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Reporting Summary

Nature Research 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 Research policies, see Authors & Referees and the Editorial Policy Checklist.

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. figure legend, table legend, main text, or Methods section).

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☒	☐	An indication of 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 *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☒	☐	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 statistics 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. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐	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 *d*, Pearson's *r*), indicating how they were calculated
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	Neurobs Presentation version 18.3 07.18.16 Neuroscan SCAN version 4.5
Data analysis	FieldTrip version 20151213 Matlab version 2012b

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/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research 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 list of figures that have associated raw data
- A description of any restrictions on data availability

All data are publically available through the Dryad Data Repository at: [YET TO INSERT CODE/DOI]. Code will be made available by the authors upon request.

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf

Life sciences study design

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

Sample size	Twenty-five healthy human volunteers (11 male; age range 19-36; mean age 25.12 years) participated in the study. No statistical methods were used to pre-determine sample sizes but our sample size is similar to those reported in previous publications from the lab that focused on similar neural signatures (e.g. ref 16).
Data exclusions	Data from all participants were retained for analysis. At the level of trials, we only considered trials in which participants pressed the correct key (which was the case in 92.07 ± 1.11 [M ± SE] % of all trials) and in which response times were within 4 SD of the mean. Remaining trials with excessive EEG variance were rejected based on visual inspection. After trial removal, it was possible that trials in which item location and response hand were associated with the same or opposite side had become slightly over-represented in the data. To re-balance the data, we finally made sure that item location and required response hand were equally often in the same or the opposite side. Trial numbers were equated by randomly subsampling from the case with more trials. On average, 955 ± 25 (M ± SE) trials (ranging between 710 and 1114) were retained for analysis per participant (out of 1200 in total). The exact values for exclusion were not pre-established. Apart from the re-balancing procedure described above, trial exclusions were always performed while considering all trials; without knowledge of the experimental condition to which individual trials belonged.
Replication	No replication was attempted as the primary results were all highly reliable.
Randomization	The location and the tilt (response hand) of the probed item were pseudo-randomised at the level of trials. This ensured that each condition (probed item left, tilt left; item left, tilt right; item right, tilt left; item right, tilt right) occurred equally often in each block of 60 trials. There were no experimental groups to randomize, as this was a within-subjects design.
Blinding	Data collection and analysis were not performed blind to the conditions of the experiments. Because there were no experimental groups, blinding was not relevant.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☒	☐ Unique biological materials
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☐	☒ Human research participants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Human research participants

Policy information about studies involving human research participants

Population characteristics	Twenty-five healthy human volunteers (11 male; age range 19-36; mean age 25.12 years) participated in the study. All participants had normal or corrected-to-normal vision. Two participants were left handed. Nearly all participants were undergraduate students at the University of Oxford or at Brookes University. Because this was a within-subjects design, none of these variables constituted a relevant co-variate.
Recruitment	Participants were recruited through flyers and an online participant database (SONA) at the University of Oxford. There was no selection bias by the experimenters. The only potential 'bias' is that the vast majority of participants were university students (as is commonly the case in cognitive neuroscience studies).