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Corresponding Author: Zhonghui Guan, Allan Basbaum

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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 #
+ -	1b	two-way ANOVA. Tukey's posthoc test	Meth para 10	5, 3, 3, 5	mice/time point, 3 replicates for each mRNA	Figure legend	error bars are mean +/- SEM media	Meth para 10	P < 0.0001 (injury)	Will add to the legend if needed	F (1, 12) = 73.11	Will add to the legend if needed
+ -	1c	two-way ANOVA, Tukey's posthoc test	Meth para 10	3, 3, 3, 3	mice/time point, 3 replicates for each mRNA	Figure legend	error bars are mean +/- SEM	Meth para 10	P = 0.629 (injury)	Will add to the legend if needed	F (1, 16) = 0.2417	Will add to the legend if needed
+ -	1d	two-way ANOVA, Tukey's posthoc test	Meth para 10	3, 3, 3, 3	mice/time point, 3 replicates for mRNA	Figure legend	error bars are mean +/- SEM	Meth para 10	P < 0.0001 (injury)	Will add to the legend if needed	F (1, 16) = 31.05	Will add to the legend if needed
	Supplementary Fig. 2e	unpaired t-test	Meth para 10	3	mice	Figure legend	error bars are mean +/- SEM	Meth para 10	P=0.0166	Will add to the legend if needed	t=3.962	Will add to the legend if needed
	Supplementary Fig. 2f	unpaired t-test	Meth para 10	4	mice	Figure legend	error bars are mean +/- SEM	Meth para 10	P=0.0005	Will add to the legend if needed	t=6.883	Will add to the legend if needed
	Supplementary Fig. 3a	unpaired t-test	Meth para 10	3	mice/genotype	Figure legend	error bars are mean +/- SEM	Meth para 10	P=0.0101	Will add to the legend if needed	t=4.585	Will add to the legend if needed
	Supplementary Fig. 3b	unpaired t-test	Meth para 10	3	mice/treatment	Figure legend	error bars are mean +/- SEM	Meth para 10	P=0.0050	Will add to the legend if needed	t=5.612	Will add to the legend if needed
+ -	4a	two-way ANOVA, Tukey's posthoc test	Meth para 10	6, 5	6 and 5 mice per genotype, tested on several days	Figure legend	error bars are mean +/- SEM	Meth para 10	p< 0.0001 (genotype)	Will add to the legend if needed	F (1, 9) = 79.74	Will add to the legend if needed
	4b	two-way ANOVA, Tukey's posthoc test	Meth para 10	7, 7	7 mice per group tested at different time points	Figure legend	Box-and-Whiskers (min/max), median	Meth para 10	P<0.0001 (saline/CSF1) p=0.0001 (time)	Will add to the legend if needed	F(1,12) = 235.2 (saline/CSF1) F(1, 12) = 31.09 (time)	Will add to the legend if needed
	4c	two-way ANOVA, Tukey's posthoc test	Meth para 10	6,4	Mice/genotype tested before and after injection	Figure legend	Box-and-Whiskers (min/max), median	Meth para 10	P<0.0001 (baseline/ CSF1) P=0.8772 (genotype)	Will add to the legend if needed	F(1,8)=74.43 (baseline/CSF1) F(1,8)=0.02546	Will add to the legend if needed
	4d	two-way ANOVA	Meth para 10	6/6	Mice pre genotype at different time points	Figure legends	Box-and-Whiskers (min/max), median	Meth para 10	P=0.1332 (genoype) P<0.0001 (time)	Will add to the legend if needed	F(1,20)=2.450 (genotype) F91,20)= 105.6 (time)	Will add to the legend if needed
+ -	4e	multiple t-tests	Meth para 10	4, 5, 7, 8	mice, 3 replicates for each mRNA	Will add to the legend	error bars are mean +/- SEM	Fig. leg, Meth para 10	P=0.0098 P=0.004 P=0.009 P=0.001	Will add to the legend if needed	t=3.71 t=3.95 t=3.08 t=3.94	Will add to the legend if needed
+ -	4f	multiple t-tests	Meth para 10	3/4 3/4 3/4 3/3	mice, 3 replicates for each mRNA	Figure legend	error bars are mean +/- SEM	Fig. leg, Meth para 10	P= 0.0003 P=0.003 P=0.005 P=0.02	Will add to the legend if needed	t=11.24 t=5.32 t=4.76 t=3.33	Will add to the legend if needed

