

|                       |  |                          |          |
|-----------------------|--|--------------------------|----------|
| Corresponding Author: | <u>Emily S. Finn (emily.finn@yale.edu)</u> | # Main Figures:          | <u>5</u> |
| Manuscript Number:    | <u>NN-A51891C</u>                          | # Supplementary Figures: | <u>0</u> |
| Manuscript Type:      | <u>Article</u>                             | # Supplementary Tables:  | <u>3</u> |
|                       |  | # Supplementary Videos:  | <u>0</u> |

## Reporting Checklist for Nature Neuroscience

This checklist is used to ensure good reporting standards and to improve the reproducibility of published results. For more information, please read [Reporting Life Sciences Research](#).

Please note that in the event of publication, it is mandatory that authors include all relevant methodological and statistical information in the manuscript.

### ► Statistics reporting, by figure

- Please specify the following information for each panel reporting quantitative data, and where each item is reported (section, e.g. Results, & paragraph number).
- Each figure legend should ideally contain an exact sample size (n) for each experimental group/condition, where n is an exact number and not a range, a clear definition of how n is defined (for example x cells from x slices from x animals from x litters, collected over x days), a description of the statistical test used, the results of the tests, any descriptive statistics and clearly defined error bars if applicable.
- For any experiments using custom statistics, please indicate the test used and stats obtained for each experiment.
- Each figure legend should include a statement of how many times the experiment shown was replicated in the lab; the details of sample collection should be sufficiently clear so that the replicability of the experiment is obvious to the reader.
- For experiments reported in the text but not in the figures, please use the paragraph number instead of the figure number.

**Note:** Mean and standard deviation are not appropriate on small samples, and plotting independent data points is usually more informative. When technical replicates are reported, error and significance measures reflect the experimental variability and not the variability of the biological process; it is misleading not to state this clearly.

|                            |                 | TEST USED             |              | n                                  |                       |                             | DESCRIPTIVE STATS (AVERAGE, VARIANCE) |             | P VALUE               |                 | DEGREES OF FREEDOM & F/t/z/R/ETC VALUE |  |
|----------------------------|-----------------|-----------------------|--------------|------------------------------------|-----------------------|-----------------------------|---------------------------------------|-------------|-----------------------|-----------------|--|--|
| FIGURE NUMBER              | WHICH TEST?     | SECTION & PARAGRAPH # | EXACT VALUE  | DEFINED?                           | SECTION & PARAGRAPH # | REPORTED?                   | SECTION & PARAGRAPH #                 | EXACT VALUE | SECTION & PARAGRAPH # | VALUE           | SECTION & PARAGRAPH #                  |  |
| example<br>1a              | one-way ANOVA   | Fig. legend           | 9, 9, 10, 15 | mice from at least 3 litters/group | Methods para 8        | error bars are mean +/- SEM | Fig. legend                           | p = 0.044   | Fig. legend           | F(3, 36) = 2.97 | Fig. legend                            |  |
| example<br>results, para 6 | unpaired t-test | Results para 6        | 15           | slices from 10 mice                | Results para 6        | error bars are mean +/- SEM | Results para 6                        | p = 0.0006  | Results para 6        | t(28) = 2.808   | Results para 6                         |  |
| +<br>-                     |                 |                       |              |                                    |                       |                             |                                       |             |                       |                 |  |  |

