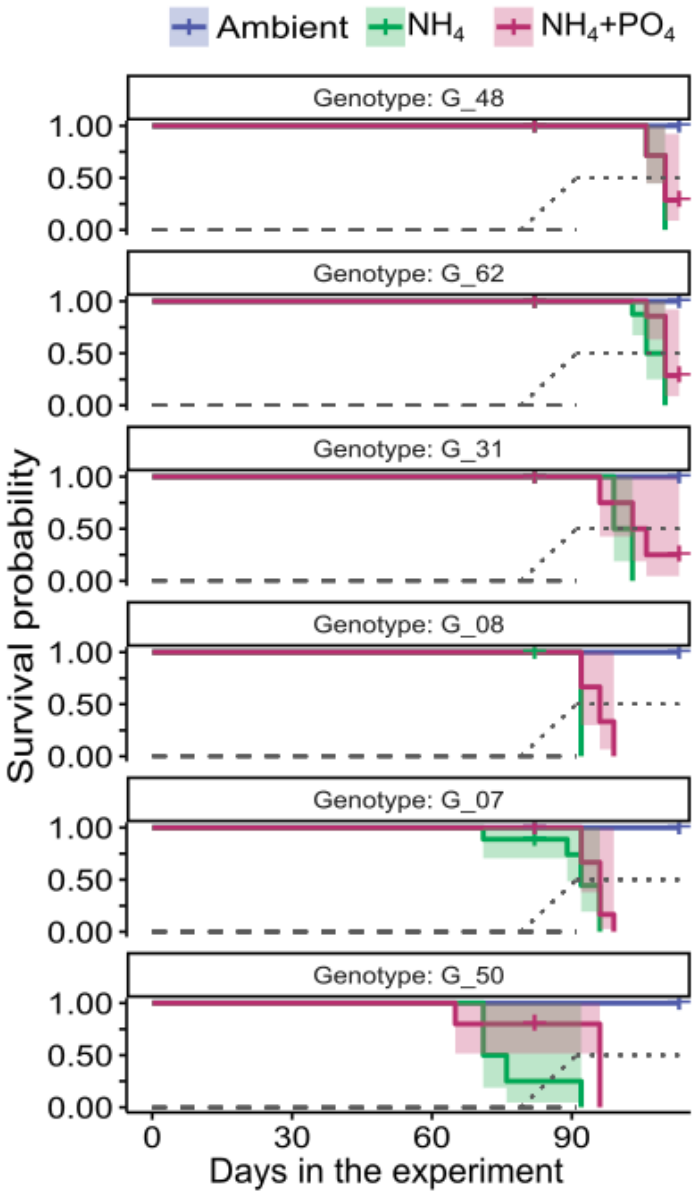

Fig. S1: Survival probability in *A. cervicornis* exposed to nutrient treatments (ambient, NH_4, and NH_4+PO_4, followed by heat stress. Survival probabilities were lower for corals exposed to elevated nutrients compared to ambient nutrients (Log-rank $p < 0.0001$), but there were no significant differences between NH_4 and NH_4+PO_4 (Log-rank $p = 0.097$).

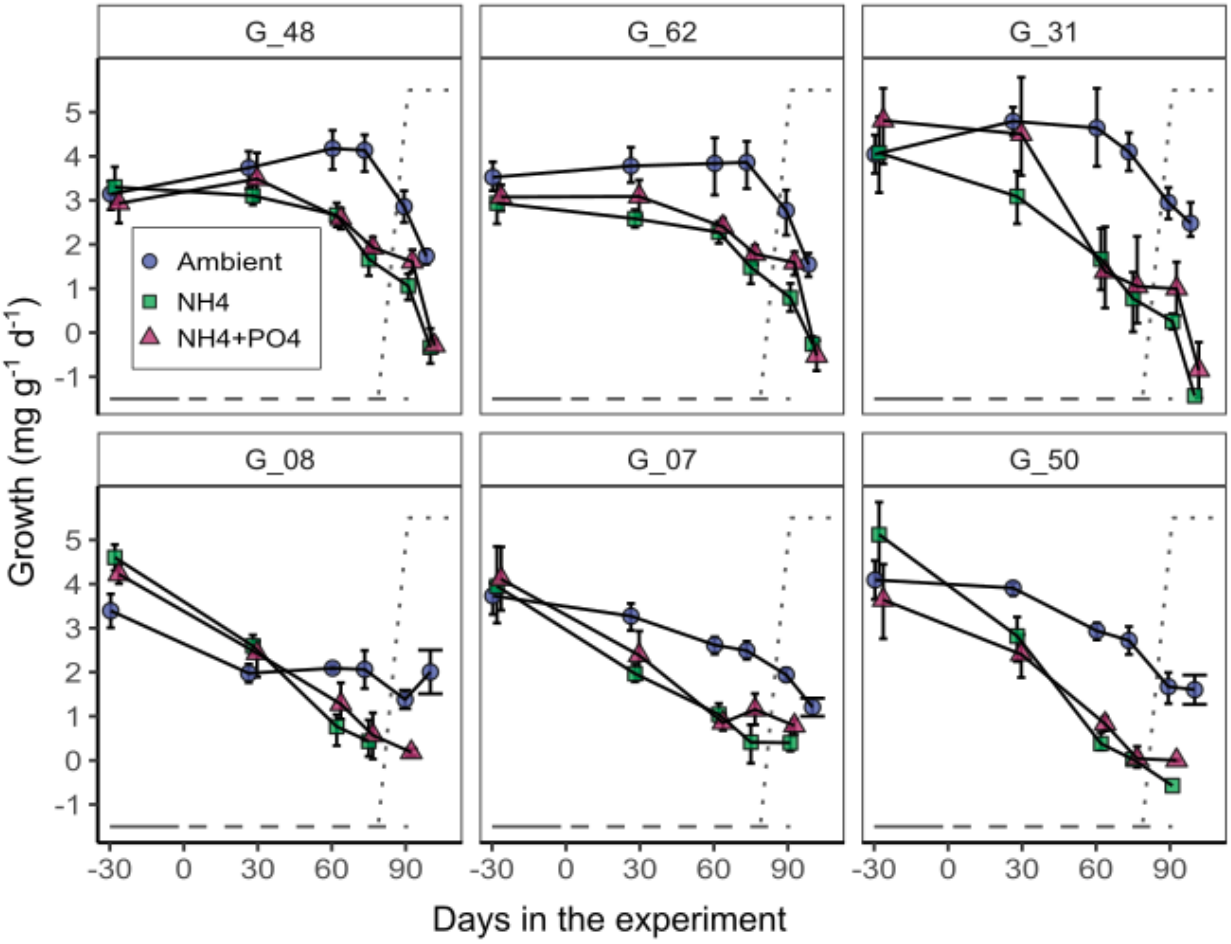

Fig. S2: *A. cervicornis* growth rates (mean mg g^{-1} d^{-1} ± 95% CI) before starting the experiment (baseline), under nutrient treatments and control temperature (days 1-75), and subsequent ramp-up (days 76-90) and heat stress (days 91-113). Each panel represents a single genotype.

