

Supplementary figures

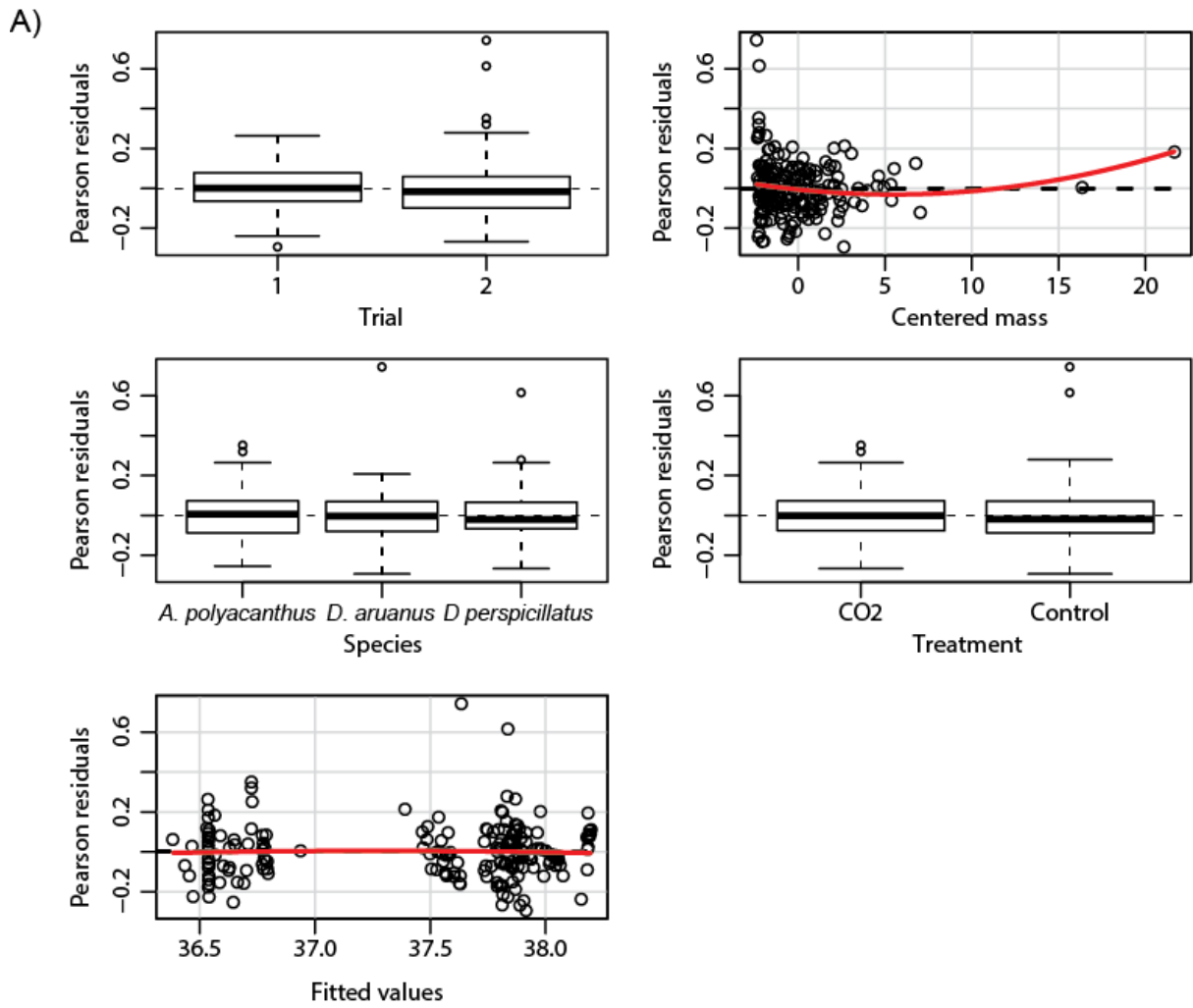