|               |             | TEST USED                          |   | n   |   |  | DESCRIPTIVE STATS (AVERAGE, VARIANCE)                 |                     | P VALUE   |                     | DEGREES OF FREEDOM & F/t/z/R/ETC VALUE                |  |
|---------------|-------------|------------------------------------|---|---|---|--|---|---------------------|---|---------------------|---|--|
| FIGURE NUMBER | WHICH TEST? | SECTION & PARAGRAPH #              | EXACT VALUE   | DEFINED?  | SECTION & PARAGRAPH #                                 | REPORTED?  | SECTION & PARAGRAPH #                                 | EXACT VALUE         | SECTION & PARAGRAPH #                                 | VALUE               | SECTION & PARAGRAPH #                                 |  |
| +<br>-        | n/a         | non-parametric permutation testing | Results (Whole-brain identification)<br>18 vs. 2,000  | 18 observed ID rates (9 session pairs each with 2 configurations of database/target); 2,000 randomized ID rates (1,000 permutations of session pairs and subject identity, each with 2 configurations of database/target) | Results (Whole-brain identification)                  | Observed data: exact values for rest-rest pair; range (min-max) for other rest-task and task-task combinations (all values visible in Fig. 3a). Permutations: average and maximum values | Results (Whole-brain identification)                  | 0                   | Results (Whole-brain identification)                  | n/a                 | n/a   |  |
| +<br>-        | 2a          | paired t-test                      | Results (Network-based identification)<br>18 paired samples (networks 1+2 versus network 1 alone) | 9 session pairs each with 2 configurations of database/target   | Results (Network-based identification)                | Exact values can be seen in the bar graphs in Fig. 2a  | Results (Network-based identification)                | 4.2e-9 (one-tailed) | Results (Network-based identification)                | df = 17.4, t = 10.4 | Results (Network-based identification)                |  |
| +<br>-        | 2a          | paired t-test                      | Results (Network-based identification)<br>18 paired samples (networks 1+2 versus network 2 alone) | 9 session pairs each with 2 configurations of database/target   | Results (Network-based identification)                | Exact values can be seen in the bar graphs in Fig. 2a  | Results (Network-based identification)                | 0.033 (one-tailed)  | Results (Network-based identification)                | df = 17.4, t = 1.97 | Results (Network-based identification)                |  |
| +<br>-        | 3c          | Mann-Whitney U test                | Results (Identification based on two-matrix database)<br>8, 8                                     | ID rates from 8 session pairs (task only vs. rest+task)   | Results (Identification based on two-matrix database) | average reported in text; average and range shown in Fig. 3c   | Results (Identification based on two-matrix database) | 1.6e-4 (two-sided)  | Results (Identification based on two-matrix database) | rank sum = 100      | Results (Identification based on two-matrix database) |  |
| +<br>-        | 3c          | Mann-Whitney U test                | Results (Identification based on two-matrix database)<br>8, 4                                     | ID rates from 8 session pairs (rest only vs. rest+task)   | Results (Identification based on two-matrix database) | average reported in text; average and range shown in Fig. 3c   | Results (Identification based on two-matrix database) | 0.004 (two-sided)   | Results (Identification based on two-matrix database) | rank sum = 68       | Results (Identification based on two-matrix database) |  |
| +<br>-        | 4b          | unpaired t-test                    | Results (Effects of parcellation scheme)<br>126 in each set (Yeo vs. Shen)                        | Non-normalized correlation coefficients between matched subjects  | Fig. legend   | mean and standard deviation shown in Fig. 4b, bottom left ("diagonal")   | n/a   | 2.1e-5 (two-tailed) | Results (Effects of parcellation scheme)              | df = 250; t = -4.3  | Results (Effects of parcellation scheme)              |  |