	mentary Fig. 4a	ANOVA, Tukey's posthoc test	para 10		tested on different time points	legend	+/- SEM	legend Meth para 10	(time) P<0.0001 (genotype)	to figure legend if needed	(time) F(1,7)=137.0	to the legend if needed
	Supplementary Fig. 4b	unpaired t-test	Meth para 10	7/7	Mice per genotype	Figure legend	Box-and-Whiskers (min/max), median	Figure legend Meth para 10	P=0.9136	Will add to figure legend if needed	t=0.1108	Will add to figure legend if needed
	Supplementary Fig. 4c	unpaired t-test	Meth para 10	7/7	Mice per genotype	Figure legend	Box-and-Whiskers (min/max), median	Figure legend Meth para 10	P=0.7646	Will add to figure legend if needed	t=0.3063	Will add to figure legend if needed
	Supplementary Fig. 4d	two-way ANOVA, Tukey's posthoc test	Meth para 10	7/7	Mice per genotype at different temperatures	Figure legend	Box-and-Whiskers (min/max), median	Figure legend Meth para 10	P<0.0001 (temperature) p=0.1762 (genotype)	Will add to figure legend if needed	F(2,24)=99.43 (temperature) F(1,12)=2.066 (genotype)	Will add to figure legend if needed
	Supplementary Fig. 4e	unpaired t-test	Meth para 10	6/6	Mice per genotype	Figure legend	Box-and-Whiskers (min/max), median	Figure legend Meth para 10	P=0.4780	Will add to figure legend if needed	t=0.7371	Will add to figure legend if needed
	Supplementary Fig. 4f	two-way ANOVA, Tukey's posthoc test	Meth para 10	6/6	Mice per genotype, different time points	Figure legend	Box-and-Whiskers (min/max), median	Figure legend Meth para 10	P=0.4635 (genotype) P<0.0001 (time)	Will add to figure legend if needed	F(1,10)=0.58 (genotype) F(1,10)=138 (time)	Will add to figure legend if needed
	Supplementary Fig. 4h	multiple t-tests	Meth para 10	3/3 3/3	Mice for each marker	Figure legend	error bars are mean +/- SEM	Figure legend Meth para 10	P=0.7673 (CGRP) P=0.4675 (NF200)	Will add to figure legend if needed	t=0.3166 (CGRP) t=0.0820 (NF200)	Will add to figure legend if needed
	Supplementary Fig. 5b	unpaired t-test	Meth para 10	3/3	Mice per treatment	Figure legend	error bars are mean +/- SEM	Figure legend Meth para 10	P=0.0014	Will add to figure legend if needed	t=7.897	Will add to figure legend if needed
