The following supplement accompanies the article

Competitive interactions moderate the effects of elevated temperature and atmospheric CO_2 on the health and functioning of oysters

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Supplement 1. Summary of statistical models

We present the data for each response variable including mean ± standard error for each treatment level.

For each response variable, we started with an initial linear regression model of the form:

[*Dependent variable*] ~ Temp + CO_2 + Oyster +
Temp×CO_2 + Temp×Oyster + CO_2×Oyster +
Temp×CO_2×Oyster

Abbreviations:
Temp = Temperature (2 levels; 12°C or 16°C)
CO_2 = atmospheric [CO_2] (2 levels; ambient [400ppm] versus elevated [1000ppm])
Oyster = species composition within each mesocosm (6 levels; two individuals of *C. gigas*; two individuals of *O. edulis*; one *C. gigas* with one *O. edulis*; one *O. edulis* with one *C. gigas*; a single *C. gigas*; a single *O. edulis*]

Where it was necessary to account for violation of homogeneity of variance, we used a linear regression with GLS estimation. All independent factors were treated as nominal and we carried out a manual backwards selection procedure to refine each model. The minimal adequate model is shown for each response variable.

Supplement 2. Model S1 | FILTRATION **(N = 140)**

Minimal adequate model:

Filtration ~ Oyster,
weights = varIdent(form = ~ 1|Oyster), method = "ML")

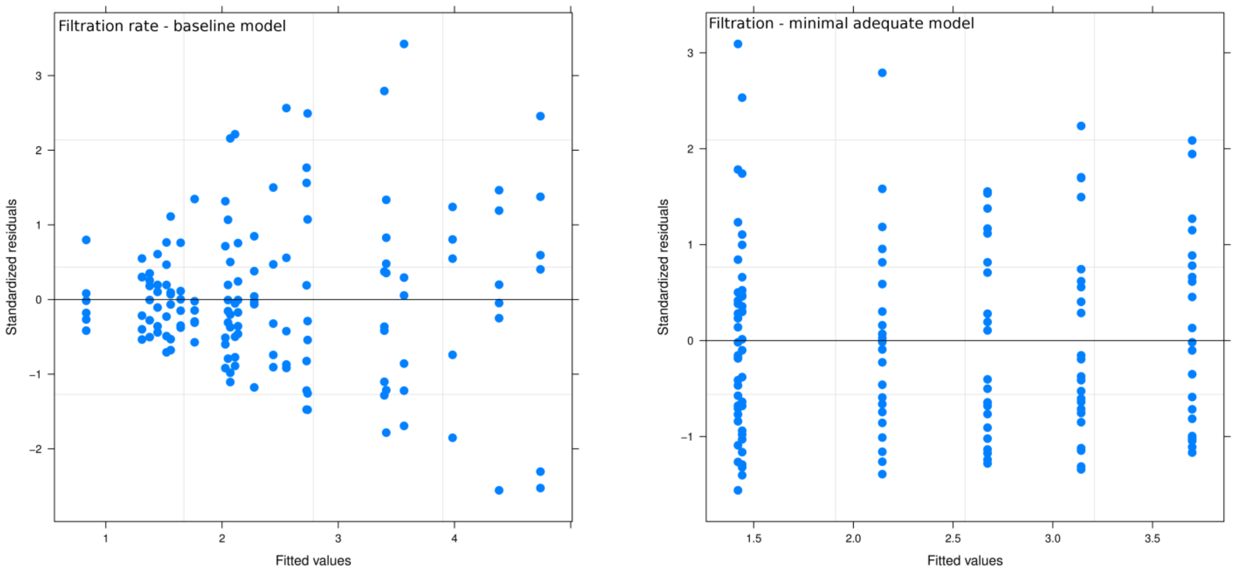

Figure S1. Variance plots of the baseline model (full factorial) and the minimal adequate linear regression model after weighting among variance covariates and backwards step-wise elimination of insignificant terms for response variable *Filtration*.

Table S1a. Contribution of factors from the minimal adequate model to *Filtration* rates.

	d.f.[1]	AIC[2]	*L*- Ratio[3]	*P*-value
Full model	30	533.5		
Oyster	5	538.7	34.47	<0.001

[1] Degrees of freedom
[2] Akaike information criterion
[3] Likelihood ratio

Table S1b. Pairwise comparisons of *Filtration* for all levels in "Oyster". Data are coefficients ± standard error (in italics) and underneath the t-values with superscript P-values in parentheses comparing row to column levels. The relevant species composition comparisons are highlighted in bold.