|        |    |                 |  |   |   |             |   |  |                                  |  |                             |  |
|--------|----|-----------------|--|---|---|-------------|---|--|----------------------------------|--|-----------------------------|--|
| +<br>- | 4b | unpaired t-test | Results (Effects of parcellation scheme)                   | 15,876 in each set (Yeo vs. Shen)       | Non-normalized correlation coefficients between unmatched subjects  | Fig. legend | mean and standard deviation shown in Fig. 4b, bottom right ("off-diagonal") | n/a                                    | 2.7e-72 (two-tailed)             | Results (Effects of parcellation scheme)                   | df = 31,750; t = -18.0      | Results (Effects of parcellation scheme)                   |
| +<br>- | 4c | unpaired t-test | Results (Effects of parcellation scheme)                   | 126 in each set (Yeo vs. Shen)          | Normalized correlation coefficients between matched subjects  | Fig. legend | mean and standard deviation shown in Fig. 4c, bottom left ("diagonal")      | n/a                                    | 2.6e-35 (two-tailed)             | Results (Effects of parcellation scheme)                   | df = 250; t = 14.6          | Results (Effects of parcellation scheme)                   |
| +<br>- | 4c | unpaired t-test | Results (Effects of parcellation scheme)                   | 15,876 in each set (Yeo vs. Shen)       | Normalized correlation coefficients between unmatched subjects  | Fig. legend | mean and standard deviation shown in Fig. 4c, bottom right ("off-diagonal") | n/a                                    | 0.79 (two-tailed)                | Results (Effects of parcellation scheme)                   | df = 31,750; t = 0.27       | Results (Effects of parcellation scheme)                   |
| +<br>- | 5a | correlation     | Results (Connectivity profiles predict cognitive behavior) | 118 in each set (predicted vs observed) | Predicted gF scores vs. observed gF scores based on whole-brain matrix  | Fig. legend | For observed behavior: mean, std, median, mode, range                       | Online methods (Behavioral prediction) | 5.70e-9                          | Results (Connectivity profiles predict cognitive behavior) | df = 116; r = 0.5046        | Results (Connectivity profiles predict cognitive behavior) |
| +<br>- | 5c | correlation     | Results (Connectivity profiles predict cognitive behavior) | 118 in each set (predicted vs observed) | Predicted gF scores vs. observed gF scores based on networks 1 and 2  | Fig. legend | For observed behavior: mean, std, median, mode, range                       | Online methods (Behavioral prediction) | 5.60e-9                          | Online methods (Behavioral prediction)                     | df = 116; r = 0.5047        | Results (Connectivity profiles predict cognitive behavior) |
| +<br>- | 5d | correlation     | Results (Connectivity profiles predict cognitive behavior) | 118                                     | Correlations were computed for each of 8 networks at 3 different feature-selection thresholds. Each set contained 118 (predicted vs observed) |             | For observed behavior: mean, std, median, mode, range                       | Online methods (Behavioral prediction) | various; p < 0.05 denoted with * | Fig. legend  | all df = 116; r values vary | Results (Connectivity profiles predict cognitive behavior) |

► Representative figures

1. Are any representative images shown (including Western blots and immunohistochemistry/staining) in the paper?

n/a

If so, what figure(s)?

2. For each representative image, is there a clear statement of how many times this experiment was successfully repeated and a discussion of any limitations in repeatability?

n/a

If so, where is this reported (section, paragraph #)?

## ▶ Statistics and general methods

1. Is there a justification of the sample size?

If so, how was it justified?

Where (section, paragraph #)?

Even if no sample size calculation was performed, authors should report why the sample size is adequate to measure their effect size.

We include all subjects from the Q2 release of the Human Connectome Project (HCP) for whom all 6 fMRI sessions are available (rest1, rest2, working memory, motor, language, & emotion task data). This is open source data, we used all the data that was available at the time this project was begun.

The sample size is well above others reported in the literature and among the largest for neuroimaging.

2. Are statistical tests justified as appropriate for every figure?

Where (section, paragraph #)?

Yes -- see chart above

- a. If there is a section summarizing the statistical methods in the methods, is the statistical test for each experiment clearly defined?

There is no section summarizing the overall statistical methods. Each statistical test performed is clearly defined and its results reported in respective subsections of Results and Fig. legends.

- b. Do the data meet the assumptions of the specific statistical test you chose (e.g. normality for a parametric test)?

Where is this described (section, paragraph #)?

We use a combination of parametric tests (i.e., t-tests, correlation) and non-parametric tests (i.e, Mann-Whitney U test, permutation testing) depending on the nature of the data; this is clearly noted.

- c. Is there any estimate of variance within each group of data?

Is the variance similar between groups that are being statistically compared?

Where is this described (section, paragraph #)?

n/a (Subjects are not divided into groups.)

- d. Are tests specified as one- or two-sided?

Where appropriate, each test is specified as one- or two-sided.

- e. Are there adjustments for multiple comparisons?

n/a

3. Are criteria for excluding data points reported?

Was this criterion established prior to data collection?

Where is this described (section, paragraph #)?

