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Supplementary Tables: 0

Supplementary Videos: 1

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 #
+ -	1h	unpaired t-test	online methods	5 for wt and 5 for het in each condition	The brain sections were from 5 different pairs of mice.	Figure legend	error bars are mean +/- SEM	Figure legend	p=0.0077 wt vs 2-4M mice; p<0.0001 wt vs het 16M; p<0.0001 het 2-4M vs 16M	Figure legend	t=3.536, df=8 for 4M t=12.38, df=8 for 16 M	Fig legend result section
+ -	4c	unpaired t test	online methods	15,11	15 cells from 11 slices from 10 wt mice, 11 cells from 8 slices from 8 het mice	Figure legend	error bars are mean +/- SEM	Figure legend	Amplitude for KI: p=0.022;	Figure legend	Fig 4C: t=2.394, df=24	Fig legend result section
+ -	4d	unpaired t test	online methods	8,9	8 cells from 6 slices from 5 wt mice and 9 cells from 7 slices from 6 het mice	Figure legend	error bars are mean +/- SEM	Figure legend	Amplitude for KO: p=0.966	Figure legend	fig 4d: t=0.0421, df=15	Fig legend result section
+ -	5e	two way ANOVA and Bonferroni posttests	online methods	5,5	tissues from 5 different pairs of littermates and 5 independent experiments	Figure legend	error bars are mean +/- SEM	Figure legend	for wt and het KI Gamma2 subunit comparison in cor and cb: P<0.05; hip and thal: P<0.001(raw p values were not calculated by GraphPad Prism 5 with Bonferroni posttests but will be provided upon request by mannual calculation).	Figure legend	t=2.921 for cor t=3.098 for cb t=7.202 for hip t=5.707 for thal	Fig legend result section
+ -	5f	two way ANOVA and Bonferroni posttests	online methods	5,5	tissues from 5 different pairs of littermates and 5 independent experiments	Figure legend	error bars are mean +/- SEM	Figure legend	for wt and het KO Gamma2 subunit comparison in cor :no difference cb and thal: P<0.05; hip: P<0.001	Figure legend	t=1.631 for cor t=3.087 for cb t=4.426 for hip t=3.145 for thal	Fig legend result section
+ -	5g	two way ANOVA and Bonferroni posttests	online methods	5,5	tissues from 5 different pairs of littermates and 5 independent experiments	Figure legend	error bars are mean +/- SEM	Figure legend	P<0.05 for cor and cb P<0.001 for hip P<0.01 for thal	Figure legend	For KI: t=2.756 for cor t=3.057 for cb t=4.56 for hip t=3.357 for thal	Fig legend result section
+ -	5h	two way ANOVA and Bonferroni posttests	online methods	5,5	tissues from 5 different pairs of littermates and 5 independent experiments	Figure legend	error bars are mean +/- SEM	Figure legend	P>0.05 for cor,cb, hip and thal	Figure legend	t=0.4974 for cor t=0.6218 for cb t=0.4353 for hip t=0.6218 for thal	Fig legend result section

