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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 (*n*) 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 *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 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. *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

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	All fMRI data was collected with MRI scanner-specific commercial software - either Siemens or GE scanners. EEG and physiological data was collected with hardware-specific commercial software.
Data analysis	All preprocessing and analysis code are provided at https://github.com/tsb46/fmri_arousal

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

Raw MRI and minimally preprocessed EEG and physiological data for ME-REST, ME-TASK and ME-TASK-CUE datasets are publicly available at https://doi.org/10.6084/m9.figshare.28225415.v3.

Instructions for obtaining HCP-REST resting-state MRI and physiological data from the Young Adult Human Connectome Project are available at https://www.humanconnectome.org/. Subject IDs used in this study are provided in the code repository https://github.com/tsb46/fmri_arousal.

ME-REST-SUPP resting-state MRI and physiological data is available via OpenNeuro (https://openneuro.org/) at doi:10.18112/openneuro.ds003592.v1.0.13. Subject IDs used in this study are provided in the code repository https://github.com/tsb46/fmri_arousal.

YALE-REST resting-state MRI and pupil diameter data is available via OpenNeuro at doi:10.18112/openneuro.ds003673.v2.0.1. Subject IDs used in this study are provided in the code repository https://github.com/tsb46/fmri_arousal.

Instructions for obtaining NATVIEW-REST resting-state simultaneous EEG-FMRI data and physiological data are available at https://fcon_1000.projects.nitrc.org/indi/retro/nat_view.html. Subject IDs used in this study are provided in the code repository https://github.com/tsb46/fmri_arousal.

Instructions for obtaining NKI-TASK breath-hold MRI and physiological data are available at https://fcon_1000.projects.nitrc.org/indi/enhanced/sharing_neuro.html. Subject IDs used in this study are provided in the code repository https://github.com/tsb46/fmri_arousal.

MRI data from the clamped CO2 and free-breathing dataset is available pending a data-sharing agreement. Please email jean.chen@utoronto.ca for instructions.

The noradrenaline transporter (NAT) density map displayed in Figure 5D is made available at https://github.com/netneurolab/hansen_receptors.

The cerebrospinal fluid probability map (along with gray and white matter) displayed in Figure 5D is made available at https://www.unil.ch/lren/home/menuinst/teaching--utilities/data--utilities.html.

The cerebral arteries probability map displayed in Figure 5D is made available at https://ucalgary.ca/labs/miplab/downloads

The cerebral veins probability map displayed in Figure 5D is made available at https://figshare.com/articles/dataset/VENAT_Probability_map_nii_gz/7205960

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	Sex and gender were not considered in study design or analysis. Sex is reported for each dataset (# of females, and # of males).
Reporting on race, ethnicity, or other socially relevant groupings	Race, ethnicity and other socially relevant groups were not considered in study design or analysis.
Population characteristics	10 separate samples of adults between ages of 18-50 are included in this study. Demographic information (sex and age range for each dataset) are provided in Supplementary Table 1.
Recruitment	All datasets utilized convenience sampling methodologies of students and members of the local community nearby the institution collecting the data.
Ethics oversight	Most datasets analyzed are publicly-available and ethics oversight was managed by the institution that collected the data. For the ME-REST, ME-TASK and ME-TASK-CUE data, ethics oversight was performed by the National Institutes of Health and Vanderbilt University. For the clamped CO2 and free breathing dataset, ethics oversight was performed by the University of Toronto.

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

Life sciences study design

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

Sample size	Ten datasets were utilized to demonstrate replicability across different data acquisition hardware and sample characteristics. No sample size calculations were performed. For smaller datasets (N < 50), all participants within the study with sufficient quality data were included in the analysis. For larger, population-level datasets (e.g. HCP, NKI-REST), a random sample was selected based on computational limits for our analysis.

Data exclusions	Participants from each dataset were excluded based on anatomical and functional MRI quality, and physiological signal artifacts. Detailed criteria for participant exclusion is described in a dedicated section of the Methods and Materials section.
Replication	Replication was ensured by replicating our results across 10 different datasets with unique data acquisition hardware and sample size characteristics.
Randomization	No experimental group randomization was performed in this study.
Blinding	No blinding was performed in this study as there was no treatment or control group in this study.

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

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

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

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, mosiacism, off-target gene editing) were examined.*

Magnetic resonance imaging

Experimental design

Design type	Resting-State and Task
Design specifications	For task-fMRI datasets, ME-TASK and ME-TASK-CUE, the experimental design was a sparse event-related design with the presentation of auditory cues separated by an inter-stimulus of interval of 29 - 131 seconds. For the ME-TASK, the auditory cue was followed by a deep breath. For the ME-CUE task, the auditory cue was followed by a button response.
Behavioral performance measures	No behavioral performance measures were analyzed in this study. For the ME-TASK-CUE task, non-responses to the auditory cue were used for filtering out non-compliant trials.

Acquisition

Imaging type(s)	Functional (T2*) and Anatomical (T1) images were collected.
Field strength	All datasets were 3T.
Sequence & imaging parameters	All datasets used different sequence and imaging parameters (TE, TR, field-of-view, spatial sampling), including single-echo and multi-echo sequences, multi-band and single-slice imaging.
Area of acquisition	Whole-brain scans were collected in each dataset.

Diffusion MRI ☐ Used ☒ Not used

Preprocessing

Preprocessing software	Preprocessing was conducted with AFNI and FSL using Nipype software (Python).
Normalization	Non-linear registration to the MNI152 template was utilized across datasets.
Normalization template	MNI152 template
Noise and artifact removal	Physiological signals (PPG, EEG, respiration, pupil, skin conductance) were collected as signals of interest, and manually examined for quality. For multi-echo fMRI datasets, motion-related artifacts were removed through multi-echo ICA (tedana software in Python).
Volume censoring	No volume censoring was performed.

Statistical modeling & inference

Model type and settings	Simple cross-correlations were computed between physiological signals the global fMRI signal, along with event-related averages of physiological signals. Standard cluster correction procedures for brain statistical maps was not applicable. Standard errors on statistical estimates of cross-correlations and averages were estimated through cluster or nested bootstrapping.
Effect(s) tested	Cross-correlations, impulse-response modeling, event-related averaging and multivariate decomposition (canonical correlation)

Specify type of analysis: ☒ Whole brain ☐ ROI-based ☐ Both

Statistic type for inference (See Eklund et al. 2016)	Mass-univariate analyses were not performed, no cluster-wise or voxel-wise corrections were performed.
Correction	Replication across datasets (N=10) was utilized as a 'correction' for any findings in our analysis versus multiple comparisons of an analysis within any single dataset.

Models & analysis

n/a	Involved in the study
☒	☐ Functional and/or effective connectivity
☒	☐ Graph analysis
☐	☒ Multivariate modeling or predictive analysis

Multivariate modeling and predictive analysis	Dimension reduction was performed with principal component analysis and complex principal component analysis. Cross-decomposition was performed with multi-set canonical correlation analysis.