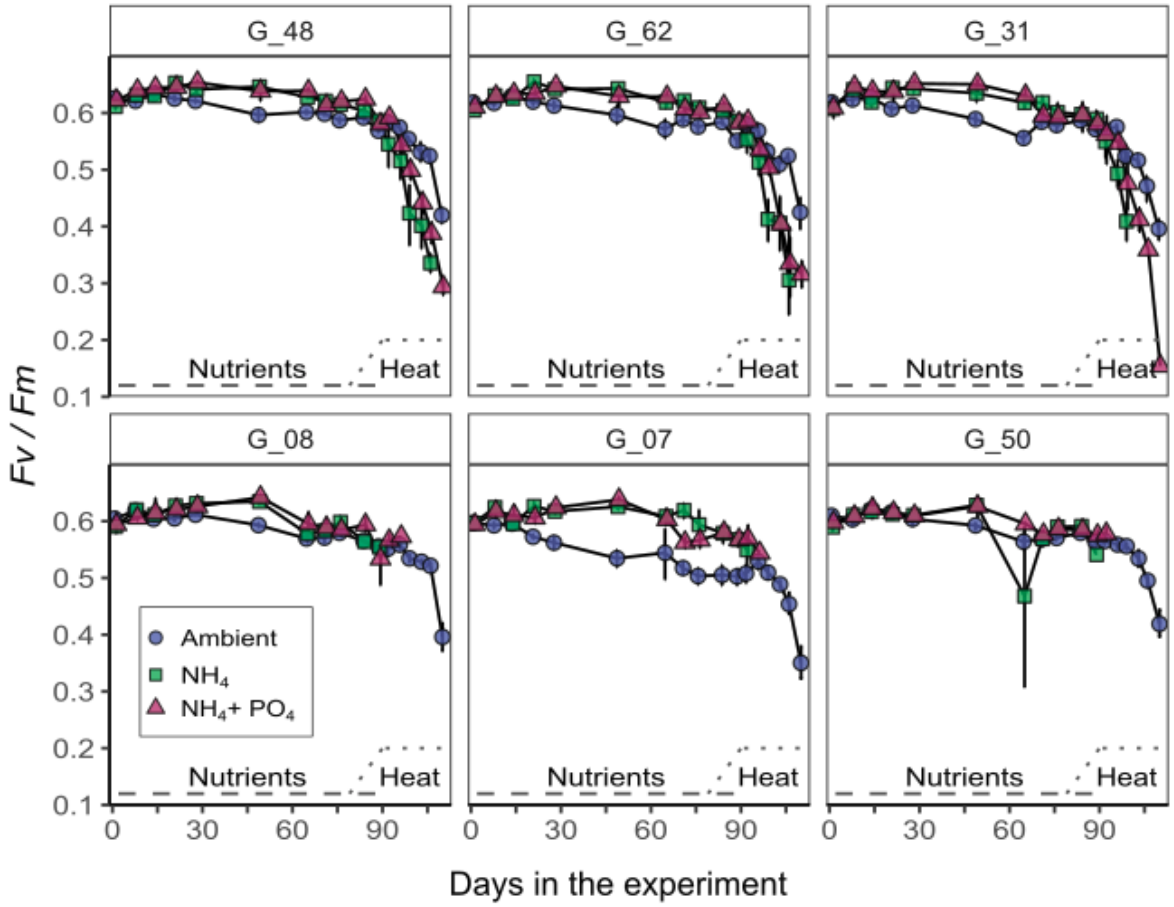

Fig. S3: *A. cervicornis* photochemical efficiency rates (*Fv/Fm* ± 95% CI) under nutrient treatments and control temperature (days 1-75), and subsequent ramp-up (days 76-90) and heat stress (days 91-113). Each panel represents a single genotype.

Prokaryotic differential abundance by nutrient treatment and days

Differential abundance analysis yielded four significant ASVs (8818, 989, 2609, and 3479) among ambient, NH_4, and NH_4+PO_4 at control temperature (phase 1; day 75), but some of these differences were driven by specific genotypes. For ASV8818 (phylum Proteobacteria and genus *Pseudoalteromonas*) the mean RA was highest in NH_4+PO_4 (0.8% ± 1.3%), but *G31* had a particularly higher mean RA (1.9% ± 2.2%) of *Pseudoalteromonas* compared to the other genotypes. ASV989 (phylum Cyanobacteria and genus *Rivularia*), had the highest RA in ambient treatment (1.9% ±3.0%) compared to NH_4 (0.15% ± 0.05%), and NH_4+PO_4 (1.2% ±1.8%) but this high abundance in ambient corals was mostly driven by *G07* (3.6% ±3.2%). ASV2609 (phylum Proteobacteria and genus *Pseudomonas*), had a similar mean RA in both ambient (1.1% ± 0.9%) and NH_4+PO_4 (1.1% ± NA) and was lower in NH_4 (0.7% ± 0.6%). The mean RA of ASV3479 (phylum Proteobacteria genus *Methylobacterium*) was highest in ambient nutrients (1.2% ± 1.5%), followed by NH_4+PO_4 (0.9% ± 0.9%), and NH_4 (0.9% ± 0.7%). While not significantly different across genotypes, *G07* had a low abundances of *Midichloriaceae* (ASV 2095; 1.0% ±0.7%) at control temperature (phase 1; day 75) , but increased in NH_4 (20.9% ±4%) and NH_4+PO_4 (38.5±52.0) treatments.