+ -	6c	unpaired t test	online methods	11, 12	tissues from 11 wt mice and 12 het mice, 7 independent experiments	Figure legend	error bars are mean +/- SEM	Figure legend	For whole field: p=0.0048 for somata: p=0.0031 for nonsomata: p=0.0136	Figure legend	Fig 6c. whole field: t=3.724 df=21 somata: t=2.469 df=21 non somata: t=2.573 df=21	Fig legend result section
+ -	6f	Unpaired t test	online methods	4,4	brain tissues from 4 different pairs of littermates, 4 independent experiments	Figure legend	error bars are mean +/- SEM	Figure legend	for GABRG2 subunit protein in SPM p=0.0334	Figure legend	For spm t=2.748, df=6	Fig legend result section
+ -	6g	single value (one sample) t test	online methods	4,4	brain tissues from 4 different pairs of littermates, 4 independent experiments, in each experiment, four brain regions were from the same mouse.	Figure legend	error bars are mean +/- SEM	Figure legend	cor:p=0.011 cb:p=0.0088 hip:p=0.0154 thal:p=0.0007	Figure legend	Fig 6g. For g2 surface cor t=5.636,df=3, for g2 surface cb, t=6.106, df=3 for g2 surface hip, t= 5.000, df=3 for g2 surface thal, t=14.25, df=3	Fig legend result section
+ -	7f	unpaired t test	online methods	12,11	12 brain sections for wt and 11 brain section for het from 6 independent staining from 7 pairs of mice. The staining was done in a genotype blind fasion. The data were pooled after all the stainings were finished.	Figure legend	error bars are mean +/- SEM	Figure legend	For gamma2 subunit intensity: p=0.005; For caspase 3 intensity: p=0.0161	Figure legend	Fig 7f. gamma2 :t=3.137, df=21 caspase 3: t=2.608 df=21	Fig legend result section
+ -	7g	unpaired t test	online methods	7,7	7 pairs of mice	Figure legend	error bars are mean +/- SEM	Figure legend	For caspase 3: p=0.0301 For caspase 3 +NeuN: p<0.0001 For TUNEL +NeuN: p=0.0127	Figure legend	For caspase 3: t=2.460, df=12 For caspase 3 +NeuN: t=6.274, df=12 For TUNEL +NeuN:t=2.926 df=12	Fig legend result section
+ -	8c	Two way ANOVA and Bonferroni posttests	online methods	4	4 different batches of transfections	Figure legend	error bars are mean +/- SEM	Figure legend	wt vs mut 0.5 p<0.05 wt vs mut 1 p<0.001 wt vs mut 2.5 p<0.001 wt vs mut 5 p<0.01 wt vs mut 10 ns (raw p values were not calculated by GraphPad Prism 5 with Bonferroni posttests but will be provided upon request by mannual calculation).	Figure legend	0.5: t=14.64, df=3 1.0: t=7.313, df=3 2.5:t=9.071 df=3 5.0: t=19.58 df=3 10:t=9.52 df=3	Fig legend result section
+ -	8e	one way ANOVA	online methods	4	4 different batches of transfections	Figure legend	error bars are mean +/- SEM	Figure legend	wt vs mut:p<0.0001	Figure legend	F=41.66, R squared=0.9124	Fig legend result section

+ -	Supplementary Fig. 6	unpaired t test	online methods	5	5 different pairs of mice and 5 independent experiments	Figure legend	error bars are mean +/- SEM	Figure legend	wt vs het p=0.2071 for Er81+NeuN wt vs het p=0.0318 for Tbr1+NeuN	Figure legend	t=2.314 df=8	Fig legend result section
+ -	Supplementary Fig. 7e	unpaired t test	online methods	5	5 different pairs of mice and 5 independent experiments	Figure legend	error bars are mean +/- SEM	Figure legend	p=0.03 wt vs het in cortex I-II/III;p=0.0012 wt vs het in cortex IV-VI; p=0.0226 wt vs het in thal	Figure legend	t=2.633 df=8 for cortex I-II/III t=4.897 df=8 for cortex IV-VI t=2.816, df=8 for thal	Fig legend result section
+ -	Supplementary fig. 7f	unpaired t test	online methods	5	5 different pairs of mice and 5 independent experiments	Figure legend	error bars are mean +/- SEM	Figure legend	p=0.3590 wt vs het dg, p=0.3924 wt vs het CA1, p=0.7008 wt vs het CA3,	Figure legend	t=0.973 df=8 for dg t=0.9040 df=8 for CA1 t=0.7008 df=8 for CA3	Fig legend result section
+ -	Supplementary fig. 7g	unpaired t test	online methods	5	5 different pairs of mice and 5 independent experiments	Figure legend	error bars are mean +/- SEM	Figure legend	p=0.0074	Figure legend	t=3.558, df=8	Fig legend result section
+ -	Supplementary fig. 8d	unpaired t test	online methods	5	5 different pairs of mice and 5 independent experiments	Figure legend	error bars are mean +/- SEM	Figure legend	p=0.0515	Figure legend	t=2.287 df=8	Fig legend result section
+ -	Supplementary fig. 11b	two way ANOVA and bonferroni posttests	online methods	5	5 different pairs of mouse pups and 5 independent experiments	Figure legend	error bars are mean +/- SEM	Figure legend	P>0.05 for all brain regions. (raw p values were not calculated by GraphPad Prism 5 with Bonferroni posttests but will be provided upon request by mannual calculation).	Figure legend	t=0.2957 for cortex, cortex-hip,cerebellum, t=0.4435 for medulla	Fig legend result section
+ -	Supplementary fig. 12b	two way ANOVA and bonferroni posttests	online methods	6 for p0 and 2-4M 8 for 4-6M and 11 for ~12M	6 pairs of mice for P0 and 2-4M 8 pairs of mice for 4-6M 11 pairs of mice for ~12M	Figure legend	error bars are mean +/- SEM	Figure legend	p>0.05 for p0 P>0.05 for 2-4M P>0.05 for 4-6M P<0.001 for ~12M (raw p values were not calculated by GraphPad Prism 5 with Bonferroni posttests but will be provided upon request by mannual calculation).	Figure legend	t=0.5204 for P0 t=0.05204 for 2-4M t=0.1202 for 4-6M t=5.284 for ~12M	Fig legend result section

