

Corresponding Author: Young-Goo Han

Manuscript Number: NN-A53823A

Manuscript Type: Article

Main Figures: 7

Supplementary Figures: 10

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	
+ -												

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 #
1d	Unpaired t-test (Assumed to be normal distribution, but not formally tested, equal variance)	Fig. legend	3,3	brains of 3 pairs of mutant and control mice	Fig. legend	error bars are mean +/- STDEV	Fig. legend	P = 0.0380 F test for variance P = 0.3510	Fig. legend	t(4) = 3.050 F(2, 2) = 4.697	Fig. legend
1e	Unpaired t test (Normal distribution by KS test, equal variance)	Fig. legend	9, 9; 9, 9; 9,9	slices from 3 pairs of mutant and control mice	Fig. legend	error bars are mean +/- STDEV	Fig. legend	P = 0.0006 (Satb2); P = 0.3634 (Ctip2); P = 0.0250 (Tbr1) F test for variance P = 4.255 (Satb2) P = 0.8609 (Ctip2) P = 0.2070 (Tbr1) KS test for normality P > 0.1	Fig. legend	t(10) = 4.877 (Satb2) t(10) = 0.9522 (Ctip2) t(10) = 2.635 (Tbr1) F(5, 5) = 0.1380 (Satb2) F(5, 5) = 1.179 (Ctip2) F(5,5) = 3.385 (Tbr1)	Fig. legend
2	Mann Whitney test	Results para 3	8, 8	slices from 3 pairs of mutant and control mice	Results para 3	Standard error	Results para 3	P = 0.0379	Results paragraph 3	Sum of ranks = 88, 48; Mann-Whitney U = 12.00	Results para 3
2b aRG	Unpaired t test (Normal distribution, equal variance)	Fig. legend	8, 8; 8, 8	Slices from 3 pairs of mutant and control mice	Fig. legend	error bars are mean +/- SEM	Fig. legend	P = 0.7888 (aRG_M); P = 0.2648 (aRG_D) F test for variance P = 0.6628 (aRG_M); P = 0.1556 (aRG_D) KS test for normality P > 0.1	Fig. legend	t(14) = 0.2730 (aRG_M); t(14) = 1.162 (aRG_D) F(7, 7) = 1.408 (aRG_M); F(7, 7) = 3.127 (aRG_D)	Fig. legend

+ -	2b bRG	Unpaired t test with Welch's correction (Normal distribution, unequal variance)	Fig. legend	8, 8; 8, 8	Slices from 3 pairs of mutant and control mice	Fig. legend	error bars are mean +/- SEM	Fig. legend	P = 0.0003 (bRG_M); P < 0.0001 (bRG_D) F test for variance P = 0.0003 (bRG_M); P = 0.0369 (bRG_D) KS test for normality P > 0.1	Fig. legend	t(7)=6.503 (bRG_M); t(9)=8.780 (bRG_D) F(7, 7) = 28.04 (bRG_M); F(7, 7) = 5.603 (bRG_D)	Fig. legend
+ -	2c (IPC-total)	Unpaired t test (Normal distribution, equal variance)	Fig. legend	8, 8; 8, 8	Slices from 3 pairs of mutant and control mice	Fig. legend	error bars are mean +/- SEM	Fig. legend	P = 0.0017 (IPC_M); P = 0.0458 (IPC_D) F test for variance P = 0.2378 (IPC_M); P = 0.6396 (IPC_D) KS test for normality P > 0.1	Fig. legend	t(13)=3.926 (IPC_M); t(13)=2.208 (IPC_D) F(6, 7) = 2.596 (IPC_M); F(6, 7) = 1.441 (IPC_D)	Fig. legend
+ -	2c (SVZ)	Unpaired t test (Normal distribution, equal variance)	Fig. legend	8, 8; 8, 8	Slices from 3 pairs of mutant and control mice	Fig. legend	error bars are mean +/- SEM	Fig. legend	P < 0.0001 (SVZ IPC_M); P < 0.0001 (SVZ IPC_D) F test for variance P = 0.7069 (SVZ IPC_M); P = 0.1388 (SVZ IPC_D) KS test for normality P > 0.1	Fig. legend	t(13)=11.92 (SVZ IPC_M); t(13)=11.52 (SVZ IPC_D) F(6, 7) = 1.336 (SVZ IPC_M); F(6, 7) = 3.350 (SVZ IPC_D)	Fig. legend
+ -	2f	Unpaired t test with Welch's correction	Fig. legend	7 (smoM2), 5 (control)	Slices from 3 pairs of mutant and control mice	Fig. legend	error bars are mean +/- SEM	Fig. legend	P = 0.0051 F test for variance P = 0.0059 KS test for normality P > 0.1	Fig. legend	t(6) = 4.300 F(6, 4) = 3.350	Fig. legend
+ -	3b proliferation	Unpaired t test (Normal distribution, equal variance)	Fig. legend	all 8, 8 control and SmoM2	Slices from 3 pairs of mutant and control mice	Fig. legend	error bars are mean +/- SEM	Fig. legend	P = 0.2680 (aRG); P = 0.0103 (bRG); P = 0.0001 (IPC) F test for variance P = 0.5533 (aRG); P = 0.3659 (bRG); P = 0.1751 (IPC) KS test for normality P > 0.1	Fig. legend	t(14)=1.154 (aRG); t(14)=2.960 (bRG); t(14)=15.75 (IPC) F(7, 7) = 1.594 (aRG); F(7, 7) = 2.045 (bRG); F(7, 7) = 2.963 (IPC)	Fig. legend