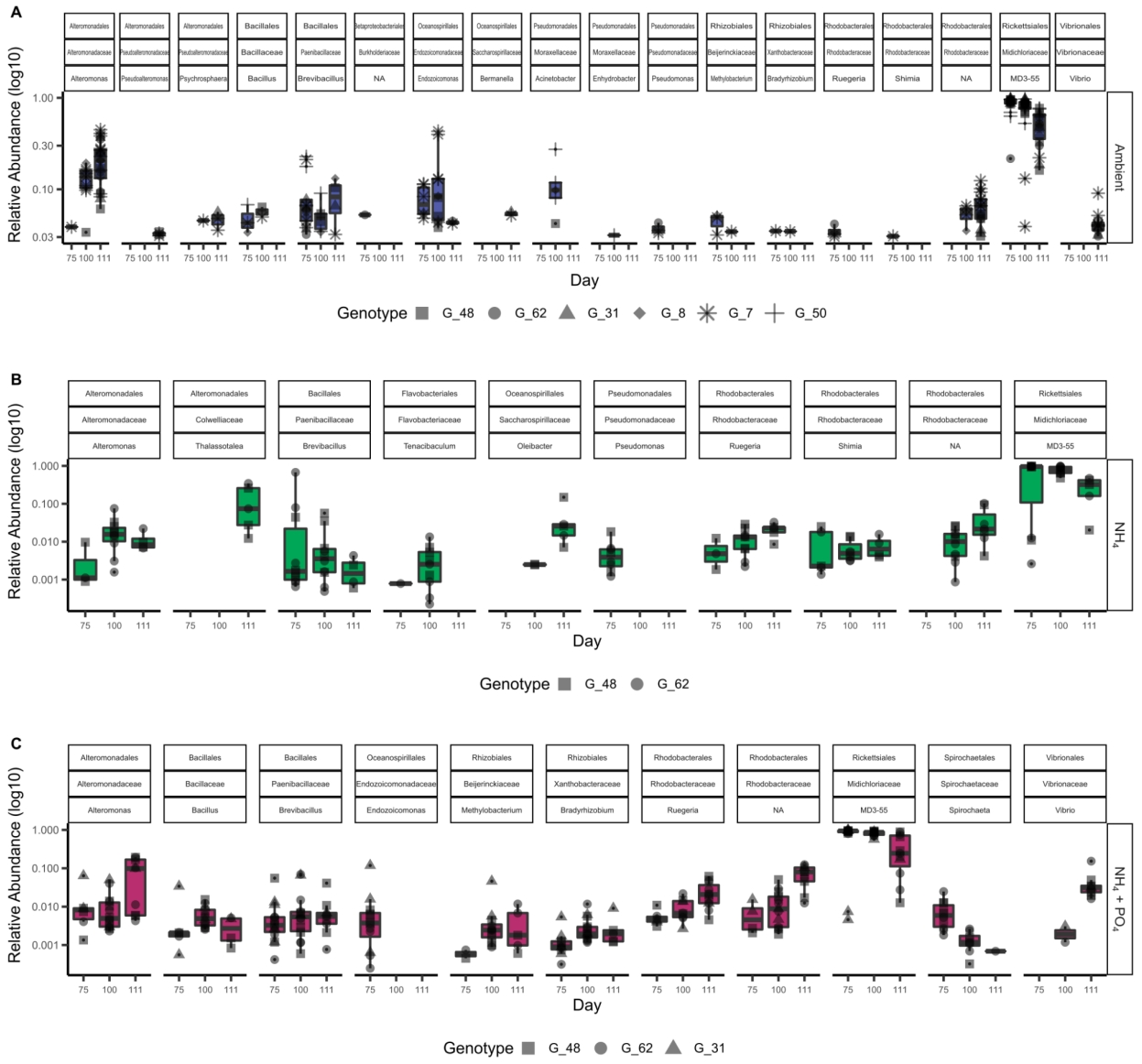

Fig. S4: Significantly differentiated ASVs across time and heat stress in the three nutrient treatments (A) Ambient (B) NH_4, and (C) NH_4,+ PO_4. Relative abundance (y-axis) of the significant taxa across time (days 75 [control], 100 [heat], and 111 [heat]). The data is parsed by the ASV's corresponding order, family, and genus. The shapes denote the six genotypes in (A), the two genotypes in (B), and the three genotypes in (C) that were used in each analysis (due to survivors across time). The genotypes are ordered by survivorship rates in each key.

3. Supplementary Tables:

Table S1: Number of fragments exposed to each nutrient treatment per *A. cervicornis* genet.

Genet	Treatment / Replicates						Total genet
	A (ambient nutrients)		**N** [ambient nutrients + 10μM NH_4]		**N+P** [ambient nutrients + 10μM NH_4 + 1μM PO_4]		
	R1	**R2**	**R1**	**R2**	**R1**	**R2**	
G_48	5	5	5	4	5	4	**28**
G_62	5	4	5	5	5	5	**29**
G_31	3	2	3	3	3	2	**16**
G_07	5	4	5	4	4	4	**26**
G_50	2	2	2	2	3	2	**13**
G_08	1	1	1	2	1	2	**8**
Total treatment	**21**	**18**	**21**	**20**	**21**	**19**	**120**

Table S2: Survival probability model used to test for differences in the mortality rates in six. *A. cervicornis* genotypes exposed to elevated nutrients (NH_4 and NH_4 + PO_4 pooled) at control temperature followed by heat stress.

Genotype	exp(coef)	exp(-coef)	lower .95	upper .95	z Pr(>|z|)
G_48 (reference)					
G_62	1.07	0.93	0.49	2.35	0.86
G_31	2.97	0.34	1.15	7.69	0.02
G_08	64.53	0.01	13.17	316.04	<0.001
G_07	76.23	0.01	17.40	333.85	<0.001
G_50	136.30	0.007	27.87	666.58	<0.001

Likelihood ratio test = 75.2 on 5 df, p<0.001
Wald test = 42.11 on 5 df, p <0.001
Score (logrank) test = 87.02 on 5 df, p=<0.001

Table S3: Generalized linear mixed models used to test for differences in the growth rate of *A. cervicornis* exposed to nutrient treatments at control temperature (days 1-78) and heat stress (days 90-113). Factor Nutrient has three levels (Ambient, NH_4 and NH_4 + PO_4), while factor Nutrients2 has two levels (Ambient, and elevated nutrients [NH_4 and NH_4 + PO_4 pooled]).

