Figure S1. Predicted versus measured parameters for *P. antarctica* (blue) and *C. flexuosus* (orange) using the 'best' (highest Bayes factor) model. Model versus observations: Before discussing the results for each treatment, we first will present the results for the fitting of the data with the multivariate model. We did this to gain confidence that the trends within the data are robust and to signify the influence individual and combined treatments have on cell growth and physiology. When the measured data are compared to the prediction of the 'best' (highest Bayes factor) model, a strong linear relationship was obtained for all measured parameters. This demonstrates that a linear model (Equation 1) is able to explain patterns in the data.

Model Selection: In the most general case, a multivariate relationship may be approximated by a first order polynomial:

$$f(x,y) = a_{11}xy + a_{10}x + a_{01}y + a_{00} \quad (1)$$

Where *x* and *y* are independent variables, *a* is a model parameter, and each additive term in the equation is termed a covariate. Given this form, we evaluate the skill of all possible combinations and permutations of model covariates against each of our dependent variables. A model with high *skill* is one which explains the most variance in the dependent variable with the fewest covariates - i.e. minimising over-fitting.

Metrics such as R^2 and χ^2 are generally used to gauge the goodness-of-fit of a model, but these two metrics neglect the number of cofactors included in the model so do not allow us to discern the *skill* of the model.

Information Criteria, such as the Aikake Information Criterion (AIC) or Bayesian Information Criterion (BIC) take the goodness-of-fit, the number of covariates, and sample size (BIC only) into consideration to give a measure of the quality of a model. These information criteria are useful but are ultimately approximations of more difficult-to-calculate metrics from information theory ('information loss' and 'Bayes factor' in the cases of AIC and BIC, respectively).

In our evaluation, we employ a method to directly calculate the Bayes Factor of a model compared to a null-model ($y=c$) based on the model R^2, the number of covariates (= degrees of freedom), and sample size (Rouder & Morey, 2013).

The Bayes Factor (Kass & Raftery, 1995) was defined as:

$$B_{01} = \frac{p(\mathrm{D}|H_1)}{p(\mathrm{D}|H_0)} \quad (2)$$

Where the probability (p) of the data (D) given your hypothesis (H_1) relative to the probability of the data given a null hypothesis. In other words, if $B_{01} = 5$, the observed data are 5 times more probable if H_1 is correct, rather than H_0. Using the Bayes Factors the relative probability of the data given for any two models may also be calculated and compared to the same null model, i.e.:

$$B_{21} = \frac{B_{20}}{B_{10}} \quad (3)$$

Using this approach, we calculate the probability of all models relative to the 'best' model (that with the highest *skill*). We then use these Bayes factors as weights when calculating an ensemble 'best fit' prediction, and in assessing the relative importance of independent variables. In this figure, the hashed line represents the 1:1 relationship between measured and predicted values.