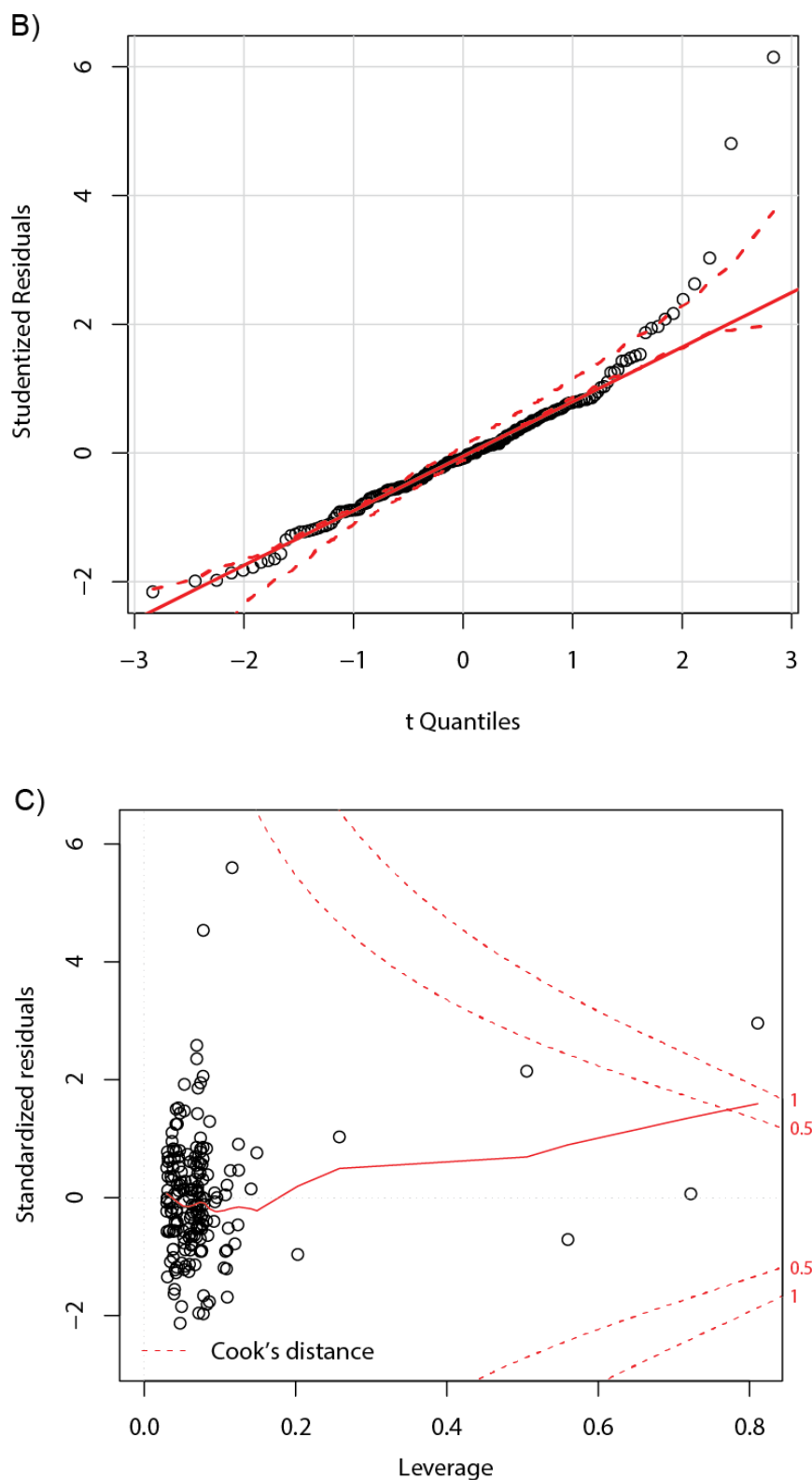