	Intra *C. gigas*	Intra *O. edulis*	Inter *C. gigas*	Inter *O. edulis*	Single *C. gigas*	Single *O. edulis*
Intra *C. gigas*[1]	-					
Intra *O. edulis*[2]	*2.227 ± 0.566* ($4.03^{<0.001}$)	-				
Inter *C. gigas*[3]	*0.557 ± 0.695* ($0.80^{0.424}$)	*-1.721 ± 0.467* ($-3.68^{<0.001}$)	-			
Inter *O. edulis*[4]	*2.256 ± 0.562* ($4.01^{<0.001}$)	*-0.021 ± 0.228* ($-0.09^{0.927}$)	*1.700 ± 0.463* ($3.67^{<0.001}$)	-		
Single *C. gigas*[5]	***1.026 ± 0.668*** **($1.54^{0.127}$)**	*-1.251 ± 0.426* ($-2.94^{0.004}$)	***0.469 ± 0.586*** **($0.80^{0.425}$)**	*-1.230 ± 0.421* ($-2.92^{0.004}$)	-	
Single *O. edulis*[6]	*1.554 ±0.605* ($2.57^{0.011}$)	***-0.724 ± 0.319*** **($-2.27^{0.025}$)**	*0.997 ± 0.514* ($1.94^{0.054}$)	***-0.703 ± 0.312*** **($-2.25^{0.026}$)**	*0.528 ± 0.476* ($1.11^{0.270}$)	-

[1] *Crassostrea gigas* in intraspecific competition (i.e. with other *C. gigas*).
[2] *Ostrea edulis* in intraspecific competition (i.e. with other *O. edulis*).
[3] *C. gigas* in interspecific competition (i.e. with *O. edulis*).
[4] *O. edulis* in interspecific competition (i.e. with *C. gigas*).
[5] *C. gigas* with no competition.
[6] *O. edulis* with no competition.

Supplement 3. Model S2 | Respiration (N = 108)

Minimal adequate model:
Respiration ~ Oyster,
weights = varIdent(form=~1|CO_2×Oyster), method = "ML")

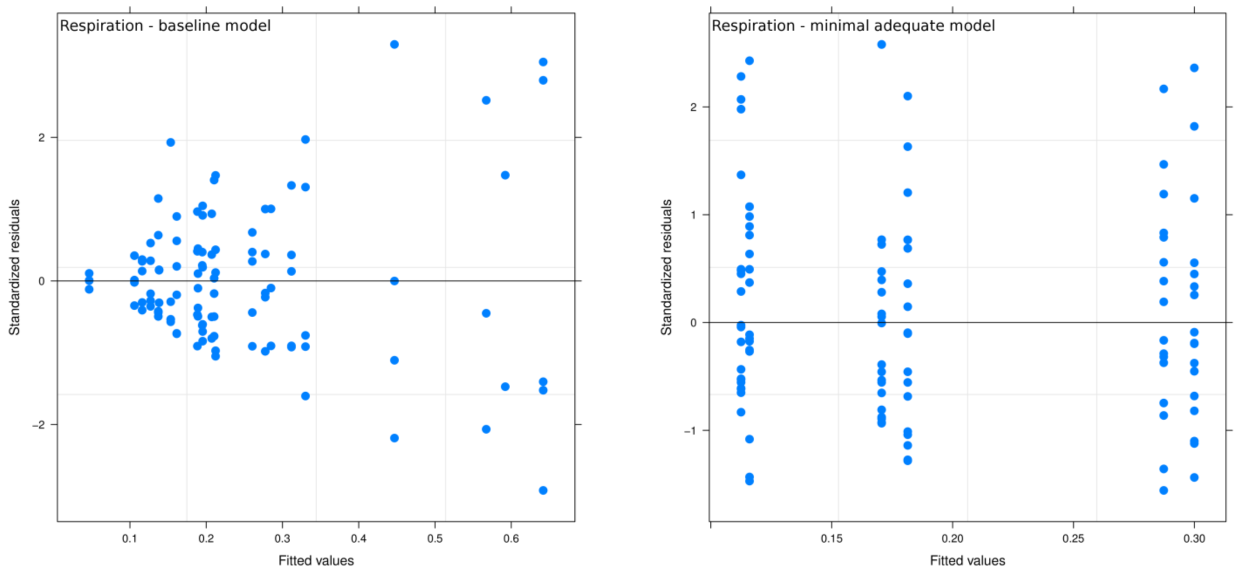

Figure S2. Variance plots of the baseline model (full factorial) and the minimal adequate linear regression model after weighting among variance covariates and backwards step-wise elimination of insignificant terms response variable *Respiration*.

