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Supplementary Figures: 2

Supplementary Tables: 0

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
+ -	1D	unpaired t-test	Fig. Legend	7, 6	neurons from 6 and 4 rats, respectively	Fig 1D, legend	error bars are mean +/- SEM	Fig. legend	p=0.02	Fig. legend	t(11)=2.67	Fig. legend

		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 #
+ -	1H	one-way ANOVA with Bonferroni posttest	Fig. Legend	9, 10,13	neurons from 6, 7, and 11 rats, respectively	Fig. 1H, legend	error bars are mean +/- SEM	Fig. legend	p=0.02	Fig legend	F(2, 28)=4.85	Fig. Legend
+ -	1I	unpaired t-test	Fig Legend	7, 7, 6, 9, 7, 7, 9, 13, 6, 7, 8, and 5	neurons from 4, 5, 4, 5, 5, 5, 6, 11, 4, 3, 4 and 4 rats, respectively	Fig. 1I, legend	error bars are mean +/- SEM	Fig. legend	p=0.01	Fig legend	t(11)=3.00	Fig Legend
+ -	2C	one-way ANOVA with Bonferroni posttest	Fig Legend	13, 11, 14	neurons from 7, 6, and 6 rats, respectively	Fig. 2C, legend	error bars are mean +/- SEM	Fig. legend	p=0.02	Fig Legend	F(2,35)=4.25	Fig Legend
+ -	2D	two-way ANOVA with Bonferroni posttest	Fig Legend	12, 10, 11	neurons from 6, 6 and 7 rats, respectively	Fig2D, Legend	error bars are mean +/- SEM	Fig. legend	p=0.00	Fig Legend	F(2,810)=15.71	Fig Legend
+ -	2F	one-way ANOVA with Bonferroni posttest	Fig Legend	10, 8, 8	neurons from 5, 4 ,5 rats, respectively	Fig. 2F, legend	error bars are mean +/- SEM	Fig. legend	p=0.01	Fig Legend	F(2,23)=6.15	Fig Legend
+ -	2H	one-way ANOVA with Bonferroni posttest	Fig Legend	19, 20, and 10	neurons from 12, 10, and 7 rats, respectively	Fig. 2H, legend	error bars are mean +/- SEM	Fig. legend	p=0.04	Fig Legend	F(2,46)=3.44	Fig Legend
+ -	3F	two-way ANOVA with Bonferroni posttest	Fig Legend	no peptide: 5, 6, 5 scrambled peptide: 7, 5 7, GluA23Y peptide: 5,5,6	rats	Fig3F, Legend	error bars are mean +/- SEM	Fig. legend	p=0.00	Fig Legend	F(2,42)=34.62	Fig Legend
+ -	3G	two-way ANOVA with Bonferroni posttest	Fig Legend	no peptide: 5, 6, 5 scrambled peptide: 7, 5 7, GluA23Y peptide: 5,5,6	rats	Fig3G, Legend	error bars are mean +/- SEM	Fig. legend	p=0.00	Fig Legend	F(2,42)=44.91	Fig Legend
+ -	3H	two-way ANOVA with Bonferroni posttest	Fig Legend	no peptide: 5, 6, 5 scrambled peptide: 7, 5 7, GluA23Y peptide: 5,5,6	rats	Fig 3H, Legend	error bars are mean +/- SEM	Fig. legend	p=0.00	Fig Legend	F(2,42)=7.2	Fig Legend

