

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 <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. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P 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 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 custom code (R and Matlab) for collecting public available datasets is included in Supplementary Data 1. There was no specific software used.
Data analysis	All custom code (R) for data analysis performed in the paper is included in Supplementary Data 2. There was no specific software used, besides opentargets.org. The software to operate BrainTrawler consists of a multitude of services, including spatial indices for gene expression and connectivity, a graph database, a web interface, and an API to handle individual parts. Hence, making the code open-source does not necessarily guarantee that it can be easily used by others. However, we believe that providing a publicly accessible, free to use instance of BrainTrawler/BrainTACO (braintrawler.vrvis.at), as well as all means to operate a custom BrainTrawler instance (see Data Availability Statement) serves the scientific community best, as it allows researchers to leverage the data without the need for extensive technical knowledge. The code for the mapping and data generation of all gene expression or connectivity data of the BrainTACO resource is provided in Supplementary Data 1. In combination with the provided Docker image (see Data Availability Statement), it is possible to reproduce the public instance running at braintrawler.vrvis.at, as well as to include one's own custom datasets. However, setting up a separate BrainTrawler instance may not be the most efficient approach for most researchers. VRVis, as a not-for-profit research center, is open to providing support in setting up a BrainTrawler instance in the scope of a research collaboration and is committed to further developing and improving the system to better serve the scientific community. We welcome initiatives for joint research and development projects and generally provide the software within these projects free of charge.

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](#)

BrainTrawler, including the BrainTACO resource, can be publicly accessed via braintrawler.vrvis.at. All means to set up a custom BrainTrawler instance (including a Docker image) is available at Zenodo (doi: 10.5281/zenodo.10400999). This does not include the 3rd party gene expression or connectivity data. All code to include these data, as well as custom datasets into BrainTrawler is provided in Supplementary Data 1, see the Code Availability Section for details.

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	not applicable
Reporting on race, ethnicity, or other socially relevant groupings	not applicable
Population characteristics	not applicable
Recruitment	not applicable
Ethics oversight	not applicable

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	not applicable
Data exclusions	not applicable
Replication	not applicable
Randomization	not applicable
Blinding	not applicable

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

not applicable

Novel plant genotypes

not applicable

Authentication

not applicable