Table S2a. Contribution of factors from the minimal adequate model to *Respiration.*

	d.f.	AIC	*L*- Ratio	*P*-value
Full model	36	-36.6		
Oyster	5	-35.8	21.44	<0.001

Table S2b. Pairwise comparisons of *Respiration* for all levels in "Oyster". Data are coefficients ± standard error (in italics) with underneath the t-values and superscript P-values in parentheses, comparing row to column levels. The relevant species composition comparisons are highlighted in bold.

	Intra *C. gigas*	Intra *O. edulis*	Inter *C. gigas*	Inter *O. edulis*	Single *C. gigas*	Single *O. edulis*
Intra *C. gigas*	-					
Intra *O. edulis*	*-0.055 ± 0.033* (-1.63$^{0.105}$)	-				
Inter *C. gigas*	*-0.004 ± 0.038* (-0.09$^{0.927}$)	*0.058 ± 0.044* (1.32$^{0.191}$)	-			
Inter *O. edulis*	*-0.184 ± 0.048* (-3.87$^{<0.001}$)	*-0.129 ± 0.052* (-2.47$^{0.015}$)	*-0.187 ± 0.056* (-3.37$^{0.001}$)	-		
Single *C. gigas*	***-0.171 ± 0.047*** **(-3.64$^{<0.001}$)**	*-0.117 ± 0.052* (-2.24$^{0.027}$)	***-0.175 ± 0.055*** **(-3.17$^{0.002}$)**	*0.013 ± 0.062* (0.20$^{0.839}$)	-	
Single *O. edulis*	*-0.065 ± 0.037* (-1.78$^{0.078}$)	***-0.011 ± 0.043*** **(-0.25$^{0.802}$)**	*-0.069 ± 0.047* (-1.47$^{0.144}$)	***0.119 ± 0.555*** **(2.17$^{0.032}$)**	*0.106 ± 0.054* (1.95$^{0.054}$)	-

Supplement 4. Model S3 | Haemocytes (N = 140)

Minimal adequate model:

Haemocytes ~ Temp + CO_2 + Oyster +
Temp×CO_2 + CO_2×Oyster,
weights = varIdent(form = ~ 1|CO_2×Oyster), method = "ML")