+ -	3I	two-way ANOVA with Bonferroni posttest	Fig Legend	no peptide: 5, 6, 5 scrambled peptide: 7, 5 7, GluA23Y peptide: 5,5,6	rats	Fig 3I, Legend	error bars are mean +/- SEM	Fig. legend	p=0.00	Fig Legend	F(2,42)=27.56	Fig Legend
+ -	3J	two-way ANOVA with Bonferroni posttest	Fig Legend	no peptide: 5, 6, 5 scrambled peptide: 7, 5 7, GluA23Y peptide: 5,5,6	rats	Fig 3J, Legend	error bars are mean +/- SEM	Fig. legend	p=0.39	Fig Legend	F(2,42)=0.97	Fig Legend
+ -	4B	two-way ANOVA with Bonferroni posttest	Fig Legend	no peptide: 6, 6, 6 scrambled peptide: 4, 7 6, GluA23Y peptide: 6,5,6	rats	Fig 4B, Legend	error bars are mean +/- SEM	Fig. legend	p=0.00	Fig Legend	F(2,42)=100.4	Fig Legend
+ -	4C	two-way ANOVA with Bonferroni posttest	Fig Legend	no peptide: 6, 6, 6 scrambled peptide: 4, 7 6, GluA23Y peptide: 6,5,6	rats	Fig 4C, Legend	error bars are mean +/- SEM	Fig. legend	p=0.00	Fig Legend	F(2,42)=25.96	Fig Legend
+ -	4D	two-way ANOVA with Bonferroni posttest	Fig Legend	no peptide: 6, 6, 6 scrambled peptide: 4, 7 6, GluA23Y peptide: 6,5,6	rats	Fig 4D, legend	error bars are mean +/- SEM	Fig. legend	p=0.00	Fig Legend	F(2,42)=41.16	Fig Legend
+ -	4E	two-way ANOVA with Bonferroni posttest	Fig Legend	no peptide: 6, 6, 6 scrambled peptide: 4, 7 6, GluA23Y peptide: 6,5,6	rats	Fig 4E, Legend	error bars are mean +/- SEM	Fig. legend	p=0.00	Fig Legend	F(2,42)=32.56	Fig Legend
+ -	4F	two-way ANOVA with Bonferroni posttest	Fig Legend	no peptide: 6, 6, 6 scrambled peptide: 4, 7 6, GluA23Y peptide: 6,5,6	rats	Fig 4F, Legend	error bars are mean +/- SEM	Fig. legend	p=0.00	Fig Legend	F(2,42)=6.944	Fig Legend

+ -	5B	two-way ANOVA with Bonferroni posttest	Fig Legend	no peptide: 6, 9, 6 scrambled peptide: 5, 5, 9, GluA23Y peptide: 5,7,10	mice	Fig 5B, Legend	error bars are mean +/- SEM	Fig. legend	p=0.00	Fig Legend	F(2,53)=62.09	Fig Legend
+ -	5C	two-way ANOVA with Bonferroni posttest	Fig Legend	no peptide: 6, 9, 6 scrambled peptide: 5, 5, 9, GluA23Y peptide: 5,7,10	mice	Fig 5C, Legend	error bars are mean +/- SEM	Fig. legend	p=0.00	Fig Legend	F(2,53)=87.71	Fig Legend
+ -	5D	two-way ANOVA with Bonferroni posttest	Fig Legend	no peptide: 6, 9, 6 scrambled peptide: 5, 5, 9, GluA23Y peptide: 5,7,10	mice	Fig 5D, Legend	error bars are mean +/- SEM	Fig. legend	p=0.02	Fig Legend	F(2,53)=4.42	Fig Legend
+ -	5E	two-way ANOVA with Bonferroni posttest	Fig Legend	no peptide: 6, 9, 6 scrambled peptide: 5, 5, 9, GluA23Y peptide: 5,7,10	mice	Fig 5E, Legend	error bars are mean +/- SEM	Fig. legend	p=0.00	Fig Legend	F(2,53)=31.49	Fig Legend
+ -	5F	two-way ANOVA with Bonferroni posttest	Fig Legend	no peptide: 6, 9, 6 scrambled peptide: 5, 5, 9, GluA23Y peptide: 5,7,10	mice	Fig 5F, Legend	error bars are mean +/- SEM	Fig. legend	p=0.45	Fig Legend	F(2,53)=0.8065	Fig Legend
+ -	5H	two-way ANOVA with Bonferroni posttest	Fig Legend	no peptide: 5, 5, 6 scrambled peptide: 4, 5, 6, GluA23Y peptide: 4,5,5	mice	Fig 5H, Legend	error bars are mean +/- SEM	Fig. legend	p=0.00	Fig Legend	F(2,36)=60.97	Fig Legend
+ -	5I	two-way ANOVA with Bonferroni posttest	Fig Legend	no peptide: 5, 5, 6 scrambled peptide: 4, 5, 6, GluA23Y peptide: 4,5,5	mice	Fig 5I, Legend	error bars are mean +/- SEM	Fig. legend	p=0.72	Fig Legend	F(2,36)=0.33	Fig Legend

