**SUPPLEMENTARY MATERIAL**

*Estimating metabolic rates at*   
We use the species-specific parameters estimated and calculated in the main text (, and ) to back calculate what the of each individual will be at their respective . To do so, for each individual, we use the following the formula:

(S1)

where and are species-specific parameters, with representing a species, and representing the highest measurement of individual (i.e. same value used to standardise between 0 and 1 in the first place).

*Estimating mass-independent metabolic rates at*   
Using the individual-specific calculated metabolic rates above ( in ml O2 h-1), we estimated species-specific mass-independent (i.e normalized) metabolic rates, (ml O2 g h-1), following the equation:

(S2),

where is the dimensionless mass-scaling exponent of metabolic rates and is body mass.

We take the natural logarithm at both sides of equation S2 to fit the model:

(S3),

where represents log-additive species-specific deviations in and .

*Model fitting*  
We follow the exact same procedure already described in the main text. We fit equation S3 above in Bayesian framework by calling *JAGS* version 4.2.0 from the R package *R2jags* version 0.05-6 (Su and Yajima 2015) in order to derive posterior distributions and associated 95% credible intervals (CIs) for the fitted parameters, , , and . Random effects, and , were assumed to be normally distributed, with means of 0. Fitted parameters were assigned priors that were vague (i.e. locally uniform over the region supported by the likelihood) (Kruschke 2014). The posterior distributions of model parameters were estimated using Markov chain Monte Carlo (MCMC) methods by constructing three chains of 1.5 106 steps each, including 7.5 105-step burn-in periods. Chains were thinned using a 375-step interval, so a total of 6,000 steps were retained to estimate posterior distributions (i.e. 3 (1.5 106 - 7.5 105)/375 = 6,000).

Finally, using the species-specific parameters estimated using equation S3 above, we estimate the oxygen consumption of native and invasive species at their respective values estimated using equation 1. Means and associated 95% credible intervals were obtained by using the full posterior MCMC sample matrix from equation S3.

**Rerefences**

Kruschke, J. K. 2014. Doing Bayesian data analysis: A tutorial with R, JAGS, and stan. Page 776. 2nd editions. Academic Press / Elsevier.

Su, Y.-S., and M. Yajima. 2015. R2jags: Using R to run ‘JAGS’.