Fig. S1A



Figs. S1B, S1C

Fig. S1 Diagnostic plots showing the distribution of residuals from the model $CT_{\max} \sim (\text{trial} + \text{mass} + \text{species} + \text{treatment})^2$ to assess (A) homoscedasticity (i.e., homogeneity of variance), (B) normality (via a quantile-quantile plot), and (C) leverage (i.e., the influence of values on model output). All data points were included in the model. T1 and T2 represent the two separate trials. For a discussion of these diagnostic plots and reasons for excluding data points from general linear models, see Kim (2015) and Prabhakaran (2016).

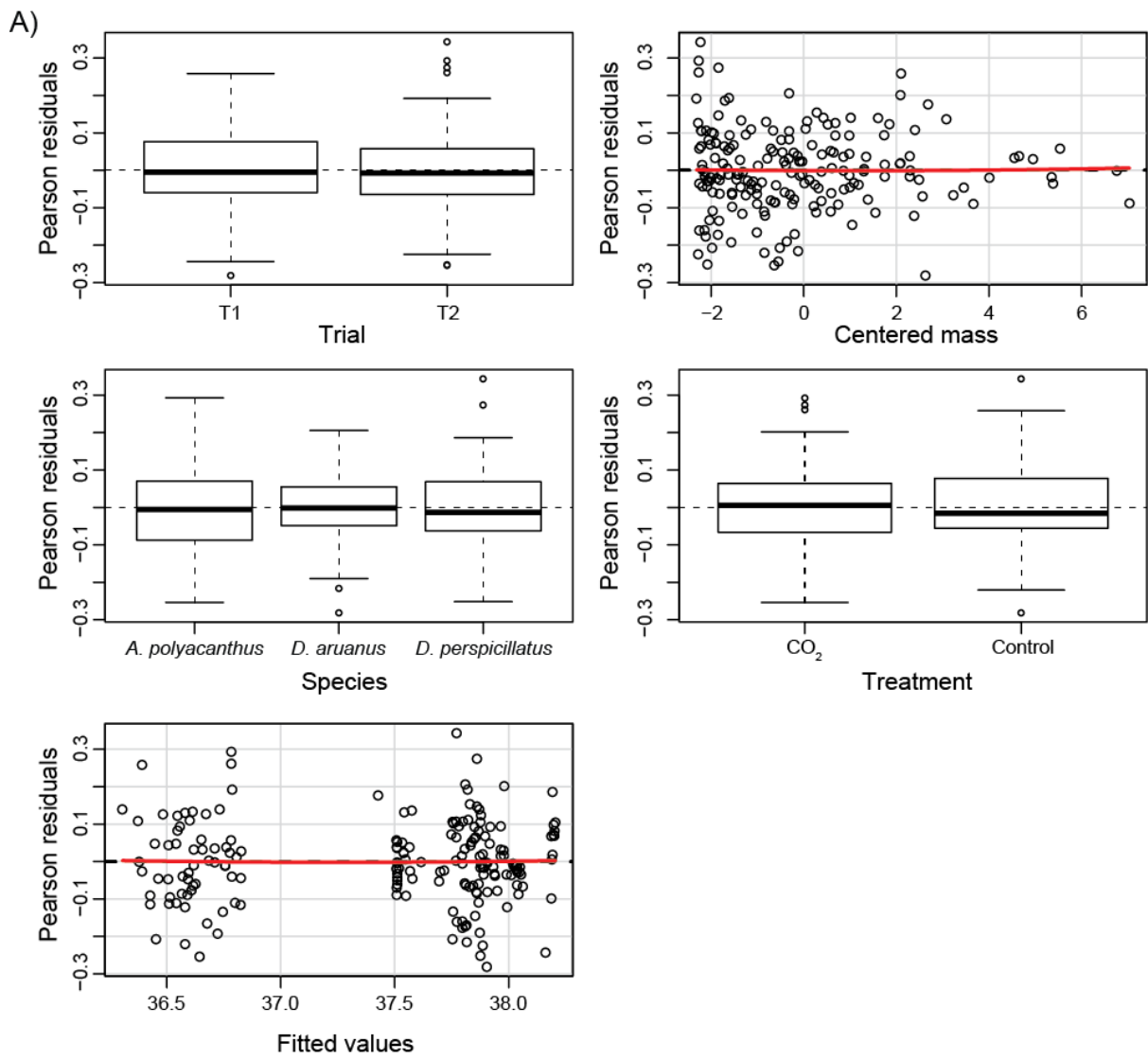
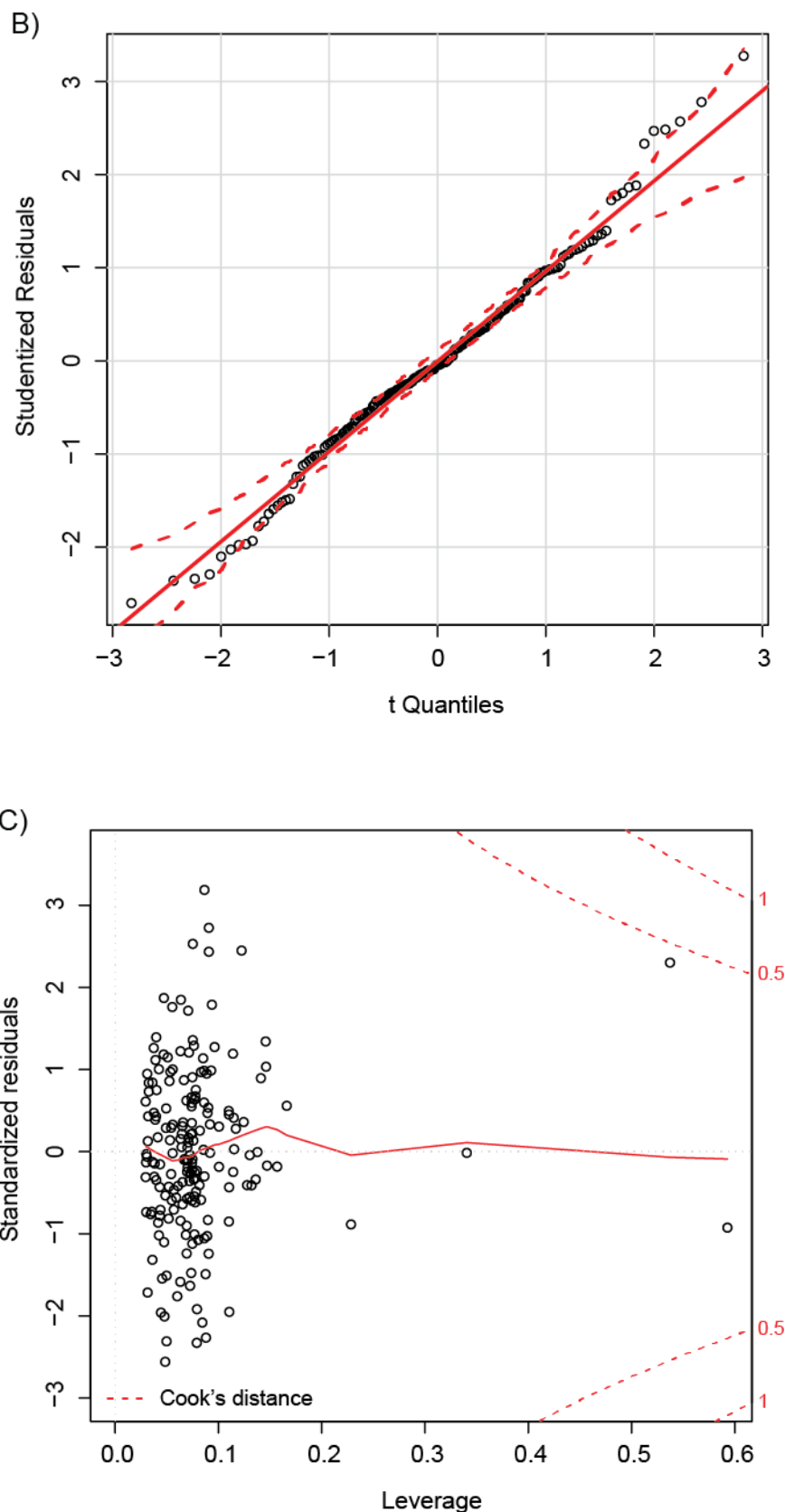