+ -	5J	two-way ANOVA with Bonferroni posttest	Fig Legend	no peptide: 5, 5, 6 scrambled peptide: 4, 5, 6, GluA23Y peptide: 4,5,5	mice	Fig 5J, Legend	error bars are mean +/- SEM	Fig. legend	p=0.00	Fig Legend	F(2,36)=20.65	Fig Legend
+ -	5K	two-way ANOVA with Bonferroni posttest	Fig Legend	no peptide: 5, 5, 6 scrambled peptide: 4, 5, 6, GluA23Y peptide: 4,5,5	mice	Fig 5K, Legend	error bars are mean +/- SEM	Fig. legend	p=0.00	Fig Legend	F(2,36)=37.17	Fig Legend
+ -	5L	two-way ANOVA with Bonferroni posttest	Fig Legend	no peptide: 5, 5, 6 scrambled peptide: 4, 5, 6, GluA23Y peptide: 4,5,5	mice	Fig 5L, Legend	error bars are mean +/- SEM	Fig. legend	p=0.37	Fig Legend	F(2,36)=1.03	Fig Legend
+ -	6B	one-way ANOVA with Bonferroni posttest	Fig Legend	9, 11, 6	neurons from 6, 7, and 6 mice, respectively	Fig. 6B, Legend	error bars are mean +/- SEM	Fig. legend	p=0.00	Fig Legend	F(2,28)=18.4	Fig Legend
+ -	6D	one-way ANOVA with Bonferroni posttest	Fig Legend	9, 10, 10	neurons from 6, 5, and 8 mice, respectively	Fig. 6D, Legend	error bars are mean +/- SEM	Fig. legend	p=0.01	Fig Legend	F(2,26)=6.14	Fig Legend
+ -	6G	one-way ANOVA with Bonferroni posttest	Fig Legend	10, 12, 10	neurons from 3, 3, and 3 mice, respectively	Fig 6G, Legend	error bars are mean +/- SEM	Fig. legend	p=0.02	Fig 6G, Legend	F(2,29)=4.57	Fig 6G, Legend
+ -	7B	two-way ANOVA	Fig Legend	10, 5, 5, 7, 8, 8	mice	Fig 7B, Legend	error bars are mean +/- SEM	Fig. legend	p=0.56	Fig 7B	F(12,120)=0.89	Fig 7B, Legend
+ -	7C	one-way ANOVA with Bonferroni posttest	Fig Legend	10, 5, 5, 7, 8, 8	mice	Fig 7C, Legend	error bars are mean +/- SEM	Fig. legend	p=0.00	Fig 7C, Legend	F(5,37)=12.87	Fig Legend
+ -	7E	one-way ANOVA with Bonferroni posttest	Fig Legend	7,5,7,7,13,18	mice	Fig 7E, Legend	error bars are mean +/- SEM	Fig. legend	p=0.00	Fig 7E, Legend	F(5,51)=7.28	Fig Legend
+ -	S1a	two-way ANOVA	Fig Legend	10,5,4,8, 10,9	mice	Fig S1A, Legend	error bars are mean +/- SEM	Fig. legend	p = 0.4836	Fig Legend	F(8,120)=0.9436	Fig Legend
+ -	S1b	one-way ANOVA	Fig Legend	10,5,4,8, 10,9	mice	Fig Legend	error bars are mean +/- SEM	Fig. legend	p=0.05	Fig Legend	F(5,40)=2.422	Fig Legend
+ -	S1e	unpaired t-test	Fig Legend	10,10	mice	Fig Legend	error bars are mean +/- SEM	Fig. legend	p=0.37	Fig Legend	t(18)=0.92	Fig Legend
+ -	S1g	unpaired t-test	Fig Legend	10,10	mice	Fig Legend	error bars are mean +/- SEM	Fig. legend	p=0.18	Fig Legend	t18=1.38	Fig Legend
+ -	S1d	two-way ANOVA	Fig Legend	10,10	mice	online method	error bars are +/- SEM	Fig. legend	p=0.99	Fig Legend	F(6,126)=0.1425	Fig Legend
+ -	S1f	two-way ANOVA	Fig Legend	10,10	mice	online method	error bars are +/- SEM	Fig. legend	p=0.8981	Fig Legend	F(6,102)=0.3672	Fig Legend
+ -	S2f	paired t-test	Fig Legend	6, 6	6 cells from 6 brain slices	online method	error bars are mean +/- SEM	Fig. legend	p=0.10	Fig Legend	t(5)=1.97	Fig Legend

+ -	S2g	paired t-test	Fig Legend	6, 6	6 cells from 6 brain slices	online method	error bars are mean +/- SEM	Fig. legend	p=0.39	Fig Legend	t(10)=0.95	Fig Legend

Representative figures

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

   If so, what figure(s)?

   Yes, representative electrophysiological recordings: Figure 1A-C, E-G; Figure 2A,B,D,E, and G; Figure 6A,C, and F; Figure S1.
   Representative spine imaging: Figure 3A-E; Figure 4A; Figure 5A and G.
   Representative dual recording setup: Figure 6E

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 #)?

   Yes, located in the supplemental figure legend section. There were no limitations in repeatability.

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.

   Yes, sample size was determined either based on our previous experience with similar experiments or those that have been routinetly used in similar studies published in this journal.

   Online Methods paragraph #15

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

   Where (section, paragraph #)?

   Yes, Online Methods, paragraph #15.

