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Main Figures: 7

Supplementary Figures: 9

Supplementary Tables: 12

Supplementary Videos: 0

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	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	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

		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 #
+ -	1a	unpaired t-test	Fig 1 legend	6	brains from 96 brain region pairs	Results para 1	Gene count	Results para 4	q<0.01, fold change >3 for every reported count	Fig 1 legend	n/a	n/a
+ -	2a	differential stability	"Genes with..." para 1	6	brains, comparison across each pair	"Genes with..." para 1	value	Supp. Table 2	n/a	n/a	n/a	n/a
+ -	2a	fraction of consistent differential relationships	Fig 2 legend	81	regions in at least 5/6 brains	Fig 2 legend	fraction of concordant differential region relationships averaged across each pair of brains	Fig 2 legend	n/a	n/a	n/a	n/a
+ -	2b	standard deviation	Fig 2 legend	132	brain structures	Fig 2 legend	value	Fig 2b	standard deviation	Fig 2 legend	n/a	n/a
+ -	2c	Multidimensional scaling	"Genes with..." para 3	132	brain structures	Fig 2 legend	First two coordinates	Fig 2c	n/a	n/a	n/a	n/a
+ -	2d	Hypergeometric test (ToppGene)	"Module enrichment..." para 1	17,348	genes, compared with the specific number of genes in each enrichment list	"Module enrichment..." para 1	Significant category count compared against multiple subsets of genes based on DS.	Fig 2d	B&H corrected, FDR q<0.01, for every reported count in each decile	Fig 2 legend	n/a	n/a
+ -	2e	% Pubmed hits	Fig 2 legend	17,348	genes	Fig 2 legend	fraction of 500 adjacent genes by DS with at least 1 Pubmed abstract also containing the word "brain"	Fig 2e / Fig 2 legend	n/a	n/a	n/a	n/a
+ -	2f	Distribution analysis	Fig 2 legend	2,288	disease states	Annotation para 1	DS location of 25th and 75th percentile disease gene in gene list ranked by DS	Fig 2f / Fig 2 legend	n/a	n/a	n/a	n/a
+ -	2f	Hypergeometric test	Fig 2 legend	2,288	disease states	Annotation para 1	Bonferroni-corrected p-value of disease gene list overlap with top 10% DS genes	Fig 2f / Fig 2 legend	Bonferroni-corrected p<0.01	Fig 2f (vertical line in plot)	n/a	n/a
+ -	3a	Consensus network	"A canonical..." para 2	6	brains	"A canonical..." para 2	Many values: gene-gene co-expression values, module assignments, module eigengenes, etc.	Throughout manuscript / Ref #22	n/a	n/a	n/a	n/a
+ -	3b (inset)	Differential stability of module eigengenes	"A canonical..." para 2	32	module eigengenes, with DS calculated as above	"A canonical..." para 2, Ref #23	Percent of genes in each module which also show at least 1.5-fold enrichment in astrocytes, neurons, or oligodendrocytes	Fig 3c	n/a	n/a	n/a	n/a

+ -	3c	Percent of marker genes for cell type	"A canonical..." para 3	3	Cell types, comparing gene lists against 32 modules	"A canonical ..." para 2, Ref #23	Percent of genes in each module which also show at least 1.5-fold enrichment in astrocytes, neurons, or oligodendrocytes	Fig 3c	n/a	n/a	n/a	n/a
+ -	3f	Number of enrichment categories	"A canonical..." para 4	32	modules, compared against all ToppGene categories	"A canonical ..." para 4	Number of significant categories for each module, with modules sorted by total count.	Fig 3f / Fig 3 legend	B&H corrected, FDR q<0.05, for every reported count	Fig 3 legend	n/a	n/a
+ -	4a	Hierarchical clustering of module eigengenes	Fig 4 legend	32	modules	Fig 4 legend	Modules clustered based on module eigengenes.	Fig 4	n/a	n/a	n/a	n/a
+ -	5	Hierarchical clustering of genes	Fig 5 legend	50	genes that have high DS but no module assignment	Fig 5 legend	Genes clustered based on z-score normalized gene expression	Fig 5	n/a	n/a	n/a	n/a
+ -	6a	Module preservation	"Differential gene..." para 1 and Ref 22	32	modules	"Differential gene..." para 1	Preservation Z-score, which is a compilation of multiple statistics into a single value	Fig 6a and Ref 22	n/a	n/a	n/a	n/a
+ -	6b	Percentage of genes agreeing between species	"Differential gene..." para 1	32	modules	"Differential gene..." para 1	% of genes in each module whose regional patterning in mouse agreed with the regional patterning in human	Fig 6b	n/a	n/a	n/a	n/a
+ -	6c-g	Pearson correlation	"Differential gene..." para 2	32	modules	"Differential gene..." para 2	Pearson correlation between human ME and corresponding mouse ME	Fig 6c-g	p-values reported in figure	n/a	n/a	n/a
+ -	7a	Parcellated connectivity matrix	"Functional connectivity" para 1	52	parcels, based on 447 subjects	"Functional connectivity" para 1	Connectivity values between pairs of 52 parcels	Fig 7a, right col.	n/a	n/a	n/a	n/a
+ -	7d	Gene co-expression values per gene	"Differential stability in cortex..." para 3-4	52	parcels, after mapping from available cortical brain regions	"Differential stability in cortex..." para 3-4	Outer product of the z-score vector obtained from gene expression across 52 parcels	"Differential stability in cortex..." para 3-4	n/a	n/a	n/a	n/a
+ -	7d	Functional genetic correlation	"Functional connectivity relates..." para 3	17,348	genes	"Functional connectivity relates..." para 3	Correlation between entries in correlation matrix from two rows above. This value is compared against DS recalculated for cortex only.	Fig 7d	n/a	n/a	n/a	n/a

Representative figures

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

   If so, what figure(s)?