For the identification experiments, our inclusion criteria was that subjects have completed all 6 functional runs in the HCP study. We did not exclude any data from this group. For the behavioral prediction, we excluded 8 subjects on the basis of head motion; this is noted in Online Methods (Behavioral prediction).

4. Define the method of randomization used to assign subjects (or samples) to the experimental groups and to collect and process data.

If no randomization was used, state so.

Where does this appear (section, paragraph #)?

n/a (Subjects are not divided into groups.)

5. Is a statement of the extent to which investigator knew the group allocation during the experiment and in assessing outcome included?

If no blinding was done, state so.

Where (section, paragraph #)?

n/a (Subjects are not divided into groups.)

6. For experiments in live vertebrates, is a statement of compliance with ethical guidelines/regulations included?  
Where (section, paragraph #)?
- The primary dataset, from the HCP, was collected under local IRB at Washington Univ. in St. Louis. The secondary dataset was collected at our institution, Yale Univ. We include statements in Online Methods (Subject information) indicating compliance with ethical guidelines and IRB approval from both institutions for each dataset, respectively.
7. Is the species of the animals used reported?  
Where (section, paragraph #)?
- n/a
8. Is the strain of the animals (including background strains of KO/transgenic animals used) reported?  
Where (section, paragraph #)?
- n/a
9. Is the sex of the animals/subjects used reported?  
Where (section, paragraph #)?
- Sex breakdown (M/F) was reported in Online Methods (Subject information).
10. Is the age of the animals/subjects reported?  
Where (section, paragraph #)?
- Age range was reported in Online Methods (Subject information).
11. For animals housed in a vivarium, is the light/dark cycle reported?  
Where (section, paragraph #)?
- n/a
12. For animals housed in a vivarium, is the housing group (i.e. number of animals per cage) reported?  
Where (section, paragraph #)?
- n/a
13. For behavioral experiments, is the time of day reported (e.g. light or dark cycle)?  
Where (section, paragraph #)?
- n/a
14. Is the previous history of the animals/subjects (e.g. prior drug administration, surgery, behavioral testing) reported?  
Where (section, paragraph #)?
- n/a
- a. If multiple behavioral tests were conducted in the same group of animals, is this reported?  
Where (section, paragraph #)?
- n/a
15. If any animals/subjects were excluded from analysis, is this reported?  
Where (section, paragraph #)?
- In the behavioral prediction analysis, 8 subjects were excluded based on head motion > 0.14 (relative RMS). This is reported in Online Methods (Behavioral prediction)
- a. How were the criteria for exclusion defined?  
Where is this described (section, paragraph #)?
- We excluded the minimum number of subjects necessary to remove any correlation between head motion and fluid intelligence, which could confound the prediction analysis. This is noted in Online Methods (Behavioral prediction).

- b. Specify reasons for any discrepancy between the number of animals at the beginning and end of the study.

n/a

Where is this described (section, paragraph #)?

## ► Reagents

1. Have antibodies been validated for use in the system under study (assay and species)?

n/a

- a. Is antibody catalog number given?

n/a

Where does this appear (section, paragraph #)?

- b. Where were the validation data reported (citation, supplementary information, Antibodypedia)?

n/a

Where does this appear (section, paragraph #)?

2. Cell line identity

n/a

- a. Are any cell lines used in this paper listed in the database of commonly misidentified cell lines maintained by [ICLAC](#) and [NCBI Biosample](#)?

Where (section, paragraph #)?

- b. If yes, include in the Methods section a scientific justification of their use--indicate here in which section and paragraph the justification can be found.

n/a

- c. For each cell line, include in the Methods section a statement that specifies:

- the source of the cell lines
- have the cell lines been authenticated? If so, by which method?
- have the cell lines been tested for mycoplasma contamination?

Where (section, paragraph #)?

n/a

## ▶ Data deposition

Data deposition in a public repository is mandatory for:

- Protein, DNA and RNA sequences
- Macromolecular structures
- Crystallographic data for small molecules
- Microarray data

Deposition is strongly recommended for many other datasets for which structured public repositories exist; more details on our data policy are available [here](#). We encourage the provision of other source data in supplementary information or in unstructured repositories such as [Figshare](#) and [Dryad](#).