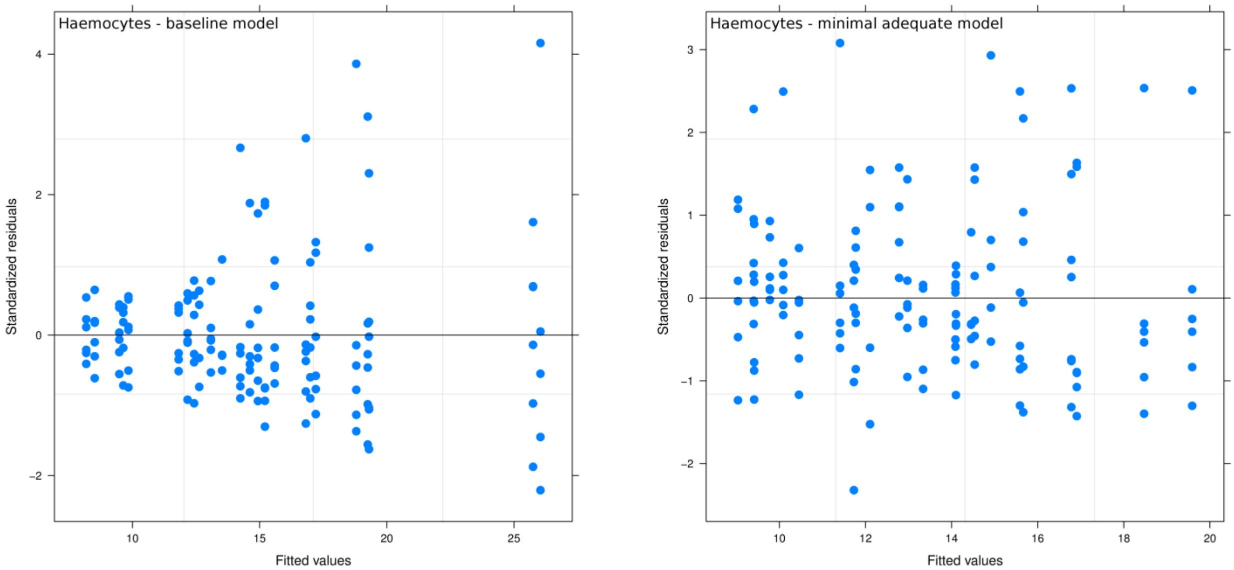

Figure S3. Variance plots of the baseline model (full factorial) and the minimal adequate linear regression model after weighting among variance covariates and backwards step-wise elimination of insignificant terms.

Table S3a. Contribution of factors from the minimal adequate model to *Haemocytes*.

	d.f.	AIC	*L*- Ratio	*P*-value
Full model	36	1034.3		
Temp	2	1095.9	9.14	0.010
CO_2	5	1029.3	23.58	0.001
Oyster	10	1021.9	22.28	0.014
Temp×CO_2	5	1023.9	14.22	0.014
CO_2×Oyster	1	1026.7	9.04	0.003

Table S3b. Pairwise comparisons of *Haemocytes* for all levels in "Temp×CO_2". Data are coefficients ± standard error (in italics) with underneath the t-values with superscript P-values in parentheses, comparing row to column levels.

	Temp	12°C		16°C	
Temp	CO_2	400 ppm	1000 ppm	400 ppm	1000 ppm
12°C	400 ppm	-			
	1000 ppm	*-2.003 ± 1.925* $(-1.04^{0.300})$	-		
16°C	400 ppm	*-5.188 ± 2.211* $(-2.35^{0.020})$	*-3.184 ± 1.907* $(-1.67^{0.097})$	-	
	1000 ppm	*1.039 ± 1.875* $(0.55^{0.580})$	*3.043 ± 1.505* $(2.02^{0.045})$	*6.277 ± 1.857* $(3.35^{0.001})$	-

Table S3c. Pairwise comparisons of *Haemocytes* for all levels in "CO_2×Oyster". Data are coefficients ± standard error (in italics) with underneath the t-values and superscript P-values in parentheses, comparing row to column levels. The relevant species composition comparisons are highlighted in bold.