	Supplementary Fig. 5c	two-way ANOVA, Bonferroni posthoc test	Methods para 10	6/6	Mice per treatment	Figure legend	Box-and-Whiskers (min/max), median	Methods para 10	P=0.0128	Will add to figure legend if needed	F (1,10) = 9.149	Will add to figure legend if needed
+ -	5a	unpaired t-test	Meth para 10	4,4	mice, 3 replicates for each mRNA	Will add to the legend	error bars are mean +/- SEM	Meth para 10	P=0.001	Will add to the legend if needed	t=5.791 df=6	Will add to the legend if needed
+ -	5b	unpaired t-test	Meth para 10	3, 4	mice, 3 replicates for each mRNA	Will add to the legend	error bars are mean +/- SEM	Meth para 10	P=0.009	Will add to the legend if needed	t=4.072 df=5	Will add to the legend if needed
+ -	5c	two-way ANOVA, Tukey's posthoc test	Meth para 10	5, 6	mice per genotype, tested at different time points	Figure legend	error bars are mean +/- SEM	Meth para 10	P = 0.0006 (time) P = 0.04 (genotype)	Will add to the legend if needed	F (4, 36) = 6.36 (time) F (1, 9) = 5.78 (genotype)	Will add to the legend if needed
+ -	5d	two-way ANOVA, Tukey's posthoc test	Meth para 10	5, 5	mice per genotype, tested at different time points	Figure legend	error bars are mean +/- SEM	Meth para 10	P < 0.0001 (time) P = 0.06 (genotype)	Will add to the legend if needed	F (4, 32) = 13.74 (time) F (1, 8) = 4.65 (genotype)	Will add to the legend if needed
+ -	5e	multiple t-tests	Meth para 10	5/5 5/5 4/4 5/5	mice, 3 replicates for each mRNA	Figure legends	error bars are mean +/- SEM	Meth para 10	P=0.17 P=0.01 P=0.096 P=0.90	Will add to the legend if needed	t=1.47 t=3.28 t=1.96 t=0.12	Will add to the legend if needed
	5f	multiple t-tests	Meth para 10	4/4 4/4 4/4 4/4	mice, 3 replicates for each mRNA	Figure legends	error bars are mean +/- SEM	Meth para 10	P=0.05 P=0.77 P=0.81 P=0.34	Will add to the legend if needed	t=2.37 t=0.30 t=0.238 t=1.027	Will add to the legend if needed
	Supplementary Fig. 6a	unpaired t-test	Meth para 10	3/3	mice, 3 replicates for each mRNA	Figure legends	error bars are mean +/- SEM	Meth para 10	P=0.0003	Will add to the legend if needed	t=11.43 df=4	Will add to the legend if needed
	Supplementary Fig. 6c	unpaired t-test	Meth para 10	7/7	Mice per genotype	Figure legends	error bars are mean +/- SEM	Meth para 10	P=0.3058	Will add to the legend if needed	t=1.070	Will add to the legend if needed

