

Life Sciences Reporting Summary

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► Experimental design

1. Sample size

Describe how sample size was determined.

For frontline studies we anticipated, based on pilot findings, that 1. only combatants who participated in the Battle of Kudilah would be tested, and 2. that approximately 20 subjects per combatant group would be needed to show statistical reliability even for robust trends. The limit of 20 subjects per combatant group was also dictated by time constraints on access to the front. No statistical model, however, was used to determine sample sizes. For the 15 online studies, no specific statistical method was used to predetermine sample size. Generally, we established a period of 5 days for data collection based on the average n usually collected in previous research for the same period as attested to in a number of previously published papers. Variations depended on the period of the year (e.g., vacations, weekends).

2. Data exclusions

Describe any data exclusions.

Exclusion criteria were pre-established. Data were pre-screened for completeness and repeat participation. Those participants that showed duplicated answers were identified (if they reported the same personal ID or code together with the same sex and age). In such cases, the duplicate case(s) was/were deleted. The primary case was left. Those participants that left in blank most important variables were also excluded. In some studies (e.g., Study 3 and 4) other criteria were additionally applied and they described in the Supplementary Information (e.g., not reporting a valid group/value).

3. Replication

Describe whether the experimental findings were reliably reproduced.

The findings presented in the manuscript have been replicated in the same report. Field and lab studies also yielded common findings .

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

Samples were randomly allocated into experimental conditions as described in Supplementary Information.

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

Investigators were unaware of the sample group allocation during experiments as the studies were run with Qualtrics, with an automatic randomization. For the analyses, investigators were initially unaware of which alternative hypotheses were expected to be validated for the for the frontline studies (value or group, spiritual formidability or physical formidability), but in the subsequent online studies they were not blinded.

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 the Methods section if additional space is needed).

n/a Confirmed

- ☐ ☒ The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
- ☐ ☒ A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly.
- ☐ ☒ A statement indicating how many times each experiment was replicated
- ☐ ☒ 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)
- ☐ ☒ A description of any assumptions or corrections, such as an adjustment for multiple comparisons
- ☐ ☒ The test results (e.g. p values) given as exact values whenever possible and with confidence intervals noted
- ☐ ☒ A summary of the descriptive statistics, including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
- ☐ ☒ Clearly defined error bars

See the web collection on [statistics for biologists](#) for further resources and guidance.

► Software

Policy information about [availability of computer code](#)

7. Software

Describe the software used to analyze the data in this study.

SPSS and R

For all studies, we encourage code deposition in a community repository (e.g. GitHub). Authors must make computer code available to editors and reviewers upon request. The *Nature Methods* [guidance for providing algorithms and software for publication](#) may be useful for any submission.

► Materials and reagents

Policy information about [availability of materials](#)

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.

There are no restrictions on availability upon request of materials for bona fide researchers, scholars and lay persons expressing legitimate interest in the studies.

9. Antibodies

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

n/a

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

n/a

b. Describe the method of cell line authentication used.

n/a

c. Report whether the cell lines were tested for mycoplasma contamination.

n/a

d. If any of the cell lines used in the paper are listed in the database of commonly misidentified cell lines maintained by [ICLAC](#), provide a scientific rationale for their use.

n/a

► Animals and human research participants

Policy information about [studies involving animals](#); when reporting animal research, follow the [ARRIVE guidelines](#)

11. Description of research animals

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

Animals were not used in these studies.

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.

This information can be found in the Supplementary Information for each study in the Participants section