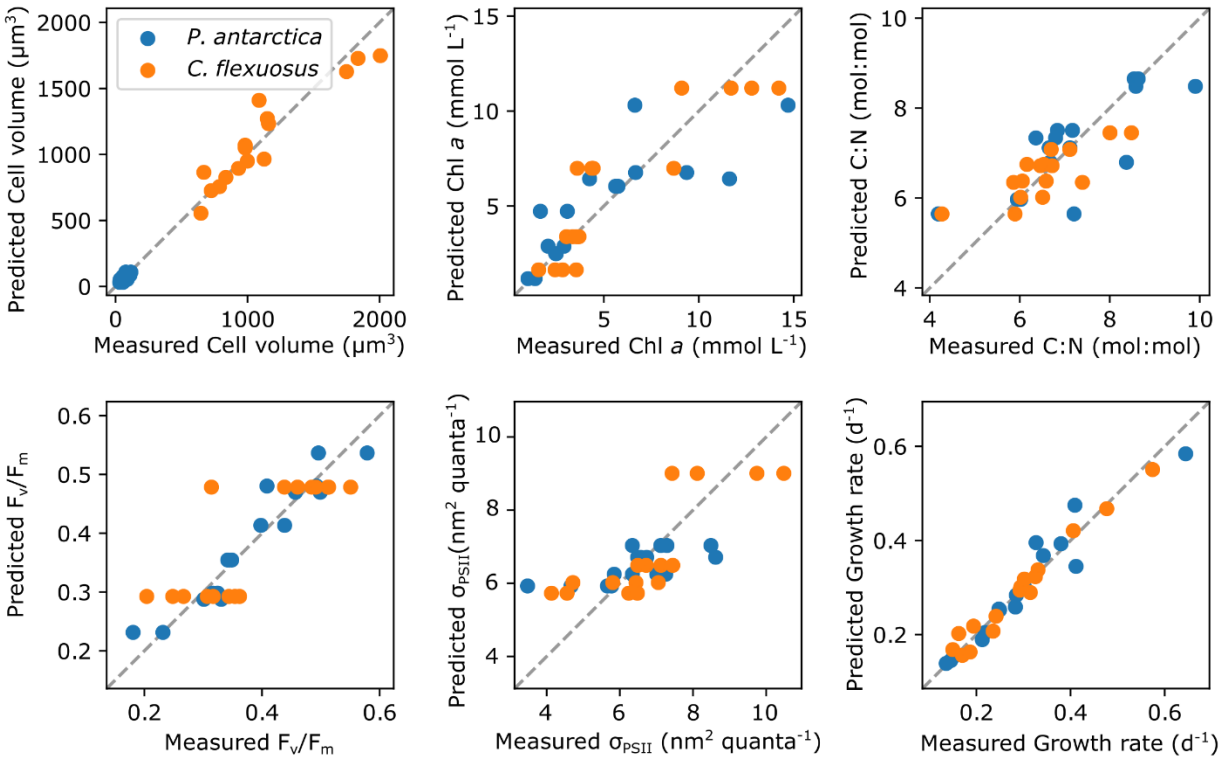


Figure S2. Predicted versus measured parameters for *P. antarctica* (orange) and *C. flexuosus* (blue) using all the model runs. While the 'best' (highest Bayes factor) model fits the measured data well, there is no *a priori* reason to assume that patterns in the data follow a particular functional form. In other words, it is not reasonable to assume trends solely on this single 'best' model. Given the uncertainty in functional form linking independent and dependent variables, a more realistic picture of the relationships in our dataset can be gained from considering *all* possible linear models. To accomplish this, we calculated the predicted values of all possible models, and calculate our 'best fit' values from the weighted average of all models using the Bayes Factors as weights. This approach allowed us to identify relationships within the data without prescribing a functional form to the relationship. We extended this weighted-ensemble approach to estimate the relative importance of each model parameter using a kernel-density estimator where the contribution of each model to the overall distribution is weighted by its Bayes Factor. This provided us with an estimate of the relative importance of each covariate. In this figure, the hashed line represents the 1:1 relationship between measured and predicted values.