	CO_2	400 ppm						1000 ppm					
CO_2	Oyster	Intra *C. gigas*	Intra *O. edulis*	Inter *C. gigas*	Inter *O. edulis*	Single *C. gigas*	Single *O. edulis*	Intra *C. gigas*	Intra *O. edulis*	Inter *C. gigas*	Inter *O. edulis*	Single *C. gigas*	Single *O. edulis*
400 ppm	Intra *C. gigas*	-											
	Intra *O. edulis*	*3.143 ± 4.708* (0.67$^{0.506}$)	-										
	Inter *C. gigas*	*5.393 ± 4.293* (1.26$^{0.211}$)	*2.250 ± 3525* (0.64$^{0.524}$)	-									
	Inter *O. edulis*	*3.631 ± 4.729* (0.77$^{0.444}$)	*0.488 ± 4.045* (0.12$^{0.904}$)	*1.763 ± 3.553* (0.50$^{0.621}$)	-								
	Single *C. gigas*	***0.889 ± 4.503*** **(0.20$^{0.844}$)**	*-2.254 ± 3.778* (-0.60$^{0.552}$)	***-4.504 ± 3.246*** **(-1.39$^{0.168}$)**	*-2.742 ± 3.804* (-0.72$^{0.472}$)	-							
	Single *O. edulis*	*-3.381 ± 6.048* (-0.56$^{0.577}$)	***-6.524 ± 5.529*** **(-1.18$^{0.240}$)**	*-8.774 ± 5.180* (-1.69$^{0.093}$)	***-7.012 ± 5.547*** **(-1.26$^{0.209}$)**	*-4.270 ± 5.356* (-0.80$^{0.427}$)	-						
1000 ppm	Intra *C. gigas*	*1.114 ± 4.674* (0.24$^{0.812}$)	*-2.029 ± 3.980* (-0.51$^{0.611}$)	*-4.279 ± 3.479* (-1.23^{221})	*-2.527 ± 4.005* (-0.63$^{0.531}$)	*0.225 ± 3.735* (0.06$^{0.952}$)	*4.495 ± 5.500* (0.82$^{0.415}$)	-					
	Intra *O. edulis*	*3.756 ± 4.533* (0.83$^{0.409}$)	*0.613 ± 3.814* (0.16$^{0.873}$)	*-1.638 ± 3.288* (-0.50$^{0.619}$)	*0.125 ± 3.840* (0.03$^{0.974}$)	*2.867 ± 3.558* (0.81$^{0.422}$)	*7.137 ± 5.381* (1.33$^{0.187}$)	*2.642 ± 3.772* (0.70$^{0.485}$)	-				
	Inter *C. gigas*	*-5.315 ± 5.631* (-0.94$^{0.347}$)	*-8.458 ± 5.069* (-1.67$^{0.098}$)	*-10.71 ± 4.686* (-2.29$^{0.024}$)	*-8.946 ± 5.089* (-1.76$^{0.081}$)	*-6.204 ± 4.879* (-1.27$^{0.206}$)	*-1.934 ± 6.333* (-0.31$^{0.761}$)	*-6.429 ± 5.038* (-1.28$^{0.204}$)	*-9.071 ± 4.907* (-1.85$^{0.067}$)	-			
	Inter *O. edulis*	*1.923 ± 4.068* (0.47$^{0.637}$)	*-1.221 ± 3.247* (-0.38$^{0.708}$)	*-3.471 ± 2.608* (-1.33$^{0.186}$)	*-1.708 ± 3.277* (-0.52$^{0.603}$)	*1.033 ± 2.941* (0.35$^{0.726}$)	*5.303 ± 4.995* (1.06$^{0.290}$)	*0.809 ± 3.197* (0.25$^{0.801}$)	*-1.833 ± 2.987* (-0.61$^{0.541}$)	*7.238 ± 4.481* (1.62$^{0.109}$)	-		
	Single *C. gigas*	*7.405 ± 3.902* (1.90$^{0.060}$)	*4.262 ± 3.036* (1.40$^{0.163}$)	*2.012 ± 2.341* (0.86$^{0.392}$)	*3.775 ± 3.069* (1.23$^{0.221}$)	*6.516 ± 2.707* (2.41$^{0.018}$)	*10.79 ± 4.861* (2.22$^{0.028}$)	***6.292 ± 2.983*** **(2.11$^{0.037}$)**	*3.650 ± 2.757* (1.32$^{0.188}$)	***12.72 ± 4.331*** **(2.94$^{0.004}$)**	*5.483 ± 1.896* (2.89$^{0.005}$)	-	
	Single *O. edulis*	*7.000 ± 4.031* (1.74$^{0.085}$)	*3.857 ± 3.201* (1.20$^{0.230}$)	*1.607 ± 2.551* (0.63$^{0.530}$)	*3.369 ± 3.232* (1.04$^{0.299}$)	*6.111 ± 2.890* (2.11$^{0.036}$)	*10.38 ± 4.966* (2.09$^{0.039}$)	*-0.405 ± 1.816* (-0.22$^{0.824}$)	***3.244 ± 2.937*** **(1.10$^{0.272}$)**	*12.32 ± 4.448* (2.77$^{0.006}$)	***5.078 ± 2.150*** **(2.36$^{0.020}$)**	*-0.405 ± 1.816* (-0.22$^{0.824}$)	-

Supplement 5. Model S4 | Phagocytosis (N = 140)

Minimal adequate model:

Phagocytosis ~ CO_2,
weights = varIdent(form = ~ 1|CO_2) , method = "ML")