	leme ntary Fig. 6d	test	para 10			legends	+/- SEM	para 10		to the legend if needed		to the legend if needed

+ -	Supp leme ntary Fig. 6e	two-way ANOVA, Tukey's Posthoc	Meth para 10	7/7	Mice per genotype at different temperatures	Figure legends	error bars are mean +/- SEM	Meth para 10	P=0.4289 (genotype) P<0.0001 (temperature)	Will add to the legend if need	F (1, 12) = 0.6704 (genotype) F (1, 24) = 130.6 (temperature)	Will add to the legend if need
	Supp leme ntary Fig. 7	multiple t-tests (unpaired, one-tailed)	Meth para 10	4/4	rats, 4 replicates for each mRNA	Will add to the legend	Box-and-Whiskers (min/max), median	Meth para 10	P=0.0106 (sham) P=0.025 (injury)	Will add to the legend if need	t=3.099 (sham) t=2.441 (injury)	Will add to the legend if needed
	Supp leme ntary Fig. 8	multiple t-tests	Meth para 10	3, 3, 3	mice, 3 replicates for each mRNA	Will add to the legend if need	error bars are mean +/- SEM	Meth para 10	P=0.0002 P=0.00064 P=0.37 not detectabl	Will add to the legend if need	t=11.77 t=9.58 t=1.0	Will add to the legend if need
+ -	6b	one-way ANOVA, multiple comparison	Meth para 10	4, 4, 4, 2	mice, 4 sections per mouse	Figure legends	error bars are mean +/- SEM	Meth para 10	P< 0.0001	Will add to the legend if needed	F=55.31	Will add to the legend if needed
+ -	6c	two-way ANOVA	Meth para 10	3, 3	mice, 4 sections per mouse	Figure legends	error bars are mean +/- SEM	Meth para 10	P < 0.0001 (genotype and injury)	Will add to the legend if needed	F (1, 8) = 167.8 (genotype) F (1, 8) = 476.4 (injury)	Will add to the legend if needed
+ -	6d	two-way ANOVA	Meth para 10	2, 4	mice, 4 sections per mouse	Figure legends	error bars are mean +/- SEM	Meth para 10	P=0.15 (genotype) P< 0.0001 (injury)	Will add to the legend if needed	F (1, 8) = 2.516 (genotype) F (1, 8) = 129.3 (injury)	Will add to the legend if needed
+ -	6e	two-way ANOVA	Meth para 10	3, 2, 3, 4	mice, 4 sections per mouse	Figure legends	error bars are mean +/- SEM	Meth para 10	P=0.34 (genotype) P=0.0001 (treatment)	Will add to the legend if needed	F (1, 8) = 1.014 (genotype) F (1, 8) = 49.68 (treatment)	Will add to the legend if needed
+ -	7k	two-way ANOVA	Meth para 10	4, 3	mice, 4 sections per mouse	Figure legends	error bars are mean +/- SEM	Meth para 10	P=0.01 (genotype) P=0.0001 (injury)	Will add to the legend if needed	F (1, 10) = 9.98 (genotype) F (1, 10) = 34.91 (injury)	Will add to the legend if needed
+ -	Supp leme ntary Fig. 12a	multiple t-tests	Meth para 10	3/4 3/4 3/3	mice, 3 replicates for each mRNA	Figure legends	error bars are mean +/- SEM	Meth para 10	P=0.015 P=0.02 P=0.004	Will add to the legend if needed	t=3.61 t=3.31 t=5.63	Will add to the legend if needed
+ -	Supp leme ntary Fig. 12b	multiple t-tests	Meth para 10	4/4 4/4 4/4	mice, 3 replicates for each mRNA	Figure legends	error bars are mean +/- SEM	Meth para 10	P=0.79 P=0.36 P=0.03	Will add to the legend if needed	t=0.27 t=0.97 t=2.75	Will add to the legend if needed

}Representative figures

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

   If so, what figure(s)?

Yes, immunostaining and fluorescent in situ hybridization

Fig. 2a-d; Supplementary Fig. 1a; Supplementary Fig. 2a-d; Fig. 3a-e; Supplementary Fig. 4g; Supplementary Fig. 5a; Supplementary Fig. 6b; Fig. 6a; Supplementary Fig. 9a-d; Fig. 7a-j; Supplementary Fig. 10; Fig. 8a-c; Supplementary Fig. 11

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, we state in the methods section that each experiment was done in at least 3 animals. For each animal, at least three different images were taken.

Methods, paragraph 4 and 5

}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.	For the qRT-PCR experiments, the sample size was 3-4 animals per gene, the minimal number required for statistical analysis. For the behavior experiments, the sample size was 4-7 animals per group. This number is based on our previous experience using these tests and is the minimum sample size given the effect size required to obtain statically significant results.
2. Are statistical tests justified as appropriate for every figure? Where (section, paragraph #)?	Yes
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 #)?	Yes, this is described in the last paragraph 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?	All tests were two-sided
e. Are there adjustments for multiple comparisons?	Post-hoc analysis
3. Are criteria for excluding data points reported? Was this criterion established prior to data collection? Where is this described (section, paragraph #)?	No
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 #)?	For behavioral experiments, animals were initially placed into one or two cages and allowed to free run for a few minutes. Next each animal was randomly picked up and placed into a separate cylinder before the behavior test. Although we wrote "All behavioral experiments were performed as previously reported", we are prepared to add this randomization method into our Method section if requested.
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 #)?	Investigators were always blinded to groups/genotypes as stated in the method section.