+ -	3b bRG, IPC self- renewal	Unpaired t test with Welch's correction for bRG (Normal distribution, unequal variance) Unpaired t test for IPC (Normal distribution, equal variance)	Fig. legend	8, 8	Slices from 3 pairs of mutant and control mice	Fig. legend	error bars are mean +/- SEM	Fig. legend	P = 0.0056 (bRG); P = 0.0001 (IPC) F test for variance P = 0.0274 (bRG); P = 0.0869 (IPC) KS test for normality P > 0.1	Fig. legend	t(9) = 3.618 (bRG); t(14) = 5.321 (IPC) F(7, 7) = 6.245 (bRG); F(7, 7) = 4.013 (IPC)	Fig. legend
+ -	3c	Mann Whitney test	Fig. legend	40 (Control), 114 (SmoM2)	Number of EdU +oRG cells from 3 pairs of mice	Fig. legend	N/A	Fig. legend	P = 0.0001	Fig. legend	Sum of ranks = 1392 , 10540; Mann-Whitney U = 571.5	Fig. legend
+ -	3e	Mann Whitney test	Fig. legend	10, 8 (Neuron); 7, 7 (IPC vs RG)	Slices from 3 pairs of mutant and control mice	Fig. legend	error bars are mean +/- SEM	Fig. legend	P = 0.0006 (Neuron); P = 0.0021 (IPC vs RG)	Fig. legend	Sum of ranks = 134 , 37 Mann-Whitney U = 1.000 (Neuron); Sum of ranks = 28 , 77 Mann-Whitney U = 0.000 (IPC vs RG)	Fig. legend
+ -	3g	Mann Whitney test	Fig. legend	71 control , 100 SmoM2	Mitotic figures of least 15 sections from 3 pairs of mutant and control mice	Fig. legend	N/A	Fig. legend	P = 0.0092	Fig. legend	Sum of ranks = 6937 and 7769; Mann-Whitney U = 2719	Fig. legend
+ -	4	Mann Whitney test	Results para 7	61 Control, 101 SMOM2	40 out of 61 control clones 72 out of 101 SMOM2 clones that contain IPC	Results para 7	N/A	N/A	P = 0.0158	Results para 7	Sum of ranks = 4390 and 1938; Mann-Whitney U = 1118	Results para 7
+ -	4c	Chi-square test/Fisher's exact test	Fig. legend	50, 61; 66, 101	50 (GFP) and 61 (SmoM2-GFP) clones (48 hours) from 4 and 3 embryos respectively; 66 (GFP) and 101 (SmoM2-GFP) clones (72 hours) from 6 and 12 embryos, respectively	Fig. legend	N/A	Fig. legend	Fisher's exact test P = 0.0823 Chi-square test P = 0.1659 (E15); Chi-square test P = 0.0002 (E16)	Fig. legend	Chi-square (2) = 3.593 (E15); Chi-square (2) = 17.61 (E16)	Fig. legend