Model 1: *A. cervicornis* growth with genotypes pooled by nutrient treatment

Fixed effects	**numDF**	**denDF**	**F-value**	**p-value**
Nutrient	2	118.2	123.6	<0.001
Days	5	491.7	247.3	<0.001
Nutrient:Day	10	492.6	22.1	<0.001
Random effects	**npar**	**logLik**	**AIC**	**Pr(>Chisq)**
none	22	-728.7	1501.3	
Genotype	21	-746.3	1534.6	<0.001
Fragment	21	-747.9	1537.8	<0.001
Replicate (Tank)	21	-728.9	1499.7	0.54

Model 2: *A. cervicornis* growth with both elevated nutrient treatments pooled by genotype

Fixed effects	**numDF**	**denDF**	**F-value**	**p-value**
Genotype	5	104.8	12.3	<0.001
Nutrients2	1	111.6	171.7	<0.001
Days	5	441.2	283.9	<0.001
Genotype:Days	5	106.9	3.2	<0.01
Treatment2:Days	25	440.2	14.5	<0.001
Nutrient:Day	5	441.9	71.8	<0.001
Genotype:Treatment2:Days	22	440.4	2.9	<0.001
Random effects	**npar**	**logLik**	**AIC**	**Pr(>Chisq)**
none	72	-555.1	1254.4	
Fragment	71	-622.1	1386.1	<0.001
Replicate (Tank)	71	-555.3	1252.7	0.6

Table S4: Estimated growth rates (mg g^{-1} d^{-1}) for *A. cervicornis* exposed to nutrient treatments, and subsequent heat stress using Model 1. Pairwise comparisons between groups were obtained using Tukey's HSD test ($\alpha = 0.05$). Stars (*) in the treatments denote the group of corals that were assigned to these treatments, but that were not exposed to elevated nutrients at the time of the measurement. Percentages of change in bold represent comparison among values that were significantly different based on the Tukey's HSD test. The model includes *nutrient* treatment, and *days* in the experiment as interacting fixed factors, as well as *genotype*, *fragment*, and *replicate* tank as random effects (see Table S3).

Days in the experiment (Phase)	Nutrient Treatment	Em mean	SE	df	Lower CL	Upper CL	Tukey Group	% change respect ambient (same day)	% change respect baseline (day -28)	% change respect control temp (day 75)
-77 to -28 (Baseline)	Ambient	3.52	0.2	11.3	3.05	3.98	7	NA	NA	NA
	* NH_4	3.64	0.2	11.1	3.18	4.10	7	3.5%	NA	NA
	*NH_4+PO_4	3.53	0.2	11.2	3.07	3.99	7	0.4%	NA	NA
1 to 28 (Control)	Ambient	3.61	0.2	11.5	3.14	4.07	7	NA	2.6%	NA
	NH_4	2.59	0.2	10.9	2.13	3.05	6	**-28.1%**	**-26.3%**	NA
	NH_4+PO_4	3.02	0.2	11.0	2.55	3.48	67	-16.4%	-14.2%	NA
29 to 62 (Control)	Ambient	3.50	0.2	11.5	3.03	3.97	7	NA	-0.5%	NA
	NH_4	1.64	0.2	10.9	1.18	2.10	45	-53.2%	**-53.4%**	NA
	NH_4+PO_4	1.67	0.2	11.2	1.20	2.13	5	-52.3%	**-52.5%**	NA
62 to 75 (Control)	Ambient	3.36	0.2	11.3	2.89	3.82	7	NA	-4.4%	NA
	NH_4	0.96	0.2	11.7	0.49	1.42	23	**-71.5%**	**-72.8%**	NA
	NH_4+PO_4	1.24	0.2	11.2	0.78	1.70	345	**-63.1%**	**-64.7%**	NA
75 to 91 (Ramp-up)	Ambient	2.36	0.2	12.9	1.89	2.84	6	NA	**-32.8%**	**-29.7%**
	NH_4	0.46	0.2	17.7	-0.04	0.96	2	**-80.5%**	**-86.9%**	-51.9%
	NH_4+PO_4	0.98	0.2	14.3	0.50	1.46	234	**-58.5%**	**-72.1%**	-21.0%
91 to 100 (Heat)	Ambient	1.63	0.2	12.9	1.15	2.10	345	NA	**-53.7%**	**-51.6%**
	* NH_4	-0.69	0.3	26.0	-1.23	-0.15	1	**-142.6%**	**-119.7%**	**-172.4%**
	*NH_4+PO_4	-0.85	0.3	24.2	-1.38	-0.32	1	**-152.3%**	**-124.2%**	**-168.5%**

Table S5: Estimated growth rates (mg g^{-1} d^{-1}) for six *A. cervicornis* genets exposed to nutrient treatments, and subsequent heat stress using Model 2. Pairwise comparisons between groups were obtained using Tukey's HSD test (α = 0.05). Stars (*) in the treatments denote the group of corals that were assigned to these treatments, but that were not exposed to elevated nutrients at the time of the measurement. Percentages of change in bold represent comparison among values that were significantly different based on the Tukey's HSD test. The model includes *genet*, *nutrient* treatment, and *days* in the experiment as interacting fixed factors, as well as *fragment*, and *replicate* tank as random effects (see Table S3).

