

Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our [Editorial Policies](#) and the [Editorial Policy Checklist](#).

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed
☐	☒ The exact sample size (<i>n</i>) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒ The statistical test(s) used AND whether they are one- or two-sided <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
☐	☒ A description of all covariates tested
☐	☒ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒ For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
☐	☒ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☐	☒ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☐	☒ Estimates of effect sizes (e.g. Cohen's <i>d</i> , Pearson's <i>r</i>), indicating how they were calculated

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

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

Data collection	The experiment was implemented in LimeSurvey (version 6.8.2+241203). For the perceptual maps, we used the web-based emBODY tool (version V1; developed by Nummenmaa et al., 2014), with additional customizations to meet the research goals of our study. Specifically, we designed figurines that allowed the armpits and soles of the feet to be colored. Data from participants with Chinese and Greek cultural backgrounds were collected via either the Prolific platform or the Radboud University SONA participation system, whereas data from Dutch participants were collected solely via the SONA system.
Data analysis	Code needed to perform the reported analyses is publicly available at http://doi.org/10.6084/m9.figshare.30751643 . Survey data were preprocessed and analyzed in R (version 4.4.1), except that open-ended responses were first translated into English using DeepL and then preprocessed in Python (version 3.11.10). Body-coloring task data were preprocessed and analyzed in Python (version 3.11.10). The core Python packages involved in the analysis were as follows: numpy (1.26.4) pandas (2.2.2) scipy (1.14.1) matplotlib (3.9.2) seaborn (0.13.2) scikit-learn (1.5.1) statsmodels (0.14.2) pingouin (0.5.5) scikit-bio (0.6.3) scikit-image (0.24.0)

opencv-python (4.10.0)
plotnine (0.14.5)

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

Survey data are available at <https://doi.org/10.34973/9naz-bv72> with open access for registered users, who must adhere to the terms of a Data Use Agreement. The agreement is deemed necessary by the Donders Institute to protect the sensitive demographic information of participants contained within the survey dataset. Other data are publicly available at <https://doi.org/10.6084/m9.figshare.30692480>.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender	Chinese participants: 74 female and 75 male. Dutch participants: 75 female, 74 male, and 1 reported "prefer not to say." Greek participants: 74 female, 73 male, and 2 reported "prefer not to say." These numbers were based on participants' self-reported sex, and informed consent was obtained from all participants.
Reporting on race, ethnicity, or other socially relevant groupings	Chinese participants: 148 Asian and 1 mixed. Dutch participants: 139 White, 5 Asian, 4 Mixed, 1 Black, and 1 reported "Other." Greek participants: 149 White. These numbers were based on participants' self-reported ethnicity. In addition, participants were prescreened based on their primary language and assigned to one of three cultural background groups (Chinese, Dutch, or Greek).
Population characteristics	All participants were aged 18–30 years. The mean age was 24.9 years for Chinese participants, 21.1 years for Dutch participants, and 25.2 years for Greek participants.
Recruitment	Chinese and Greek participants were recruited via the Prolific platform and SONA system, while Dutch participants were recruited via SONA system.
Ethics oversight	The study was approved by the ethics committee of the Faculty of Social Sciences at Radboud University Nijmegen.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☐ Life sciences ☒ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Behavioural & social sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	The study consists of an online survey and a web-based body-colouring task. The collected data are a combination of qualitative and quantitative data.
Research sample	The age and sex information for the sample are reported above. Chinese and Greek participants were recruited via SONA system or Prolific. The Prolific is an online participation platform with an international pool. Dutch participants were registered users in the Radboud University SONA system. The sample was recruited based on their primary languages to represent the targetted cultural groups (Chinese, Dutch, and Greek) in the present study.
Sampling strategy	We recruited participants using a convenience sample approach targeting three cultural background groups. We predetermined N=150 per group. The sample size was chosen for pragmatic reasons while ensuring balanced comparisons across the three cultural groups. In addition, we restricted recruitment to participants aged 18–30 years to narrow the age distributions across cultural groups.
Data collection	Data were collected entirely online. Participants were required to perform the study using a computer and a mouse. Participants first

Data collection	read the study information and provided digital informed consent before performing the study. The researchers were not blinded to the study design or hypothesis.
Timing	Data collection began in November 2023 and finished in February 2024.
Data exclusions	One Chinese and one Greek participant were excluded due to inattentive performance in the body-coloring task (e.g., doodling).
Non-participation	No participants dropped out from the study.
Randomization	Participants were prescreened based on their primary language and completed the study in that language (Mandarin Chinese, Greek, or Dutch).

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems		Methods	
n/a	Involved in the study	n/a	Involved in the study
☒	☐ Antibodies	☒	☐ ChIP-seq
☒	☐ Eukaryotic cell lines	☒	☐ Flow cytometry
☒	☐ Palaeontology and archaeology	☒	☐ MRI-based neuroimaging
☒	☐ Animals and other organisms		
☒	☐ Clinical data		
☒	☐ Dual use research of concern		
☒	☐ Plants		

Plants

Seed stocks	Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.
Novel plant genotypes	Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.
Authentication	Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.