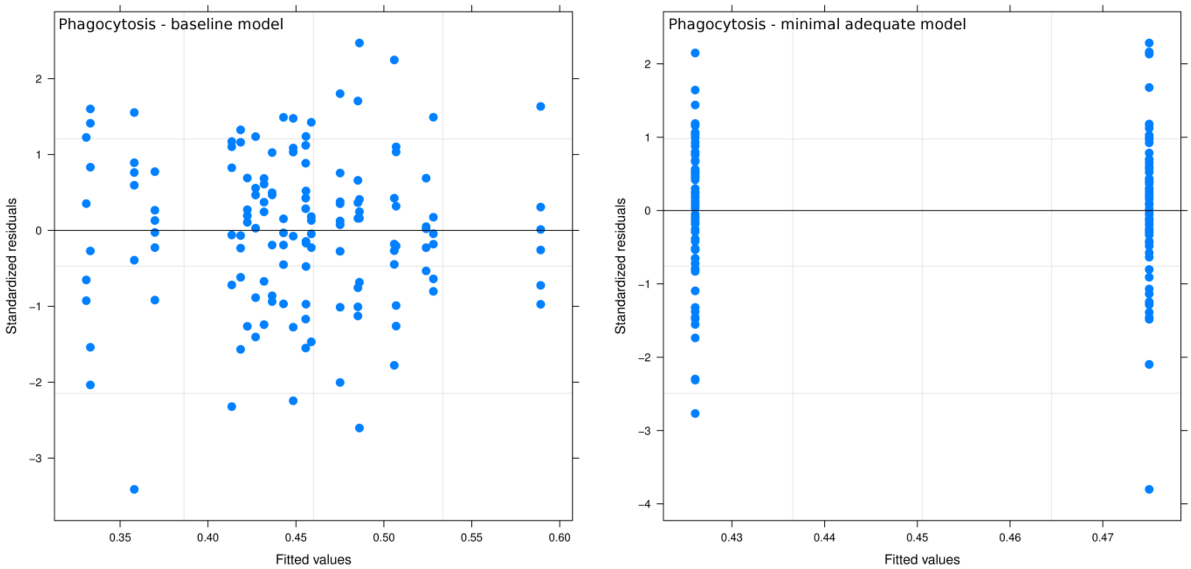

Figure S4. Variance plots of the baseline model (full factorial) and the minimal adequate linear regression model after weighting among variance covariates and backwards step-wise elimination of insignificant terms.

Table S4. Contribution of factors from the minimal adequate model to *Phagocytosis.*

	d.f	AIC	L Ratio	P-value
Full model	26	-188.4		
CO_2	1	-193.8	6.07	0.014

Supplement 6. Model S5 | PROTEINS (N = 140)

Minimal adequate model:

Proteins ~ Temp + Oyster +
Temp×Oyster
weights = NULL , method = "ML")

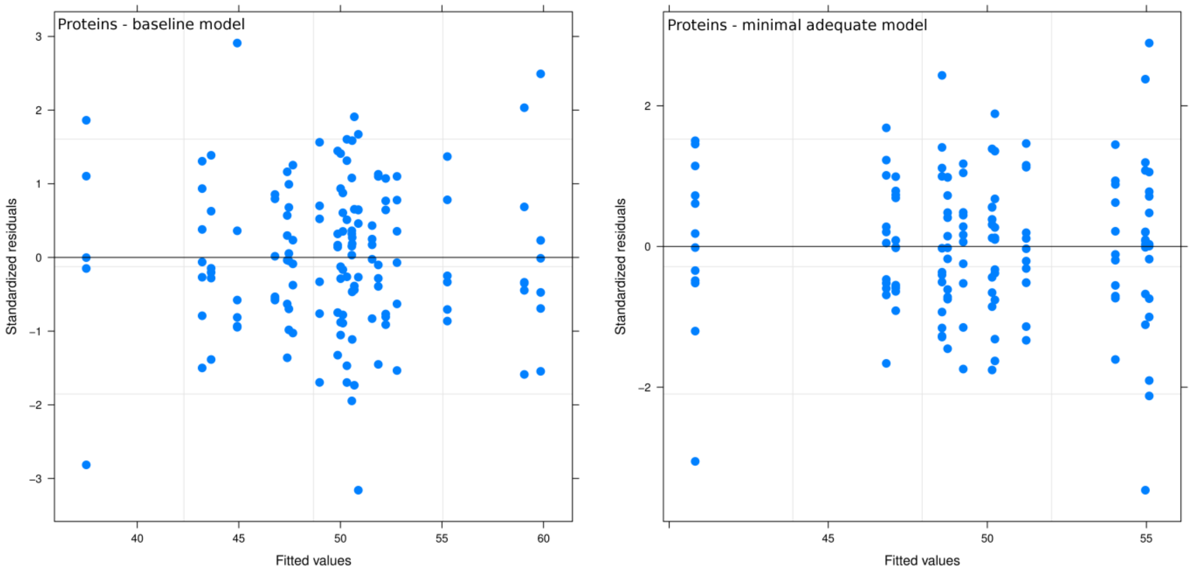

Figure S5. Variance plots of the baseline model (full factorial) and the minimal adequate linear regression model after weighting among variance covariates and backwards step-wise elimination of insignificant terms.