+ -	5b	Mann Whitney test	Fig. legend	9, 9; 9,9; 9, 9	Slices from 3 pairs of mutant and control mice	Fig. legend	error bars are mean +/- SEM	Fig. legend	P = 0.5076 (aRG_M); P = 0.3401 (aRG_D); P = 0.0005 (bRG_M); P = 0.0002 (bRG_D)	Fig. legend	Sum of ranks = 93.50 , 77.50 Mann-Whitney U = 32.50 (aRG_M); Sum of ranks = 97 , 74 Mann-Whitney U = 29.00 (aRG_D); Sum of ranks = 122 , 49 Mann-Whitney U = 4.000 (bRG_M); Sum of ranks =124 , 47 Mann-Whitney U = 2.000 (bRG_D)	Fig. legend
+ -	5c	Mann Whitney test	Fig. legend	9, 9; 9, 9	Slices from 3 pairs of mutant and control mice	Fig. legend	error bars are mean +/- SEM	Fig. legend	P = 0.0188 (IPC_M); P = 0.0078 (IPC_D)	Fig. legend	Sum of ranks = 112 , 59 Mann-Whitney U = 14.00 (IPC_M); Sum of ranks = 115 , 56 Mann-Whitney U = 11.00 (IPC_D)	Fig. legend
+ -	5d	Unpaired t test with Welch's correction (Normal distribution, unequal variance)	Fig. legend	7, 7	190 (control) 144 (Mut) mitotic spindles of 7 slices from 3 pairs of mutant and control mice	Fig. legend	error bars are mean +/- SEM	Fig. legend	P = 0.0124 KS test for normality P > 0.1 F test for variance P = 0.0098	Fig. legend	t(7) = 3.343 F(6, 6) = 11.18	Fig. legend
+ -	5e	Unpaired t test (Normal distribution, equal variance for Tbr1, ctip2) and Unpaired t test with Welch's correction (Normal distribution, unequal variance for for Satb2)	Fig. legend	9,9;9,9; 9,9	Slices from 3 pairs of mutant and control mice	Fig. legend	error bars are mean +/- STDEV	Fig. legend	P < 0.0001 (Tbr1); P = 0.0271 (Ctip2); P < 0.0001 (Satb2) KS test for normality P > 0.1 F test for equal variance P = 0.4990 (Tbr1); P = 0.0701 (Ctip2); P < 0.0418 (Satb2)	Fig. legend	t(16)=5.244 (Tbr1); t(16)=2.432 (Ctip2); t(11)=7.947 (Satb2) F (8,8) = 1.642 (Tbr1); F (8,8) = 3.928 (Ctip2); F (8,8) = 4.719 (Satb2)	Fig. legend
+ -	7a	Wilcoxon rank sum test (Mann Whitney test)	Fig. legend	123 (DMSO), 135 (SANT-1), 133 (SAG)	Mitotic figures from 15 organoids from 3 independent experiments	Fig. legend	N/A	Fig. legend	P = 0.0007 (DMSO vs. SANT-1); P = 0.2681 (DMSO vs. SAG)	Fig. legend	Sum of ranks = 14080 , 19590, Mann-Whitney U = 6330 (DMSO vs.SANT-1); Sum of ranks = 15336 , 17817 Mann-Whitney U = 7586 (DMSO vs. SAG)	Fig. legend

+ -	7b	Mann Whitney test	Fig. legend	21 (DMSO), 21 (SANT-1)	Mini 'cortices' of 11 (DMSO), 15 (SANT-1) cerebral organoids from 3 independent experiments	Fig. legend	error bars are mean +/- SEM	Fig. legend	P < 0.0001 (DMSO vs. SANT-1)	Fig. legend	Sum of ranks = 627.5 , 275.5, Mann-Whitney U = 44.50	Fig. legend
+ -	7b	Mann Whitney test	Fig. legend	21 (DMSO), 20 (SAG)	Mini 'cortices' of 11 (DMSO), 13 (SAG) cerebral organoids from 3 independent experiments	Fig. legend	error bars are mean +/- SEM	Fig. legend	P = 0.2565 (DMSO vs. SAG)	Fig. legend	Sum of ranks = 485 , 376, Mann-Whitney U = 166.0	Fig. legend
+ -	7c	Fisher's exact test	Fig. legend	294 (DMSO), 292 (SANT-1), 400 (SAG)	Total number of cilia of each group	Fig. legend	N/A	Fig. legend	P < 0.0001 (DMSO vs. SANT-1); P = 0.6454 (DMSO vs. SAG)	Fig. legend	N/A	Fig. legend
+ -	7c	Descriptive: (percent of cilia containing Smo in each organoids)	Fig. legend	4 (DMSO), 3 (SANT-1), 3 (SAG)	Number of organoids of each group	Fig. legend	error bars are mean +/- SD	Fig. legend	N/A	Fig. legend	N/A	Fig. legend
+ -	S3d	Mann Whitney test	Fig. legend	9, 9	Slices from 4 pairs of mutant and control mice	Fig. legend	error bars are mean +/- SEM	Fig. legend	P = 0.0004 (PH3+ Tbr2+)	Fig. legend	Sum of ranks = 45, 126, Mann-Whitney U = 0.0000	Fig. legend
+ -	S3d	Mann Whitney test	Fig. legend	9, 9	Slices from 4 pairs of mutant and control mice	Fig. legend	error bars are mean +/- SEM	Fig. legend	P = 0.2878 (AP PH3+Sox2 +Tbr2-)	Fig. legend	Sum of ranks = 98, 73, Mann-Whitney U = 28.00	Fig. legend
+ -	S3d	Mann Whitney test	Fig. legend	9, 9	Slices from 4 pairs of mutant and control mice	Fig. legend	error bars are mean +/- SEM	Fig. legend	P = 0.0016 (nonAP PH3 +Sox2+Tbr2-)	Fig. legend	Sum of ranks = 50, 121, Mann-Whitney U = 5.000	Fig. legend
+ -	S10b	Unpaired t test (Normal distribution, equal variance)	Fig. legend	10 (DMSO); 12 (SANT-1)	10 (DMSO) and 12 (SANT-1) 'cortical' regions of 4 organoids each from 2 independent experiments	Fig. legend	N/A	Fig. legend	P < 0.0001 KS normality test P > 0.1 F test for variance P = 0.5469	Fig. legend	t(20) = 5.126 F(9, 11) = 1.458	Fig. legend
+ -												