Days in the experiment (Phase)	Nutrient Treatment	Genet	Em mean	SE	df	Lower CL	Upper CL	% change respect ambient (same day)	% change respect baseline	% change respect control temp (Day 75)	% respect G_48	% respect G_50
-77 to -28 (Baseline)	Ambient	G_48	3.14	0.22	90.6	2.71	3.58	NA	NA	NA	NA	-23.2%
		G_62	3.52	0.23	104.2	3.07	3.97	NA	NA	NA	12.0%	-14.0%
		G_31	4.04	0.30	193.4	3.44	4.64	NA	NA	NA	28.4%	-1.4%
		G_08	3.39	0.48	285.8	2.45	4.33	NA	NA	NA	7.9%	-17.1%
		G_07	3.73	0.23	104.2	3.27	4.18	NA	NA	NA	18.6%	-8.9%
		G_50	4.09	0.34	226.3	3.42	4.76	NA	NA	NA	30.2%	NA
	Nutrients (N and N+P pooled)	G_48	3.11	0.17	36.1	2.78	3.45	-1.0%	NA	NA	NA	-27.5%
		G_62	3.01	0.16	30.4	2.68	3.33	-14.6%	NA	NA	-3.5%	-30.0%
		G_31	4.41	0.21	78.8	3.99	4.82	9.1%	NA	NA	41.5%	2.6%
		G_08	4.38	0.32	239.9	3.74	5.02	29.1%	NA	NA	40.6%	2.0%
		G_07	4.02	0.17	39.8	3.68	4.37	7.9%	NA	NA	29.3%	-6.3%
		G_50	4.29	0.23	104.2	3.84	4.75	4.9%	NA	NA	37.9%	NA
1 to 28 (Control)	Ambient	G_48	3.74	0.22	90.6	3.30	4.17	NA	18.8%	NA	NA	-4.4%
		G_62	3.64	0.24	118.6	3.17	4.12	NA	3.6%	NA	-2.4%	-6.7%
		G_31	4.79	0.30	193.4	4.19	5.39	NA	18.6%	NA	28.1%	22.5%
		G_08	1.98	0.48	285.8	1.04	2.91	NA	**-41.8%**	NA	-47.1%	-49.5%
		G_07	3.27	0.23	104.2	2.81	3.72	NA	-12.3%	NA	-12.5%	-16.4%
		G_50	3.91	0.34	226.3	3.24	4.58	NA	-4.5%	NA	4.6%	NA
	Nutrients (N and N+P pooled)	G_48	3.29	0.17	36.1	2.96	3.63	-11.9%	5.7%	NA	NA	27.3%
		G_62	2.84	0.16	30.4	2.51	3.16	-22.2%	-5.7%	NA	-13.8%	9.7%
		G_31	3.73	0.21	78.8	3.31	4.14	-22.1%	-15.4%	NA	13.2%	44.2%
		G_08	2.52	0.28	162.5	1.97	3.08	**27.8%**	-42.3%	NA	-23.3%	-2.3%
		G_07	2.16	0.17	39.8	1.82	2.50	**-33.9%**	-46.3%	NA	-34.3%	-16.4%
		G_50	2.58	0.23	104.2	2.13	3.04	**-33.9%**	-39.8%	NA	-21.5%	NA
29 to 62 (Control)	Ambient	G_48	4.18	0.22	90.6	3.74	4.61	NA	**32.8%**	NA	NA	42.1%
		G_62	3.83	0.23	104.2	3.38	4.29	NA	8.9%	NA	-8.2%	30.5%
		G_31	4.63	0.30	193.4	4.03	5.23	NA	14.8%	NA	11.0%	57.7%
		G_08	2.09	0.48	285.8	1.15	3.03	NA	**-38.4%**	NA	-49.9%	-28.8%
		G_07	2.61	0.24	119.0	2.14	3.08	NA	**-30.0%**	NA	-37.5%	-11.2%
		G_50	2.94	0.34	226.3	2.27	3.61	NA	**-28.2%**	NA	-29.6%	NA
	Nutrients (N and N+P pooled)	G_48	2.62	0.17	36.1	2.29	2.96	**-37.2%**	-15.8%	NA	NA	446.3%
		G_62	2.34	0.16	30.4	2.02	2.66	**-39.0%**	-22.2%	NA	-10.8%	387.2%
		G_31	1.53	0.21	78.8	1.12	1.95	**-66.9%**	-65.2%	NA	-41.5%	219.6%
		G_08	1.03	0.28	162.5	0.48	1.58	**-50.6%**	-76.4%	NA	-60.6%	115.2%
		G_07	0.95	0.17	39.8	0.61	1.30	**-63.5%**	-76.3%		-63.7%	98.4%
		G_50	0.48	0.24	120.3	0.01	0.95	**-83.7%**	-88.8%	NA	-81.7%	NA

Table S5 (continuation): Estimated growth rates (mg g^{-1} d^{-1}) for six *A. cervicornis* genets exposed to nutrient treatments, and subsequent heat stress using Model 2. Stars (*) in the treatments denote the group of corals that were assigned to these treatments, but that were not exposed to elevated nutrients at the time of the measurement. Percentages of change in bold represent comparison among values that were significantly different based on the Tukey's HSD test. The model includes *genet*, *nutrient* treatment, and *days* in the experiment as interacting fixed factors, as well as *fragment*, and *replicate* tank as random effects (see Table S3).