We encourage publication of Data Descriptors (see [Scientific Data](#)) to maximize data reuse.

- Are accession codes for deposit dates provided?

Where (section, paragraph #)?

n/a

## ▶ Computer code/software

Any custom algorithm/software that is central to the methods must be supplied by the authors in a usable and readable form for readers at the time of publication. However, referees may ask for this information at any time during the review process.

- Identify all custom software or scripts that were required to conduct the study and where in the procedures each was used.

Matlab code was written to conduct the study. The computations were clearly described in the Methods section and can be reproduced in a straightforward way. The authors are happy to share the code upon readers' request.

- If computer code was used to generate results that are central to the paper's conclusions, include a statement in the Methods section under "**Code availability**" to indicate whether and how the code can be accessed. Include version information as necessary and any restrictions on availability.

A code availability statement is included at the end of Online Methods.

## ▶ Human subjects

- Which IRB approved the protocol?

Where is this stated (section, paragraph #)?

For the HCP data, local IRB (Wash U St Louis). For the Yale data, Human Research Protection Program of Yale University. See Online Methods (Subject information).

- Is demographic information on all subjects provided?

Where (section, paragraph #)?

Yes -- Online Methods (Subject information)

- Is the number of human subjects, their age and sex clearly defined?

Where (section, paragraph #)?

The number of subjects is clearly defined for the two datasets used in the study. The group average, standard deviation and range of age is clearly defined for the Yale dataset. Due to limited access to the demographic information of the HCP dataset, we include only the range of age for the HCP dataset. The number of male and female subjects is clearly defined for both sets. See Online Methods (Subject information).

- |   |  |
|---|--|
| <p>4. Are the inclusion and exclusion criteria (if any) clearly specified?<br/>Where (section, paragraph #)?</p>  | <p>Yes, inclusion criteria for the identification analyses and motion-based exclusions for the behavioral prediction analyses are both described in Online Methods (Subject information and Behavioral prediction sections, respectively).</p> |
| <p>5. How well were the groups matched?<br/>Where is this information described (section, paragraph #)?</p>   | <p>n/a (Data was not divided into groups.)</p>   |
| <p>6. Is a statement included confirming that informed consent was obtained from all subjects?<br/>Where (section, paragraph #)?</p>                    | <p>Yes, see Online Methods (Subject information)</p>   |
| <p>7. For publication of patient photos, is a statement included confirming that consent to publish was obtained?<br/>Where (section, paragraph #)?</p> | <p>n/a</p>   |

## ► fMRI studies

For papers reporting functional imaging (fMRI) results please ensure that these minimal reporting guidelines are met and that all this information is clearly provided in the methods:

- |   |   |
|---|---|
| <p>1. Were any subjects scanned but then rejected for the analysis after the data was collected?</p>  | <p>No HCP Q2 subjects with all 6 functional runs were rejected from the identification analyses. Eight subjects were rejected from the behavioral analysis due to head motion.</p>  |
| <p>a. If yes, is the number rejected and reasons for rejection described?<br/>Where (section, paragraph #)?</p>   | <p>Yes (see Online Methods, Behavioral prediction)</p>  |
| <p>2. Is the number of blocks, trials or experimental units per session and/or subjects specified?<br/>Where (section, paragraph #)?</p>                                  | <p>We include a summary of this information in the Results section and Online Methods (Subject information). Specifics of the experimental design can be found in published HCP documentation (which we cite) and HCP release manual.</p> |
| <p>3. Is the length of each trial and interval between trials specified?</p>  | <p>The length of the different sessions was reported, see Results (Identification using shorter timecourses).</p>   |
| <p>4. Is a blocked, event-related, or mixed design being used? If applicable, please specify the block length or how the event-related or mixed design was optimized.</p> | <p>We did not include this information as it is not relevant to the current study. Specifics of the experimental design can be found in published HCP documentation and the HCP release manual.</p>                                       |
| <p>5. Is the task design clearly described?<br/>Where (section, paragraph #)?</p>   | <p>We did not include this information as it is not relevant to the current study. Specifics of the experimental design can be found in published HCP documentation and the HCP release manual.</p>                                       |
| <p>6. How was behavioral performance measured?</p>  | <p>Behavioral performance (fluid intelligence) was measured as number of items correct on a 24-item Raven's progressive matrices test. This is noted in Online Methods (Behavioral prediction).</p>                                       |
| <p>7. Is an ANOVA or factorial design being used?</p>   | <p>n/a</p>  |