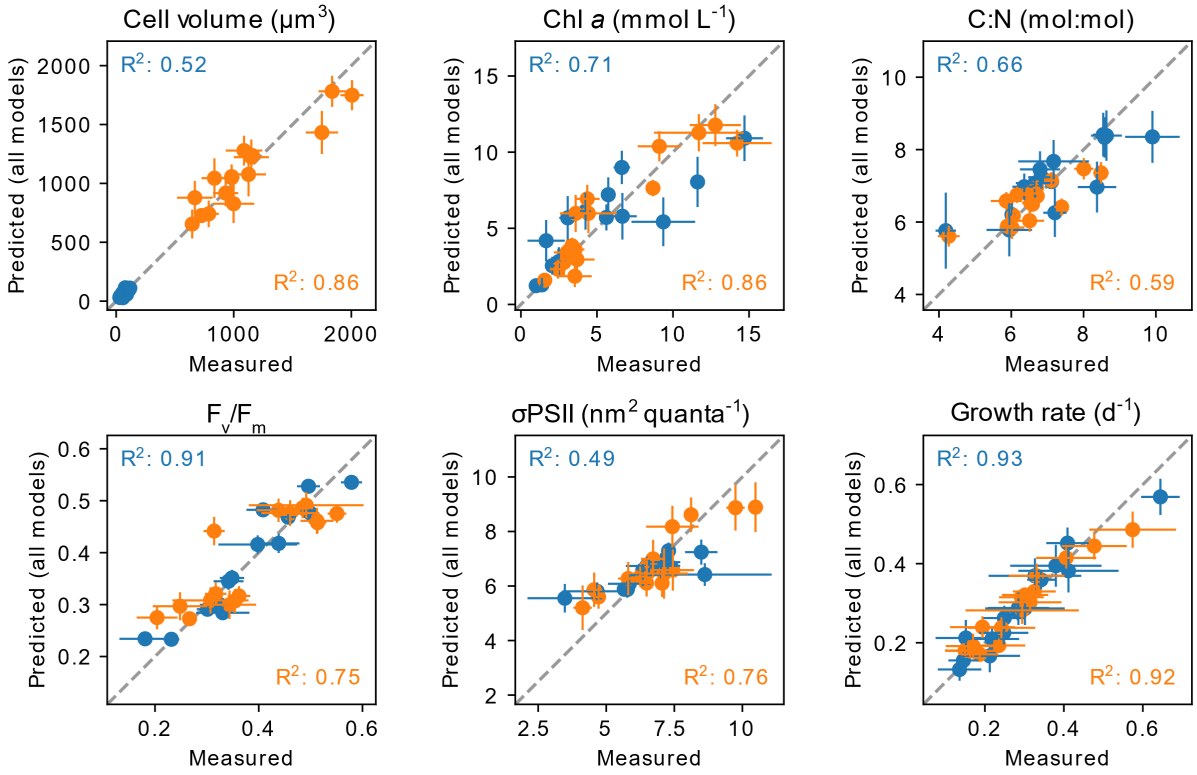
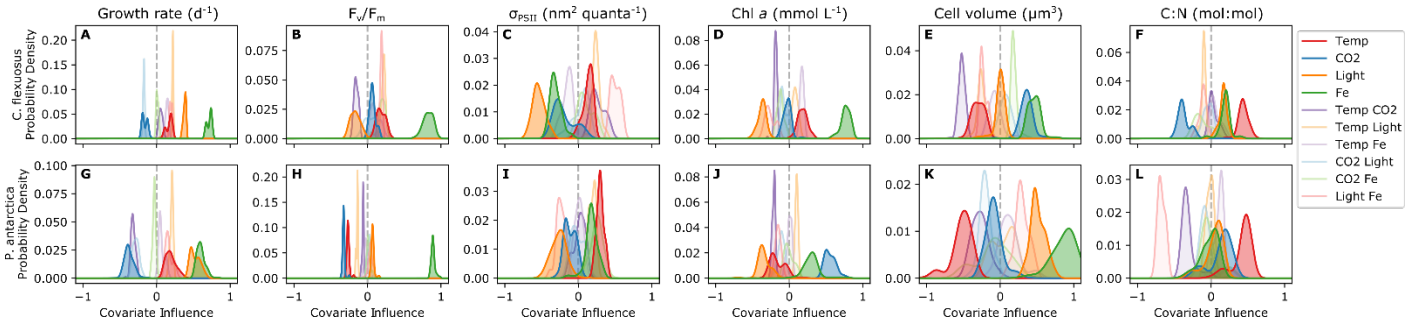


Figure S3. Probability density plots of the size of covariate effects on measured physiological parameters for *C. flexuosus* (A-F) and *P. antarctica* (G-L), as determined by fitting a multivariate linear model to all data simultaneously (*p*=1). The distribution of effect sizes is calculated from the size of each parameter in all 112 models weighted by the skill of each model. Sharp peaks represent consistent effect size across all high-skill models, whereas broad distributions have less confidence across models. Probability distributions centered above zero indicate a positive influence on cell physiology.



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Kass, R. E., & Raftery, A. E. (1995). Bayes factor and model uncertainty. *Journal of the American Statistical Association*, *90*(430), 773-795.

Rouder, J. N., & Morey, R. D. (2012). Default Bayes factors for model selection in regression. *Multivariate Behavioral Research*, *47*(6), 877-903.