Days in the experiment (Phase)	Nutrient Treatment	Genet	Em mean	SE	df	Lower CL	Upper CL	% change respect ambient (same day)	% change respect baseline	% change respect control temp (Day 75)	% respect G_48	% respect G_50
62 to 75 (Control)	Ambient	G_48	4.14	0.22	90.6	3.70	4.57	NA	**31.5%**	NA	NA	**52.1%**
		G_62	3.86	0.23	104.2	3.40	4.31	NA	9.6%	NA	-6.7%	**41.9%**
		G_31	4.09	0.30	193.4	3.49	4.69	NA	1.4%	NA	-1.0%	**50.5%**
		G_08	2.06	0.48	285.8	1.12	3.00	NA	**-39.2%**	NA	**-50.1%**	-24.2%
		G_07	2.49	0.23	104.2	2.03	2.94	NA	**-33.3%**	NA	**-39.9%**	-8.6%
		G_50	2.72	0.34	226.3	2.05	3.39	NA	**-33.5%**	NA	**-34.2%**	NA
	Nutrients (N and N+P pooled)	G_48	1.79	0.17	36.1	1.46	2.13	**-56.7%**	-42.4%	NA	NA	-1477.9%
		G_62	1.63	0.16	30.4	1.31	1.95	**-57.7%**	-45.7%	NA	-8.9%	-1355.7%
		G_31	0.90	0.21	78.8	0.48	1.31	**-78.1%**	-79.7%	NA	-50.0%	-788.9%
		G_08	0.51	0.28	162.5	-0.04	1.06	**-75.1%**	-88.3%	NA	-71.4%	-494.7%
		G_07	0.79	0.17	42.9	0.44	1.13	**-68.4%**	-80.5%	NA	-56.1%	-704.4%
		G_50	-0.13	0.28	204.8	-0.69	0.43	**-104.8%**	-103.0%	NA	-107.3%	0.0%
75 to 91 (Ramp-up)	Ambient	G_48	2.90	0.23	117.4	2.43	3.36	NA	-7.8%	-29.94%	NA	73.2%
		G_62	2.82	0.25	138.8	2.33	3.31	NA	-19.9%	-26.95%	-2.7%	68.5%
		G_31	3.07	0.33	241.9	2.43	3.72	NA	-23.9%	-24.94%	6.0%	83.7%
		G_08	1.38	0.48	285.8	0.44	2.32	NA	-59.3%	-33.01%	-52.3%	-17.4%
		G_07	1.88	0.25	138.7	1.39	2.37	NA	-49.6%	-24.46%	-35.2%	12.3%
		G_50	1.67	0.34	226.3	1.00	2.34	NA	-59.1%	-38.50%	-42.3%	NA
	Nutrients (N and N+P pooled)	G_48	1.43	0.18	53.8	1.07	1.80	**-50.5%**	-53.9%	-19.98%	NA	-502.2%
		G_62	1.19	0.17	43.4	0.85	1.54	**-57.6%**	-60.3%	-26.88%	-16.7%	-434.9%
		G_31	0.55	0.23	115.0	0.09	1.01	**-82.0%**	-87.5%	-38.29%	-61.4%	-255.1%
		G_08	0.11	0.42	418.4	-0.72	0.95	**-91.9%**	-97.4%	-78.21%	-92.2%	-131.4%
		G_07	0.43	0.22	103.3	-0.01	0.87	**-77.3%**	-89.4%	-45.74%	-70.3%	-219.6%
		G_50	-0.36	0.31	255.0	-0.97	0.25	**-121.3%**	-108.3%	174.16%	-124.9%	NA
91 to 100 (Heat)	Ambient	G_48	1.77	0.23	117.4	1.31	2.24	NA	-43.6%	-57.14%	NA	10.5%
		G_62	1.60	0.25	138.8	1.11	2.09	NA	-54.6%	-58.58%	-9.8%	-0.3%
		G_31	2.60	0.33	241.9	1.96	3.25	NA	-35.6%	-36.44%	46.8%	62.3%
		G_08	2.01	0.48	285.8	1.07	2.94	NA	-40.9%	-2.74%	13.2%	25.1%
		G_07	1.15	0.25	138.7	0.65	1.64	NA	-69.3%	-53.90%	-35.3%	-28.5%
		G_50	1.60	0.34	226.3	0.94	2.27	NA	-60.8%	-41.05%	-9.5%	0.0%
	Nutrients (N and N+P pooled)	G_48	-0.27	0.18	49.1	-0.63	0.09	**-115.0%**	-108.6%	-114.88%	NA	NA
		G_62	-0.38	0.18	47.3	-0.74	-0.03	**-123.8%**	-112.7%	-123.32%	42.7%	NA
		G_31	-1.70	0.34	317.9	-2.37	-1.03	**-165.3%**	-138.6%	-289.62%	536.9%	NA
		G_08	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
		G_07	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
		G_50	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Table S6: Generalized linear mixed models used to test for differences in the photochemical efficiency (*Fv/Fv*) of *A. cervicornis* exposed to nutrient treatments at control temperature (days 1-78) and heat stress (days 90-113). Factor Nutrient (Model 1) has three levels (Ambient, NH_4 and NH_4 + PO_4), while factor Nutrients2 (Model 2) has two levels (Ambient, and elevated nutrients [NH_4 and NH_4 + PO_4 pooled]).

Model 1: *Fv/Fm* with genets as a random effect

Fixed effects	**numDF**	**denDF**	**F-value**	**p-value**
Nutrient	2	120.5	19.6	<0.001
Days	16	1460.5	666.7	<0.001
Nutrient:Day	31	1460.6	69.3	<0.001
Random effects	**npar**	**logLik**	**AIC**	**Pr(>Chisq)**
none	54	3541.1	-6974.2	
Genotype	53	3541.1	-6899.2	<0.001
Fragment	53	3465.9	-6825.8	<0.001
Replicate (Tank)	53	3502.6	-6974.8	0.080

Model 2: *Fv/Fm* with genotype as fix effect (elevated nutrient treatments pooled)

Fixed effects	**numDF**	**denDF**	**F-value**	**p-value**
Genotype	5	111.1	35.4	<0.001
Nutrients2	1	136.8	22.7	<0.001
Days	16	1329.7	316.8	<0.001
Genotype:Nutrients	5	116.8	10.6	<0.01
Genotype:Days	80	1326.6	2.2	<0.001
Nutrient:Days	16	1331.0	50.1	<0.001
Genotype:Nutrients2:Days	67	1327.4	1.7	<0.001
Random effects	**npar**	**logLik**	**AIC**	**Pr(>Chisq)**
none	194	3134.2	5880.5	
Fragment	193	3133.0	5880.0	<0.001
Replicate (Tank)	193	3094.7	5883.3	0.11

Table S7: Estimated *Fv/Fm* for six *A. cervicornis* genets exposed to nutrient treatments, and subsequent heat stress using Model 2 (see Table S6). Stars (*) in the treatments denote the group of corals that were assigned to these treatments, but that were not exposed to elevated nutrients at the time of the measurement. Percentages of change in bold represent comparison among values that were significantly different based on the Tukey's HSD test. The model includes *genet*, *nutrient* treatment, and *days* in the experiment as interacting fixed factors, as well as *fragment*, and *replicate* tank as random effects.