6. For experiments in live vertebrates, is a statement of compliance with ethical guidelines/regulations included? Where (section, paragraph #)?	Yes, in the Methods section, paragraph 1.
7. Is the species of the animals used reported? Where (section, paragraph #)?	Yes, in the Methods section, paragraph 1.
8. Is the strain of the animals (including background strains of KO/ transgenic animals used) reported? Where (section, paragraph #)?	No. All mice were on a BL6 background. We will add this information to the Methods section. The HA/LA rats were selected from Wistar-derived Sabra strain rats.
9. Is the sex of the animals/subjects used reported? Where (section, paragraph #)?	Yes, in the method section paragraph 1
10. Is the age of the animals/subjects reported? Where (section, paragraph #)?	No. All experiments were performed with young adult mice (11-14 week-old). We will add this information to the Methods section.
11. For animals housed in a vivarium, is the light/dark cycle reported? Where (section, paragraph #)?	No. It was a typical 12-hour light/dark cycle. IF necessary, we will add this information to the method section.
12. For animals housed in a vivarium, is the housing group (i.e. number of animals per cage) reported? Where (section, paragraph #)?	No. It was typically 1-5 animals per housing group. IF necessary, we will add this information to the method section.
13. For behavioral experiments, is the time of day reported (e.g. light or dark cycle)? Where (section, paragraph #)?	Yes. All behavioral experiments were performed during the light cycle. Methods, paragraph 2
14. Is the previous history of the animals/subjects (e.g. prior drug administration, surgery, behavioral testing) reported? Where (section, paragraph #)?	Yes, in Methods section, paragraph 2.
a. If multiple behavioral tests were conducted in the same group of animals, is this reported? Where (section, paragraph #)?	We wrote "All behavioral experiments were performed as performed as previously reported". Here, mice underwent repeated testing with von Frey filaments at different time points. Different baseline behavior was also tested in the same group of animals. We can add this information to the Methods section if needed.
15. If any animals/subjects were excluded from analysis, is this reported? Where (section, paragraph #)?	No
a. How were the criteria for exclusion defined? Where is this described (section, 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 #)?

No discrepancy.

}Reagents

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

Yes.

a. Is antibody catalog number given?

Where does this appear (section, paragraph #)?

No. We can add this information to the Methods section if necessary.

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

Where does this appear (section, paragraph #)?

The anti-CSF1 antibody did not detect any immunostaining signal in the sensory neurons of Adv-Cre; Csf1 fl/fl mice. Characteristics of the ATF3, NPY and NF200 antibody have been reported previously (Braz et al., J. Comp. Neurol. 2011 519:2648-57.)

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

Where (section, paragraph #)?

No cell lines were used.

a. Were they recently authenticated?

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

}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 #)?

No. Our RNA-Seq data were submitted to GEO: series entry number GSE66619. We will add this information to the Methods section.

}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.

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.

}Human subjects

1. Which IRB approved the protocol?

   Where is this stated (section, paragraph #)?

2. Is demographic information on all subjects provided?

   Where (section, paragraph #)?

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

   Where (section, paragraph #)?

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

   Where (section, paragraph #)?

5. How well were the groups matched?

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

6. Is a statement included confirming that informed consent was obtained from all subjects?

   Where (section, paragraph #)?

7. For publication of patient photos, is a statement included confirming that consent to publish was obtained?

   Where (section, paragraph #)?

}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?

    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 #)?

3. Is the length of each trial and interval between trials specified?

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.

5. Is the task design clearly described?

    Where (section, paragraph #)?

6. How was behavioral performance measured?

7. Is an ANOVA or factorial design being used?

8. For data acquisition, is a whole brain scan used?

    If not, state area of acquisition.

    a. How was this region determined?

9. Is the field strength (in Tesla) of the MRI system stated?

    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?

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 #)?

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 #)?

13. How were anatomical locations determined, e.g., via an automated labeling algorithm (AAL), standardized coordinate database (Talairach daemon), probabilistic atlases, etc.?

14. Were any additional regressors (behavioral covariates, motion etc) used?

15. Is the contrast construction clearly defined?

16. Is a mixed/random effects or fixed inference used?

    a. If fixed effects inference used, is this justified?

17. Were repeated measures used (multiple measurements per subject)?

    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?

19. Are statistical inferences corrected for multiple comparisons?

    a. If not, is this labeled as uncorrected?

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

    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?

22. For cluster-wise significance, is the cluster-defining threshold and the corrected significance level defined?