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

      yes

   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 #)?

      Normal distribution was assumed based on previous and current results: in Online Methods, Data acquisition and statistics 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 #)?

      Yes, in Online Methods section, Data acquisition and statistics subsection.

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

      two sided, specified.

   e. Are there adjustments for multiple comparisons?

      yes, Bonferroni, specified

3. To promote transparency, *Nature Neuroscience* has stopped allowing bar graphs to report statistics in the papers it publishes. If you have bar graphs in your paper, please make sure to switch them to dot-plots (with central and dispersion statistics displayed) or to box-and-whisker plots to show data distributions.	all switched.
4. Are criteria for excluding data points reported? Was this criterion established prior to data collection? Where is this described (section, paragraph #)?	Yes, criteria was reported before data were collected and described in Online Methods, paragraph #6 and 14
5. 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 #)?	Yes, throughout the Results and Online Methods Paragraph
6. 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 #)?	Yes, #2 paragraph in Data acquisition subsection, Online Methods
7. For experiments in live vertebrates, is a statement of compliance with ethical guidelines/regulations included? Where (section, paragraph #)?	Yes, first paragraph in Online Methods
8. Is the species of the animals used reported? Where (section, paragraph #)?	Yes, first paragraph in Online Methods, first paragraph
9. Is the strain of the animals (including background strains of KO/ transgenic animals used) reported? Where (section, paragraph #)?	Yes, first paragraph in Online Methods, first paragraph
10. Is the sex of the animals/subjects used reported? Where (section, paragraph #)?	Yes, first paragraph in Online Methods, first paragraph
11. Is the age of the animals/subjects reported? Where (section, paragraph #)?	Yes, first paragraph in Online Methods, first paragraph
12. For animals housed in a vivarium, is the light/dark cycle reported? Where (section, paragraph #)?	Yes, first paragraph in Online Methods, first paragraph
13. For animals housed in a vivarium, is the housing group (i.e. number of animals per cage) reported? Where (section, paragraph #)?	Yes, first paragraph in Online Methods, first paragraph

14. For behavioral experiments, is the time of day reported (e.g. light or dark cycle)?

    Where (section, paragraph #)?

Yes, Online Methods,

15. Is the previous history of the animals/subjects (e.g. prior drug administration, surgery, behavioral testing) reported?

    Where (section, paragraph #)?

Yes, first paragraph in Online Methods, Drug-induced locomotor response sub section and Conditioned place preference subsection.

    a. If multiple behavioral tests were conducted in the same group of animals, is this reported?

       Where (section, paragraph #)?

yes, reported, Online Methods section, Drug-induced locomotor response sub section and Conditioned place preference subsection.

16. If any animals/subjects were excluded from analysis, is this reported?

    Where (section, paragraph #)?

yes Online Methods, Online Methods Data acquisition and statistics section #1 paragraph..

    a. How were the criteria for exclusion defined?

       Where is this described (section, paragraph #)?

Health, misplacement of cannula, specified in Online Methods Data acquisition and statistics section #1 paragraph.

    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 #)?

Online Methods Data acquisition and statistics section #1 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?

       Where does this appear (section, paragraph #)?

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

       Where does this appear (section, paragraph #)?

2. Cell line identity

    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 #)?

n/a

    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.

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 #)?

Data availability

Provide a Data availability statement in the Methods section under "Data availability", which should include, where applicable:
• Accession codes for deposited data
• Other unique identifiers (such as DOIs and hyperlinks for any other datasets)
• At a minimum, a statement confirming that all relevant data are available from the authors
• Formal citations of datasets that are assigned DOIs
• A statement regarding data available in the manuscript as source data
• A statement regarding data available with restrictions

See our data availability and data citations policy page for more information.

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.

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

Where is the Data Availability statement provided (section, paragraph #)?

Data Availability: The data that support the findings of this study are available from the corresponding author upon request.

Code Availability: not applicable.

Accession codes: not applicable.

provided by the end of the Online Methods

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.

n/a

2. 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.

n/a

Human subjects

1. Which IRB approved the protocol?

   Where is this stated (section, paragraph #)?

n/a

2. Is demographic information on all subjects provided?

   Where (section, paragraph #)?

n/a

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

   Where (section, paragraph #)?

n/a

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

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

   a. If yes, is the number rejected and reasons for rejection described?

      Where (section, paragraph #)?

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?	
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?	
b. Are the field-of-view, matrix size, slice thickness, and TE/TR/flip angle clearly stated?	
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?

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?

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?

20. Are the results based on an ROI (region of interest) analysis? — n/a

    a. If so, is the rationale clearly described?

    b. How were the ROI's defined (functional vs anatomical localization)?

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