



## **eLife's transparent reporting form**

We encourage authors to provide detailed information *within their submission* to facilitate the interpretation and replication of experiments. If you have any questions, please contact us: [editorial@elifesciences.org](mailto:editorial@elifesciences.org).

### **Sample-size estimation**

- You should state whether an appropriate sample size was computed when the study was being designed
- You should state the statistical method of sample size computation and any required assumptions
- If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Please outline where this information can be found within the submission (e.g., page numbers or figure legends), or explain why this information doesn't apply to your submission:

The minimum sample size for each replicate (i.e., species) was 30. This is noted in manuscript Methods paragraph 2 sentence 1. This sample size was chosen due to being near the upper end of the range of number of individuals analyzed in typical previous studies on Bergmann's rule.

### **Replicates**

- You should report how often each experiment was performed
- You should include a definition of biological versus technical replication
- The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
- If you encountered any outliers, you should describe how these were handled
- Criteria for exclusion/inclusion of data should be clearly stated
- High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

Please outline where this information can be found within the submission (e.g., page numbers or figure legends), or explain why this information doesn't apply to your submission:

Information on how data was filtered for replicates (i.e., species) is in manuscript Methods paragraph 1-2, with the resulting number of replicates and corresponding data description in manuscript Methods paragraph 3 sentences 1-2. All outliers were included, with outlier sensitivity analysis shown in Figure 2—figure supplement 3.

### **Statistical reporting**

- Statistical analysis methods should be described and justified



- Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
- For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's  $r$ , Cohen's  $d$ ))
- Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to page numbers in the

Linear regression analysis described in manuscript Methods paragraph 4. Results for each replicate (i.e., species) including raw data are presented in Figure 1-figure supplement 1. Summary statistics for aggregate replicates (i.e., all species) in manuscript Results paragraph 1. manuscript.)

#### **Additional data files (“source data”)**

- We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
- Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
- Include model definition files including the full list of parameters used
- Include code used for data analysis (e.g., R, MatLab)
- Avoid stating that data files are “available upon request”

Please indicate the figures or tables for which source data files have been provided: No source data provided as all figures were derived from the same major generated datasets, which will be available on Dryad (licenses permitting). Analysis code is available on GitHub (<https://github.com/KristinaRiemer/MassResponseToTemp>) and will be available on Dryad also.