Life Sciences Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form is intended for publication with all accepted life science papers and provides structure for consistency and transparency in reporting. Every life science submission will use this form; some list items might not apply to an individual manuscript, but all fields must be completed for clarity.

For further information on the points included in this form, see Reporting Life Sciences Research. For further information on Nature Research policies, including our data availability policy, see Authors & Referees and the Editorial Policy Checklist.

1. Sample size
   
   Describe how sample size was determined.
   
   Large sample sizes of approximately 100 participants per cell were specified a priori based on past research.

2. Data exclusions
   
   Describe any data exclusions.
   
   Data for Experiment 2 were collected in two rounds. In the first round, the gender and spoon scenarios were replicated. In the second round the remaining scenarios were tested. In the second round, 131 participants were mistakenly recruited who had taken part in the first round. Thus, these participants were excluded. This exclusion criterion was not pre-specified.

   Data from Experiments 4, 6, and 7 were collected simultaneously. Five participants were excluded for not completing the procedure. This exclusion criterion was pre-specified.

3. Replication
   
   Describe whether the experimental findings were reliably reproduced.
   
   All replication attempts were successful. They are included in the paper as separate experiments.

4. Randomization
   
   Describe how samples/organisms/participants were allocated into experimental groups.
   
   Participants were randomly assigned to condition using Qualtrics.

5. Blinding
   
   Describe whether the investigators were blinded to group allocation during data collection and/or analysis.
   
   All data were collected on Amazon Mechanical Turk and no analyses for an experiment began until after data collection was complete. During data collection, we did not know which conditions participants were assigned to. During analysis, we knew which conditions participants were assigned to.

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.
6. Statistical parameters
   For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

<table>
<thead>
<tr>
<th>n/a</th>
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<tbody>
<tr>
<td>☑</td>
<td>The exact sample size ((n)) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)</td>
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<td>☑</td>
<td>A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly</td>
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<td>A statement indicating how many times each experiment was replicated</td>
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<td>☑</td>
<td>The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)</td>
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<td>A description of any assumptions or corrections, such as an adjustment for multiple comparisons</td>
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<td>The test results (e.g. (P) values) given as exact values whenever possible and with confidence intervals noted</td>
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<td>☑</td>
<td>A clear description of statistics including <strong>central tendency</strong> (e.g. median, mean) and <strong>variation</strong> (e.g. standard deviation, interquartile range)</td>
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<td>Clearly defined error bars</td>
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See the web collection on statistics for biologists for further resources and guidance.

7. Software
   Policy information about availability of computer code
   Describe the software used to analyze the data in this study.

   All analyses were conducted using R statistical computing, specifically the nlme package by Pinheiro et al. (2017) and the lme4 package by Bates et al. (2015).

   For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). Nature Methods guidance for providing algorithms and software for publication provides further information on this topic.

8. Materials availability
   Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.

   No unique materials were used. All materials used are available on the Open Science Framework (see manuscript for URL).

9. Antibodies
   Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

   No antibodies were used.

10. Eukaryotic cell lines
   a. State the source of each eukaryotic cell line used.
   b. Describe the method of cell line authentication used.
   c. Report whether the cell lines were tested for mycoplasma contamination.
   d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by ICLAC, provide a scientific rationale for their use.

   No eukaryotic cell lines were used.

11. Description of research animals
    Provide details on animals and/or animal-derived materials used in the study.

    No animals were used.
All participants were recruited from Amazon Mechanical Turk. Approximately 50% of all participants were female and the mean age was in the early to mid 30s, depending on experiment. The standard deviation for age was approximately 11 years, again depending on experiment. We provide exact gender distributions and age information in the Supplementary Information.