Days in the experiment (Phase)	Nutrient Treatment	Genet	Em mean	SE	df	Lower CL	Upper CL	% change respect ambient (same day)	% change respect day 1	% change respect control temp (Day 76)	% respect G_48	% respect G_50
1 (baseline)	Ambient	G_48	0.63	0.01	134.52	0.61	0.64	NA	NA	NA	NA	2.7%
		G_62	0.62	0.01	160.13	0.60	0.63	NA	NA	NA	-1.2%	1.4%
		G_31	0.62	0.01	387.81	0.60	0.64	NA	NA	NA	-1.2%	1.4%
		G_08	0.60	0.02	890.40	0.57	0.64	NA	NA	NA	-3.4%	-0.9%
		G_07	0.60	0.01	160.13	0.58	0.61	NA	NA	NA	-4.7%	-2.1%
		G_50	0.61	0.01	510.83	0.59	0.63	NA	NA	NA	-2.6%	NA
	Nutrients	G_48	0.62	0.01	49.29	0.60	0.63	-1.5%	NA	NA	NA	3.8%
		G_62	0.61	0.01	41.20	0.60	0.62	-1.7%	NA	NA	-1.5%	2.3%
		G_31	0.61	0.01	114.54	0.59	0.62	-1.7%	NA	NA	-1.4%	2.4%
		G_08	0.59	0.01	300.03	0.57	0.61	-1.9%	NA	NA	-3.8%	-0.1%
		G_07	0.60	0.01	54.38	0.58	0.61	-0.3%	NA	NA	-3.5%	0.2%
		G_50	0.59	0.01	160.13	0.58	0.61	-2.6%	NA	NA	-3.7%	NA
28 (Control)	Ambient	G_48	0.62	0.01	134.52	0.61	0.64	NA	-0.7%	NA	NA	2.9%
		G_62	0.61	0.01	160.13	0.60	0.63	NA	-0.9%	NA	-1.4%	1.5%
		G_31	0.61	0.01	387.81	0.59	0.63	NA	-0.9%	NA	-1.4%	1.5%
		G_08	0.61	0.02	890.40	0.58	0.65	NA	1.2%	NA	-1.6%	1.3%
		G_07	0.56	0.01	160.13	0.55	0.58	NA	-5.8%	NA	**-9.6%**	**-6.9%**
		G_50	0.60	0.01	510.83	0.58	0.63	NA	-1.0%	NA	-2.8%	NA
	Nutrients	G_48	0.65	0.01	49.29	0.64	0.66	4.2%	5.0%	NA	NA	6.2%
		G_62	0.64	0.01	41.20	0.63	0.66	5.2%	6.1%	NA	-0.4%	5.7%
		G_31	0.65	0.01	114.54	0.63	0.66	5.5%	6.4%	NA	-0.1%	6.0%
		G_08	0.63	0.01	300.03	0.61	0.65	2.9%	6.1%	NA	-2.8%	3.2%
		G_07	0.62	0.01	54.38	0.61	0.63	**10.4%**	4.2%	NA	-4.2%	1.7%
		G_50	0.61	0.01	160.13	0.59	0.63	1.0%	2.7%	NA	-5.8%	NA
65 (Control)	Ambient	G_48	0.60	0.01	134.52	0.59	0.62	NA	-3.9%	NA	0.0%	6.7%
		G_62	0.57	0.01	160.13	0.55	0.59	NA	-7.5%	NA	-5.0%	1.3%
		G_31	0.56	0.01	387.81	0.53	0.58	NA	**-10.2%**	NA	-7.7%	-1.5%
		G_08	0.57	0.02	890.40	0.54	0.60	NA	-5.8%	NA	-5.3%	1.0%
		G_07	0.54	0.01	160.13	0.53	0.56	NA	-8.8%	NA	**-9.6%**	-3.5%
		G_50	0.56	0.01	510.83	0.54	0.59	NA	-7.5%	NA	-6.2%	0.0%
	Nutrients	G_48	0.63	0.01	49.29	0.62	0.65	5.2%	2.7%	NA	0.0%	19.4%
		G_62	0.62	0.01	41.20	0.61	0.64	9.1%	2.6%	NA	-1.5%	17.6%
		G_31	0.62	0.01	114.54	0.61	0.64	**12.3%**	2.6%	NA	-1.5%	17.6%
		G_08	0.59	0.01	300.03	0.57	0.61	3.1%	-1.0%	NA	-7.3%	10.7%
		G_07	0.61	0.01	54.38	0.59	0.62	**11.3%**	1.8%	NA	-4.3%	14.2%
		G_50	0.53	0.01	192.86	0.51	0.55	-6.0%	**-10.7%**	NA	**-16.2%**	0.0%
76 (Control)	Ambient	G_48	0.59	0.01	134.52	0.57	0.60	NA	-6.2%	NA	0.0%	2.9%
		G_62	0.58	0.01	160.13	0.56	0.59	NA	-6.9%	NA	-2.0%	0.9%
		G_31	0.58	0.01	387.81	0.56	0.60	NA	-6.5%	NA	-1.5%	1.4%
		G_08	0.58	0.02	890.40	0.55	0.61	NA	-4.1%	NA	-1.3%	1.6%
		G_07	0.50	0.01	160.13	0.49	0.52	NA	**-15.7%**	NA	**-14.3%**	**-11.8%**
		G_50	0.57	0.01	510.83	0.55	0.59	NA	-6.4%	NA	-2.9%	0.0%
	Nutrients	G_48	0.62	0.01	49.29	0.61	0.63	5.2%	0.1%	NA	0.0%	6.6%
		G_62	0.61	0.01	41.20	0.59	0.62	5.1%	-0.4%	NA	-2.0%	4.4%
		G_31	0.60	0.01	114.54	0.58	0.61	3.3%	-1.8%	NA	-3.3%	3.0%
		G_08	0.59	0.01	300.03	0.57	0.61	2.2%	-0.2%	NA	-4.1%	2.2%
		G_07	0.58	0.01	59.96	0.57	0.59	**15.3%**	-2.6%	NA	-6.1%	0.1%
		G_50	0.58	0.01	387.18	0.56	0.60	1.6%	-2.4%	NA	-6.2%	0.0%

Table S7 (continuation): Estimated *Fv/Fm* for six *A. cervicornis* genets exposed to nutrient treatments, and subsequent heat stress using Model 2 (see Table S6).