Representative figures

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

   If so, what figure(s)?

Yes.
Representative images of Western blots in Figure 1, 5,6,8 and supplementary figure 10 and 13.
Representative images of immunohistochemistry in Figure 1, 2,6,7,8 and Supplementary Figure 2,5,6,7,8,9,11,12.

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. There is a clear statement of how many times the experiment was successfully repeated if there is a quantification involved. For those data without quantification (Fig1c,Supplementary Figure10 and 13), we successfully repeated at least three to four times with no limitations of reproducibility.

PCR gel (Fig 2a) were also done multiple times with no limitation of reproducibility.

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 referred to previous similar studies from our own and other groups to determine the sample size. The details are stated in Statistical analysis in Online Methods section.
Statistical analysis indicates whether the effects were significant at the sample size used.

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

   Where (section, paragraph #)?

Yes. We deem the statistical tests used in each figure are appropriate. Similar information is stated in statistical analysis in Online Methods section.

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

Yes. There is a paragraph of statistical analysis in the methods section. It clearly defined the statistical tests used for each experiment.

   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 #)?

Yes. Based on our preliminary data and previous studies, most of our experiments were distributed symmetrically or bell-shape like. This information is included in the manuscript in 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 #)?

Standard error of the mean (S.E.M) is reported with each mean in the text and figures.

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

The tests were two-sided.

   e. Are there adjustments for multiple comparisons?

We used Bonferroni correction.

3. Are criteria for excluding data points reported? Was this criterion established prior to data collection? Where is this described (section, paragraph #)?	The only mice excluded from the study were those mice recommended by the veterinarians to sacrifice due to health concerns such as severe fighting wounds in Vanderbilt University Medical Center. This criterion was established prior to data collection. This information is not included in the manuscript.
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 #)?	All the behavior tests were done based on the availability of the mice in Vanderbilt University Mouse Neurobehavior core and the availability of the behavior testing rooms. This information is not included in the manuscript.
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 #)?	All the Elevated Zero Maze and Open Field tests were conducted by the personnel without knowing the mouse genotypes. The data were organized based on genotype. This information is not included in the manuscript.
6. For experiments in live vertebrates, is a statement of compliance with ethical guidelines/regulations included? Where (section, paragraph #)?	All the experiments in live animals were approved by IACUC in Vanderbilt University Medical Center. This information is not included in the manuscript.
7. Is the species of the animals used reported? Where (section, paragraph #)?	Yes. We used mice. This information is included in online methods section.
8. Is the strain of the animals (including background strains of KO/ transgenic animals used) reported? Where (section, paragraph #)?	In the study, all the data of biochemistry, immunohistochemistry and electrophysiology were from mouse littermates in mixed C57BL/6j/129Svj or C57Bl/6j background. The data were pooled. All the mice subject to EEG recordings, Elevated Zero Maze and Open Field tests were in pure C57Bl/6j background. This information is included in online methods in page 29 in the manuscript.
9. Is the sex of the animals/subjects used reported? Where (section, paragraph #)?	Both male and female mice were used in the study. There was no special comparison between different genders.
10. Is the age of the animals/subjects reported? Where (section, paragraph #)?	Yes. The age of mice were reported in the figures and/or in the figure legends.
11. For animals housed in a vivarium, is the light/dark cycle reported? Where (section, paragraph #)?	All the mice were housed in a vivarium monitored by IACUC in Vanderbilt University Medical Center. The housing facility has light on from 6am to 6pm. This information is not reported in the manuscript.
12. For animals housed in a vivarium, is the housing group (i.e. number of animals per cage) reported? Where (section, paragraph #)?	The animal housing is based on the guidelines from IACUC in Vanderbilt University Medical Center. The mice were group housed with a maximum number of 5 per cage. All the mice were single housed after headmount affixation surgery for EEG recordings. This information is not included in the manuscript.