8. For data acquisition, is a whole brain scan used?  
If not, state area of acquisition.
- Yes
- a. How was this region determined?
- n/a
9. Is the field strength (in Tesla) of the MRI system stated?
- Yes, for the Yale dataset.
- a. Is the pulse sequence type (gradient/spin echo, EPI/spiral) stated?
- Yes, for the Yale dataset.
- b. Are the field-of-view, matrix size, slice thickness, and TE/TR/flip angle clearly stated?
- Yes, for the Yale dataset.
10. Are the software and specific parameters (model/functions, smoothing kernel size if applicable, etc.) used for data processing and pre-processing clearly stated?
- Yes (see "Preprocessing" subsection of Online Methods). HCP preprocessing pipeline is extensively documented elsewhere; we include a citation to this paper.
11. Is the coordinate space for the anatomical/functional imaging data clearly defined as subject/native space or standardized stereotaxic space, e.g., original Talairach, MNI305, ICBM152, etc? Where (section, paragraph #)?
- All analyses were based on data normalized to MNI space, as the HCP provides individual-subject data already normalized to this space. This is noted in Online Methods (Preprocessing; Functional parcellation and network definition).
12. If there was data normalization/standardization to a specific space template, are the type of transformation (linear vs. nonlinear) used and image types being transformed clearly described? Where (section, paragraph #)?
- Yes, see Online Methods (Preprocessing; Functional parcellation and network definition).
13. How were anatomical locations determined, e.g., via an automated labeling algorithm (AAL), standardized coordinate database (Talairach daemon), probabilistic atlases, etc.?
- We used a 268-node functional brain parcellation developed by our group with a previously published algorithm (citation included). The parcellation image is available online.
14. Were any additional regressors (behavioral covariates, motion etc) used?
- 6 or 12 motion parameters, cerebro-spinal fluid signal, white matter signal, global signal (see Online Methods, Preprocessing)
15. Is the contrast construction clearly defined?
- n/a
16. Is a mixed/random effects or fixed inference used?
- n/a
- a. If fixed effects inference used, is this justified?
- n/a
17. Were repeated measures used (multiple measurements per subject)?
- n/a
- a. If so, are the method to account for within subject correlation and the assumptions made about variance clearly stated?
- n/a
18. If the threshold used for inference and visualization in figures varies, is this clearly stated?
- The choice of thresholds is clearly stated, and where possible, we report results across a range of thresholds.

19. Are statistical inferences corrected for multiple comparisons?
- No. The primary finding for the identification analyses is a single measure of accuracy, which represents the average of many trials. The primary finding for the behavioral prediction analyses is a correlation between predicted and observed behavioral scores, which is derived from a fully cross-validated leave-one-subject-out analysis. Thus, multiple comparison correction is not relevant here.
- a. If not, is this labeled as uncorrected?
- n/a
20. Are the results based on an ROI (region of interest) analysis?
- No, a whole brain connectivity analysis is performed.
- a. If so, is the rationale clearly described?
- n/a
- b. How were the ROI's defined (functional vs anatomical localization)?
- Nodes and networks were defined based on resting-state functional connectivity data. No individual ROI analysis is performed. This is clearly stated.
21. Is there correction for multiple comparisons within each voxel?
- n/a
22. For cluster-wise significance, is the cluster-defining threshold and the corrected significance level defined?
- n/a

## ► Additional comments

### Additional Comments

The main results presented in the paper used data from the Human Connectome Project (HCP) led by Washington University, University of Minnesota, and Oxford University. The data is publicly available and is well documented. Therefore we give only a minimal description of the HCP data regarding fMRI acquisition parameters, experiment design, data normalization and preprocessing, etc., with citations to publications containing the full details of these features of the dataset.