► Representative figures

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

If so, what figure(s)?

All the immunostainings micrographs

- 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 #)?

Figure legends

► 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.

No statistical methods were used to pre-determine sample sizes but our sizes are similar to those reported in previous publications

We analyzed at least three different mice from different breeding pairs. The mutant phenotypes were strong enough to show significant differences from comparing three control and three mutant mice.

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

Where (section, paragraph #)?

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

Figure legends, methods statistics, paragraph 19

 - 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 #)?

Statistical methods were summarized in the 'Statistics' section in Methods (paragraph 19). Statistical test for each experiment was defined in the figure legend or in the text.

 - 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 #)?

All the parametric analyses were formally tested for normal distribution and equal variance, except for the data in Figure 1d, of which we only had 3 pair of MRI samples and the n is too small for normality test.

'Statistics' section in Methods (paragraph 19)

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

Figure legends

 - e. Are there adjustments for multiple comparisons?

'Statistics' section in Methods (paragraph 19) All are two-sided

 - f. Are there adjustments for multiple comparisons?

N/A

3. Are criteria for excluding data points reported?

Was this criterion established prior to data collection?

Where is this described (section, paragraph #)?

We have not excluded any data or animals

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 #)?

No randomization was done (Statistics subsection in Methods).

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 #)?
- No blinding was done for in vivo experiments; it was impossible because mutant phenotype was too obvious.
For in vitro study, blinding was done (Legends for Figure 2 and 4).
6. For experiments in live vertebrates, is a statement of compliance with ethical guidelines/regulations included?
Where (section, paragraph #)?
- Methods, paragraph 1
7. Is the species of the animals used reported?
Where (section, paragraph #)?
- Methods, paragraph 1
8. Is the strain of the animals (including background strains of KO/transgenic animals used) reported?
Where (section, paragraph #)?
- Methods, paragraph 1
9. Is the sex of the animals/subjects used reported?
Where (section, paragraph #)?
- Methods, paragraph 1
10. Is the age of the animals/subjects reported?
Where (section, paragraph #)?
- Methods, paragraph 1
11. For animals housed in a vivarium, is the light/dark cycle reported?
Where (section, paragraph #)?
- Methods, paragraph 1
12. For animals housed in a vivarium, is the housing group (i.e. number of animals per cage) reported?
Where (section, paragraph #)?
- Methods, paragraph 1
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 #)?
15. If any animals/subjects were excluded from analysis, is this reported?
Where (section, paragraph #)?
- We haven't excluded any animals

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 #)?

► 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 #)?

Methods, paragraph 5

b. Where were the validation data reported (citation, supplementary information, Antibodypedia)?
Where does this appear (section, paragraph #)?

Company product literature including related citations can be readily found using the catalog number.

Methods, paragraph 5

2. Cell line identity

NO

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

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

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 #)?

Human cerebral organoids section in Methods

▶ Data deposition

Data deposition in a public repository is mandatory for:

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

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

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

- Are accession codes for deposit dates provided?

Where (section, paragraph #)?

Accession codes section at the end of discussion

▶ Computer code/software

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

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

N/A

- 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

- Which IRB approved the protocol?

Where is this stated (section, paragraph #)?

The St. Jude Children's Research Hospital Institutional Review Board approved the use of fixed human fetal brain samples. It is stated in Human fetal brain samples subsection in Methods.

- Is demographic information on all subjects provided?

Where (section, paragraph #)?

n/a

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

Where (section, paragraph #)?

n/a

- 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?

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?

► Additional comments

Additional Comments