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

    Where (section, paragraph #)?

Both Open Field test and Elevated Zero test were conducted in day time (between 6am to 6pm). This information was not reported in the manuscript.

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

    Where (section, paragraph #)?

Most mice used for Open Field test had been tested with Elevated Zero Maze before Open Field test. Only those mice were recommended to sacrifice by the veterinarian Vanderbilt animal housing and the Neurobehavior core facilities were removed. This information was not reported in the manuscript.

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

       Where (section, paragraph #)?

Most mice used for Open Field test had been tested with Elevated Zero Maze before Open Field test. The order of the test is based on the different stress level of each test. This information was not reported in the manuscript.

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

    Where (section, paragraph #)?

We used age, gender and strain matched mice in all the experiments. Only those mice were recommended to sacrifice by the veterinarian Vanderbilt animal housing and the Neurobehavior core facilities were excluded from the study.

    a. How were the criteria for exclusion defined?

       Where is this described (section, paragraph #)?

This is based on the Vanderbilt University Medical Center IACUC guidelines.

    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 #)?

In Fig 2e, the discrepancy between the number of animals in the het KI mice at the beginning and the end of the study was likely due to SUDEP (sudden unexpected death in epilepsy). This was described in the results section paragraph 5.

Reagents

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

Yes. All the antibodies used in the study have been validated and are commercially available. The mouse monoclonal anti GABRG2 antibody used in Fig 7d is a gift from Dr. Jadeep Kapur's lab. However, it has been validated by Dr. Kapur's lab and it is also commercially available.

    a. Is antibody catalog number given?

       Where does this appear (section, paragraph #)?

The catalog number of all the antibodies are provided in online methods section.

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

       Where does this appear (section, paragraph #)?

The monoclonal anti-GABRG2 antibody has been reported by Dr. Jadeep Kapur's lab (Joshi S, Sun C, Kapur J. A mouse monoclonal antibody against the γ2 subunit of GABAA receptors. Hybridoma (Larchmt). 2011 Dec;30(6):537-42. doi: 10.1089/hyb.2011.0035.
PMID: 22149279
We used this antibody in Fig 7d. The antibody was reported in the methods section paragraph 8.

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.

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

1. Are accession codes for deposit dates provided?

   Where (section, paragraph #)?

For the protein modeling data Fig. 1a and Supplementary Fig. 1c-d, please visit http://figshare.com/articles/Kang_et_al_/1037721 for more information.

The sequences for the wild-type and the mutant GABRG2 subunits are as below. The protein structure modeling in Figure 1a and supplementary Fig. c-d is based on the later part of sequences starting from L (LSRRM...) as marked by asterisk because the N-termini of the wild-type and the mutant GABRG2 subunit protein are identical.

The sequences of the GABRG2 wild-type:

QKSDDDYEDYASNKTWVLTPKVPEGDV
TVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINMEYTIDIFFAQ
TWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAHWITTPNRML
RIWNDGRVLYTLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEIVYQW
KRSSVEVGDTRSWRLYQFSFVGLRNTTEVVKTTSGDYVVMSVYFD
*LSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAVPARTSLGITTVLTMTTLST
IARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTL
HYFVSNRKPSKDKDKKKKNPAPTIDIRPRSATI Q
MNNATHLQERDEEYGYECLDGKDC
ASFFCCFEDCRTGAWRHGRIHIRIAKMDSYARIFFPTAFCLFNLVYWVSYLYL

The sequences of the mutant protein GABRG2(390X)

QKSDDDYEDYASNKTWVLTPKVPEGDV
TVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINMEYTIDIFFAQ
TWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAHWITTPNRML
RIWNDGRVLYTLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEIVYQW
KRSSVEVGDTRSWRLYQFSFVGLRNTTEVVKTTSGDYVVMSVYFD
*LSRRMGYFTIQTYIPCTLIVVLSWVSFWINK
DAVPARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFSALVE
YGTLHYFVSNRKPSKDKDKKKKNPAPTIDIRPRSATI

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 #)?	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