   All images in the paper (in Figure 6) are available as part of the Allen Mouse Brain Atlas.

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?

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

   N/A; however, please see the Documentation tab at the atlas website for more experimental details.

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.

   A more complete description of the resource, including information on sample size is available in the Methods section, in the Documentation tab of the Allen Human Brain Atlas, and in Reference #3.

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

   Where (section, paragraph #)?

   The statistical methods used are described in the text. To the best of our knowledge the statistical tests used are appropriate.

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

      Standard methods are presented without detailed description. Less standard methods are described in the text, in separate Methods sections, or through citations to references where they are described in detail.

   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 #)?

      To the best of our knowledge, statistical tests were chosen such that the data meet assumptions of the specific statistical test. This is described in the "Statistics of the methods" section.

   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 #)?

      No.

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

      n/a

   e. Are there adjustments for multiple comparisons?

      Yes, when appropriate.

3. Are criteria for excluding data points reported?

   Was this criterion established prior to data collection?

   Where is this described (section, paragraph #)?

   n/a. All data included in the atlas are used in this analysis, unless otherwise specified. Data points are averaged together as described in the text.

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

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. All brains come from neurotypical donors.

6. For experiments in live vertebrates, is a statement of compliance with ethical guidelines/regulations included?

   Where (section, paragraph #)?

   n/a. All data come from atlases that are freely available to the public.

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 #)?

   This information is available through the Documentation tabs of the relevant Allen Brain Atlas.

10. Is the age of the animals/subjects reported?

    Where (section, paragraph #)?

    This information is available through the Documentation tabs of the relevant Allen Brain Atlas.

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 #)?

n/a

a. How were the criteria for exclusion defined?

Where is this described (section, paragraph #)?

n/a

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

Where is this described (section, paragraph #)?

n/a

Reagents

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

n/a

a. Is antibody catalog number given?

Where does this appear (section, paragraph #)?

n/a

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

Where does this appear (section, paragraph #)?

n/a

2. If cell lines were used to reflect the properties of a particular tissue or disease state, is their source identified?

Where (section, paragraph #)?

n/a

a. Were they recently authenticated?

Where is this information reported (section, paragraph #)?

n/a

Data deposition

Data deposition in a public repository is mandatory for:

a. Protein, DNA and RNA sequences
b. Macromolecular structures
c. Crystallographic data for small molecules
d. 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.

1. Are accession codes for deposit dates provided?

   Where (section, paragraph #)?

All data is freely available as part of the Allen Brain Atlas data portal, or as part of Supplementary Data Set 1.

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.

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

R is required to reproduce nearly all the figure panels.

2. Is computer source code/software provided with the paper or deposited in a public repository? Indicate in what form this is provided or how it can be obtained.

Code is available as part of Supplementary Data Set 1.

Human subjects

1. Which IRB approved the protocol?

   Where is this stated (section, paragraph #)?

n/a; however, please see the Documentation tab at the atlas website for additional details.

2. Is demographic information on all subjects provided?

   Where (section, paragraph #)?

Please see the Documentation tab at the atlas website for additional details.

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

   Where (section, paragraph #)?

Please see the Documentation tab at the atlas website.

4. Are the inclusion and exclusion criteria (if any) clearly specified?

   Where (section, paragraph #)?

n/a

5. How well were the groups matched?

   Where is this information described (section, paragraph #)?

n/a

6. Is a statement included confirming that informed consent was obtained from all subjects? Where (section, paragraph #)?	n/a; however, please see the Documentation tab at the atlas website for additional details.
7. For publication of patient photos, is a statement included confirming that consent to publish was obtained? Where (section, paragraph #)?	n/a

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:

1. Were any subjects scanned but then rejected for the analysis after the data was collected?	n/a; however, please see the cited publications for information on the published fMRI data set used in this analysis.
a. If yes, is the number rejected and reasons for rejection described? Where (section, paragraph #)?	n/a
2. Is the number of blocks, trials or experimental units per session and/or subjects specified? Where (section, paragraph #)?	n/a
3. Is the length of each trial and interval between trials specified?	n/a
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.	n/a
5. Is the task design clearly described? Where (section, paragraph #)?	n/a
6. How was behavioral performance measured?	n/a
7. Is an ANOVA or factorial design being used?	n/a
8. For data acquisition, is a whole brain scan used? If not, state area of acquisition.	n/a
a. How was this region determined?	n/a

9. Is the field strength (in Tesla) of the MRI system stated?	n/a
a. Is the pulse sequence type (gradient/spin echo, EPI/spiral) stated?	n/a
b. Are the field-of-view, matrix size, slice thickness, and TE/TR/ flip angle clearly stated?	n/a
10. Are the software and specific parameters (model/functions, smoothing kernel size if applicable, etc.) used for data processing and pre-processing clearly stated?	n/a
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 #)?	n/a
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 #)?	n/a
13. How were anatomical locations determined, e.g., via an automated labeling algorithm (AAL), standardized coordinate database (Talairach daemon), probabilistic atlases, etc.?	n/a
14. Were any additional regressors (behavioral covariates, motion etc) used?	n/a
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?	n/a
19. Are statistical inferences corrected for multiple comparisons?	n/a
a. If not, is this labeled as uncorrected?	n/a

20. Are the results based on an ROI (region of interest) analysis?	n/a
a. If so, is the rationale clearly described?	n/a
b. How were the ROI's defined (functional vs anatomical localization)?	n/a
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	Extensive documentation is available as part of the Allen Brain Atlas data resources. These white papers are freely available to the public. Due to the unique nature of this data set, more extensive information on methods and statistical tests is available in the main manuscript, online methods, and supplemental code than can be supplied in this checklist.