Fig. S2A



Figs. S2B, S2C

Fig. S2 Diagnostic plots showing the distribution of residuals from the model $CT_{\max} \sim (\text{trial} + \text{mass} + \text{species} + \text{treatment})^2$ to assess (A) homoscedasticity (i.e., homogeneity of variance), (B) normality (via a quantile-quantile plot), and (C) leverage (i.e., the influence of values on model output). *Five outliers were excluded from the model* (identified as dotted green circles in Figs. 2, 3 and S3). T1 and T2 represent the two separate trials.

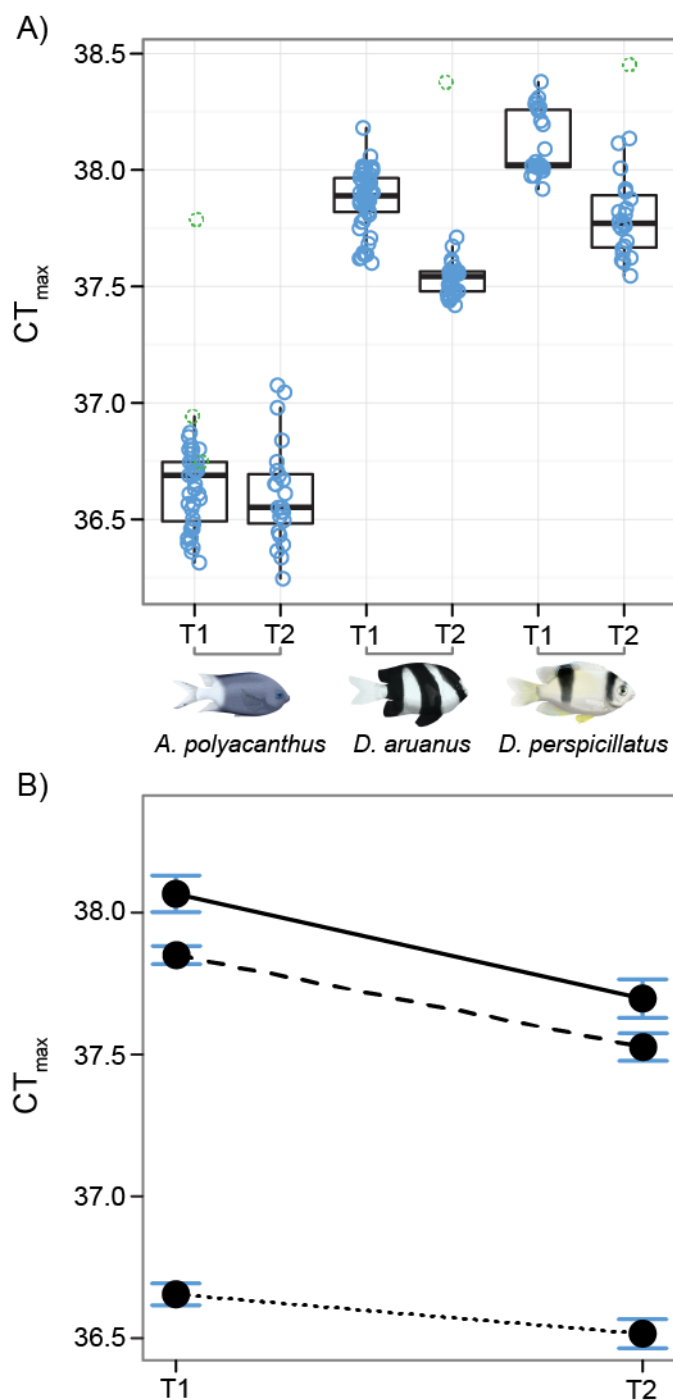


Fig. S3

Fig. S3 CT_{max} of three damselfish species across two trials (T1 and T2). (A) Box-and-whisker plots showing the distribution of the raw data with five outliers (excluded from the model) indicated with dotted green circles. (B) Model predictions for *A. polyacanthus* (dotted line), *D. aruanus* (dashed line) and *D. perspicillatus* (solid line). Error bars are 95% confidence intervals.

References

Kim, B. (2015). Understanding diagnostic plots for linear regression analysis.

University of Virginia Library <http://data.library.virginia.edu/diagnostic-plots/>

Prabhakaran, S. (2016). Outlier detection and treatment with R. R-bloggers

<https://www.r-bloggers.com/outlier-detection-and-treatment-with-r/>