Table S5a. Contribution of factors from the minimal adequate model to *Proteins.*

	d.f.	AIC	*L*- Ratio	*P*-value
Full model	25	1082.2		
Temp	6	1072.8	16.03	0.014
Oyster	10	1065.9	17.16	0.071
Temp×Oyster	5	1073.6	12.77	0.025

Table S5b. Pairwise comparisons of *Proteins* for all levels in “Temp×Oyster”. Data are coefficients ± standard error (in italics) with underneath the t-values and superscript P-values in parentheses, comparing row to column levels. The relevant species composition comparisons are highlighted in bold.

	Temp	12°C						16°C					
Temp	Oyster	Intra *C. gigas*	Intra *O. edulis*	Inter *C. gigas*	Inter *O. edulis*	Single *C. gigas*	Single *O. edulis*	Intra *C. gigas*	Intra *O. edulis*	Inter *C. gigas*	Inter *O. edulis*	Single *C. gigas*	Single *O. edulis*
12°C	Intra *C. gigas*	-											
	Intra *O. edulis*	*-6.006 ± 4.169* $(-1.44^{0.152})$	-										
	Inter *C. gigas*	*-14.15 ± 4.169* $(-3.39^{0.001})$	*-8.143 ± 4.169* $(-1.95^{0.053})$	-									
	Inter *O. edulis*	*-6.303 ± 4.169* $(-1.51^{0.133})$	*-0.297 ± 4.169* $(-0.07^{0.943})$	*7.846 ± 4.169* $(1.88^{0.062})$	-								
	Single *C. gigas*	***-8.426 ± 4.263*** **$(-1.98^{0.050)}$**	*-2.419 ± 4.263* $(-0.57^{0.571})$	***5.724 ± 4.263*** **$(1.34^{0.182})$**	*-2.122 ± 4.263* $(-0.50^{0.619})$	-							
	Single *O. edulis*	*-9.420 ± 4.263* $(-2.21^{0.029})$	***-3.414 ± 4.263*** **$(-0.80^{0.425})$**	*4.729 ± 4.263* $(1.11^{0.269})$	***-3.117 ± 4.263*** **$(-0.73^{0.466})$**	*-0.995 ± 4.263* $(0.23^{0.820})$	-						
16°C	Intra *C. gigas*	*-13.21 ± 4.169* $(-3.17^{0.002})$	*-7.201 ± 4.169* $(-1.73^{0.087})$	*0.943 ± 4.169* $(0.23^{0.821})$	*-6.904 ± 4.169* $(-1.66^{0.100})$	*-4.781 ± 4.263* $(-1.12^{0.264})$	*-3.786 ± 4.263* $(-0.89^{0.376})$	-					
	Intra *O. edulis*	*-10.40 ± 4.169* $(-2.50^{0.014})$	*-4.398 ± 4.169* $(-1.05^{0.293})$	*3.745 ± 4.169* $(0.90^{0.371})$	*-4.101 ± 4.169* $(-0.98^{0.327})$	*-1.979 ± 4.263* $(-0.46^{0.643})$	*-0.984 ± 4.263* $-0.23^{0.818}$	*2.803 ± 4.169* $(0.67^{0.503})$	-				
	Inter *C. gigas*	*-7.758 ± 4.169* $(-1.86^{0.065})$	*-1.752 ± 4.169* $(-0.42^{0.675})$	*6.391 ± 4.169* $(1.53^{0.128})$	*-1.455 ± 4.169* $(-0.35^{0.728})$	*0.667 ± 4.263* $(0.16^{0.876})$	*1.662 ± 4.263* $(0.39^{0.697})$	*5.449 ± 4.169* $(1.31^{0.194})$	*2.646 ± 4.169* $(0.63^{0.527})$	-			
	Inter *O. edulis*	*-7.934 ± 4.169* $(-1.90^{0.059})$	*-1.928 ± 4.269* $(-0.46^{0.645})$	*6.216 ± 4.169* $(-0.39^{0.696})$	*-1.630 ± 4.169* $(-0.39^{0.696})$	*0.492 ± 4.263* $(0.12^{0.908})$	*1.487 ± 4.263* $(0.35^{0.728})$	*5.273 ± 4.169* $(1.26^{0.208})$	*2.471 ± 4.169* $(0.59^{0.554})$	*-0.176 ± 4.169* $(-0.04^{0.966})$	-		
	Single *C. gigas*	*-14.27 ± 4.169* $(-3.42^{0.001}$	*-8.264 ± 4.169* $(-1.98^{0.050})$	*-0.121 ± 4.169* $(-0.03^{0.977})$	*-7.967 ± 4.169* $(-1.91^{0.058})$	*-5.845 ± 4.263* $(-1.37^{0.173})$	*-4.850 ± 4.263* $(-1.14^{0.257})$	***-1.064 ± 4.169*** **$(-0.26^{0.799})$**	*-3.866 ± 4.169* $(-0.93^{0.355})$	***-6.512 ± 4.169*** **$(-1.56^{0.121})$**	*-6.337 ± 4.169* $(-1.52^{0.131})$	-	
	Single *O. edulis*	*-9.332 ± 4.263* $(-2.19^{0.030})$	*-3.326 ± 4.263* $(-0.78^{0.437})$	*4.817 ± 4.263* $(1.13^{0.261})$	*-3.029 ± 4.263* $(-0.71^{0.479})$	*-0.907 ± 4.354* $(-0.21^{0.835})$	*0.088 ± 4.354* $(0.02^{0.984})$	*3.875 ± 4.263* $(0.91^{0.365})$	***1.072 ± 4.263*** **$(0.25^{0.802})$**	*-1.574 ± 4.263* $(-0.37^{0.713})$	***-1.398 ± 4.263*** **$(-0.33^{0.743})$**	*-4.938 ± 4.263* $(1.16^{0.249})$	-