Days in the experiment (Phase)	Nutrient Treatment	Genet	Em mean	SE	df	Lower CL	Upper CL	% change respect ambient (same day)	% change respect day 1	% change respect control (Day 76)	% respect G_48	% respect G_50
89 (ramp-up)	Ambient	G_48	0.57	0.01	191.22	0.55	0.59	NA	-9.0%	-3.05%	0.0%	1.1%
		G_62	0.55	0.01	236.28	0.53	0.57	NA	**-10.8%**	-4.21%	-3.1%	-2.0%
		G_31	0.57	0.01	517.23	0.55	0.59	NA	-7.8%	-1.42%	0.1%	1.2%
		G_08	0.56	0.02	890.40	0.52	0.59	NA	-8.1%	-4.14%	-2.4%	-1.3%
		G_07	0.50	0.01	236.28	0.48	0.52	NA	**-15.7%**	0.04%	**-11.6%**	**-10.6%**
		G_50	0.56	0.01	510.83	0.54	0.59	NA	-7.7%	-1.31%	-1.1%	0.0%
	Nutrients	G_48	0.58	0.01	73.93	0.57	0.60	2.5%	-5.4%	-5.53%	0.0%	4.1%
		G_62	0.58	0.01	65.45	0.57	0.60	6.0%	-3.8%	-3.41%	0.2%	4.3%
		G_31	0.59	0.01	190.00	0.57	0.60	2.9%	-3.6%	-1.79%	0.5%	4.7%
		G_08	0.54	0.01	387.95	0.52	0.56	-2.3%	-8.5%	-8.35%	-7.0%	-3.2%
		G_07	0.57	0.01	110.30	0.55	0.58	**12.8%**	-4.6%	-2.11%	-2.7%	1.3%
		G_50	0.56	0.01	516.89	0.54	0.58	-0.5%	-5.7%	-3.32%	-4.0%	0.0%
96 (Heat)	Ambient	G_48	0.58	0.01	191.22	0.56	0.59	NA	-8.1%	-2.03%	0.0%	3.0%
		G_62	0.57	0.01	236.28	0.55	0.59	NA	-8.0%	-1.15%	-1.1%	1.8%
		G_31	0.57	0.01	517.23	0.55	0.60	NA	-7.2%	-0.73%	-0.2%	2.7%
		G_08	0.56	0.02	890.40	0.52	0.59	NA	-7.6%	-3.62%	-2.9%	0.0%
		G_07	0.53	0.01	236.28	0.51	0.55	NA	**-11.3%**	5.26%	**-8.0%**	-5.2%
		G_50	0.56	0.01	510.83	0.53	0.58	NA	-8.4%	-2.06%	-2.9%	0.0%
	Nutrients	G_48	0.53	0.01	73.93	0.52	0.54	-8.0%	-14.2%	**-14.29%**	0.0%	NA
		G_62	0.52	0.01	65.45	0.51	0.54	-7.9%	-13.8%	**-13.43%**	-1.0%	NA
		G_31	0.52	0.01	233.53	0.50	0.53	**-10.1%**	-15.1%	**-13.57%**	-2.5%	NA
		G_08	0.57	0.02	1282.44	0.53	0.62	2.4%	-3.6%	-3.43%	8.0%	NA
		G_07	0.54	0.02	1262.71	0.49	0.59	2.1%	-9.2%	-6.81%	2.1%	NA
99 (Heat)	Ambient	G_48	0.55	0.01	191.22	0.54	0.57	NA	-11.4%	-5.54%	0.0%	-0.2%
		G_62	0.53	0.01	236.28	0.51	0.55	NA	-13.9%	-7.51%	-4.0%	-4.2%
		G_31	0.52	0.01	517.23	0.50	0.55	NA	-15.5%	-9.60%	-5.8%	-6.0%
		G_08	0.53	0.02	890.40	0.50	0.57	NA	-11.6%	-7.77%	-3.7%	-3.9%
		G_07	0.51	0.01	236.28	0.49	0.53	NA	-14.6%	1.34%	**-8.1%**	**-8.3%**
		G_50	0.56	0.01	510.83	0.53	0.58	NA	-8.8%	-2.54%	0.2%	0.0%
	Nutrients	G_48	0.46	0.01	73.93	0.45	0.47	**-16.9%**	-25.2%	**-25.32%**	0.0%	NA
		G_62	0.46	0.01	65.45	0.44	0.47	**-14.5%**	-25.1%	**-24.75%**	-1.2%	NA
		G_31	0.45	0.01	381.88	0.43	0.47	**-14.1%**	-26.1%	**-24.80%**	-2.6%	NA
106 (Heat)	Ambient	G_48	0.53	0.01	191.22	0.51	0.54	NA	-16.1%	**-10.57%**	0.0%	6.1%
		G_62	0.52	0.01	236.28	0.51	0.54	NA	-15.1%	**-8.87%**	-0.1%	5.9%
		G_31	0.47	0.01	517.23	0.45	0.49	NA	**-24.0%**	**-18.76%**	**-10.6%**	-5.2%
		G_08	0.52	0.02	890.40	0.49	0.56	NA	-13.7%	**-10.01%**	-0.7%	5.3%
		G_07	0.45	0.01	236.28	0.44	0.47	NA	**-23.8%**	**-9.67%**	**-13.5%**	**-8.2%**
		G_50	0.50	0.01	510.83	0.47	0.52	NA	-18.8%	**-13.19%**	-5.7%	0.0%
	Nutrients	G_48	0.36	0.01	110.46	0.34	0.37	**-31.8%**	-42.0%	**-42.04%**	0.0%	NA
		G_62	0.32	0.01	126.44	0.31	0.34	**-38.6%**	-47.0%	**-46.79%**	**-10.0%**	NA
		G_31	0.35	0.02	1264.08	0.31	0.40	**-24.8%**	-41.9%	**-40.85%**	-1.3%	NA
110 (Heat)	Ambient	G_48	0.42	0.01	191.22	0.40	0.44	NA	-32.8%	**-28.36%**	0.0%	0.4%
		G_62	0.43	0.01	236.28	0.41	0.44	NA	-31.2%	**-26.07%**	1.2%	1.6%
		G_31	0.39	0.01	517.23	0.37	0.42	NA	**-36.2%**	**-31.78%**	-6.2%	-5.8%
		G_08	0.40	0.02	890.40	0.36	0.43	NA	-34.5%	**-31.67%**	-5.9%	-5.5%
		G_07	0.35	0.01	236.28	0.33	0.37	NA	**-41.2%**	**-30.26%**	**-16.6%**	**-16.3%**
		G_50	0.42	0.01	510.83	0.39	0.44	NA	-31.3%	**-26.56%**	-0.4%	0.0%
	Nutrients	G_48	0.29	0.02	957.33	0.25	0.32	**-31.6%**	-53.4%	**-53.42%**	0.0%	NA
		G_62	0.31	0.02	954.51	0.28	0.35	**-26.3%**	-48.4%	**-48.16%**	9.1%	NA
		G_31	0.15	0.02	1264.08	0.10	0.19	**-62.4%**	-75.6%	**-75.18%**	**-48.5%**	NA

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