Supplement 7. Model S6 | GLUCOSE (N = 140)

Intercept only model. Data are shown for information only, as no significant terms were found.

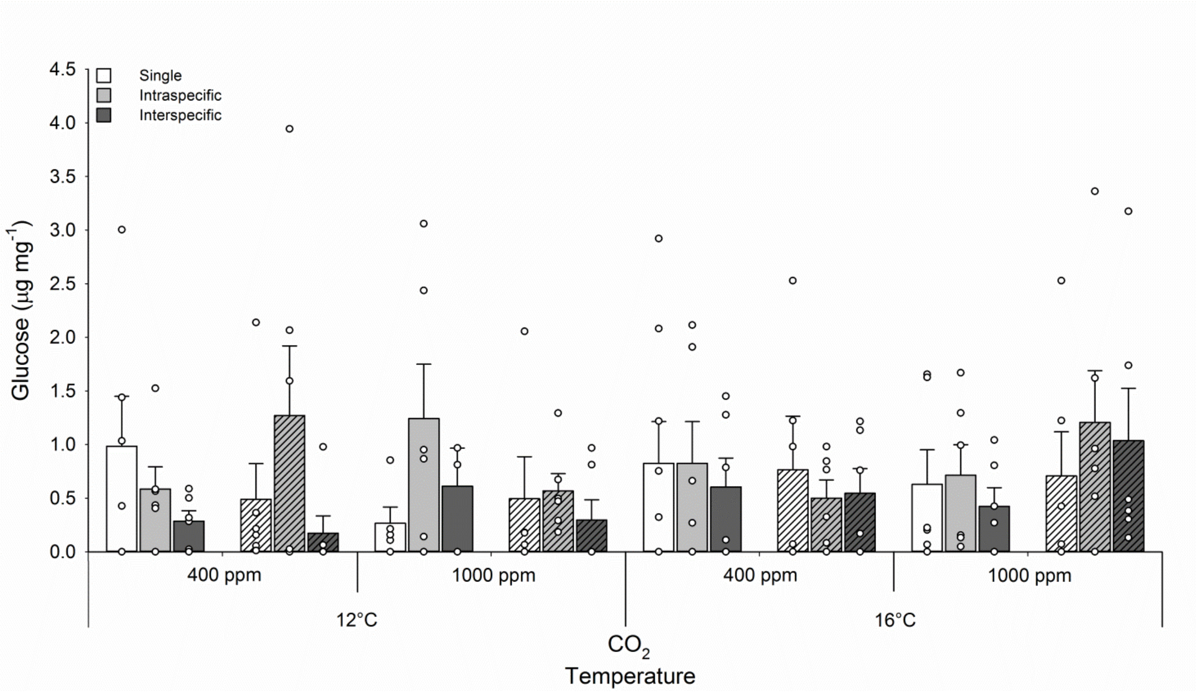

Figure S6. Glucose concentration in haemolymph of *C. gigas* (no hashed bars) and *O. edulis* (hashed bars) maintained alone and in intra- and inter-specific mixtures under elevated temperature and concentration of CO_2. Bars indicate mean (± SEM) and dots are raw data values.