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Manuscript Number: NN-A51416

Manuscript Type: Article

Main Figures: 6

Supplementary Figures: 11

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 #	
+ -	supp 6	2-way ANOVA	results para 6	35	6 mice, 1 recording session each	methods para 6	L4 FS mean rate change	results para 6	3.5e-7	results para 6	f(1) = 26.6	
+ -	1	2-way ANOVA	results para 6	11	6 mice, 1 recording session each	methods para 6	L4 RS mean rate change	results para 6	9.1e-6	results para 6	f(1) = 21	
+ -	2	paired t-test	results para 8	33	5 mice, 1 recording session each	methods para 6	L2/3 RS percent decrease	results para 8	3.9e-6	results para 8	t(32) = 5.5	
+ -	2	2-way ANOVA	results para 9	75	9 mice, 1 recording session each	methods para 6	L5 RS rate change population effect	fig legend	2.26e-7	results and fig leg	f(1) = 27	
+ -	2	2-way ANOVA	results para 9	on average 15 trials/unit	75 units, 6 mice, 1 recording session each	methods para 6	L5 RS spike rate - individual unit tuning curve	results para 9	depends on unit	results para 7	depends on unit	
+ -	2	wilcoxon sign-rank	results para 10	20	3 mice, 1 recording session each	methods para 6	L4 Chr2 effect	results para 10	0.0026	results para 10	z = 3.0	
+ -	2c	wilcoxon sign-rank	results para 10	19	3 mice, 1 recording session each	methods para 6	L2/3 Chr2 effect	results para 10	0.0148	results para 10	z = 2.4	
+ -	2c	wilcoxon sign-rank	results para 10	49	3 mice, 1 recording session each	methods para 6	L5 Chr2 effect	results para 10	0.0455	results para 10	z = 2.0	
+ -	supp fig 3	2-way ANOVA	results para 4	16	3 mice, 1 recording session each	fig legen	L4 spike rate tuning curve population effect	fig legend	0.5001	fig leg	f(1) = 0.45	
+ -	supp fig 3	2-way ANOVA	results para 4	33	3 mice, 1 recording session each	fig legen	L5 RS spike rate tuning curve population effect	fig legen	0.3585	fig legen	f(1) = 0.8445	
+ -	supp fig 3	2-way ANOVA	results para 4	19	3 mice, 1 recording session each	fig legen	L5 FS spike rate tuning curve population effect	fig legen	0.7395	fig legen	f(1) = 0.1108	
+ -	3	Kruskal-wallis	results para 15	33	5 mice, 1 recording session each	methods para 6	L2/3 RS OMI rank change	results and fig leg	0.65	results para 12	chi(7) = 5.0	
+ -	3	Kruskal-wallis	results para 15	75	9 mice, 1 recording session each	methods para 6	L5 RS OMI rank change	results and fig leg	4.1e-15	results para 12	chi(7) = 82	
+ -	para 17	Wilcoxon sign rank	results para 17	75	9 mice, 1 recording session each	methods para 6	L5 RS spike rate no touch	results para 17	5.2e-11	results para 17	z = 6.5	
+ -	4	2-way ANOVA	results para 18	53	9 mice, 1 recording session each	methods para 6	L5 FS spike rate tuning curve population effect	results para 17	1.1e-6	results para 14	f(1) = 24	
+ -	4	Wilcoxon sign rank	results para 18	35	3 mice, 1 recording session each	methods para 6	L5 FS spike rate effect Chr2 stimulation	results para 14	0.001	results para 14	z = 3.4	
+ -	3	paired t-test	results para 12	75	9 mice, 1 recording session each	methods para 6	L5 RS spatial tuning index	results para 14	0.003	results para 14	t(74) = 3.1	

+	-	supp 5	paired t-test	results para 16	75	9 mice, 1 recording session each	methods para 6	OMI vs OMI stim preference	results para 16	4.1e-12	fig leg	t(74) = 8.2	
+	-	supp 5	paired t-test	results para 13	75	9 mice, 1 recording session each	methods para 6	Most Preferred Spike Rate comparison	results para 13	5.5e-4	fig leg	t(74) = 3.7	
+	-	supp 5	paired t-test	results para 13	75	9 mice, 1 recording session each	methods para 6	Least Preferred Spike Rate comparison	results para 13	1.4e-11	fig leg	t(74) = 7.9	
+	-	supp 4	2-way anova	results para 13	422 whisks	4 mice, 1 behavioral session each	fig leg	whisk amplitude CDF with 95% interval	fig leg	0.7121	fig leg	f(1) = .14	
+	-	supp 4	2-way anova	results para 13	422 whisks	4 mice, 1 behavioral session each	fig leg	whisker set-point CDF with 95% interval	fig leg	0.5637	fig leg	f(1) = .33	
+	-	supp 4	2-way anova	results para 13	422 whisks	4 mice, 1 behavioral session each	fig leg	whisk frequency CDF with 95% interval	fig leg	0.4742	fig leg	f(1) = .51	
+	-	2	Wilcoxon sign rank	results para 13	123	11 mice, 1 recording each	fig leg	L5RS mean FR change	results para 13	9.7848e-05	results para 13	z = 3.9	
+	-	5b	Paired t-test	Legend	13	13 pairs of cells, from 10 slices prepared from 5 mice	fig legend	mean+/-SEM	results para 16	0.4949	results para 16	t(12)=0.7039	
+	-	3d	Wilcoxon	results para 12	45	9 mice, 1 recording session each	results para 12	FWHM of Gaussian fits with r-squared > 0.75	results para 12	0.0155	results para 12	z = 2.42	
+	-	Supp fig 6	2-Way ANOVA	results para 18	25	3 mice, 1 recording session each	results para 18	L6 FS cell mean rate change	results para 18	0.55	results para 18	f(1) = 0.36	
+	-	Supp fig 6	2-Way ANOVA	results para 18	50	5 mice, 1 recording session each	results para 18	L2/3 FS cell mean rate change	results para 18	0.005	results para 18	f(1) = 9.13	
+	-	Supp 5	unpaired t test	fig legend	24 vs 75	9 mice, 1 recording session each	fig leg	L5 RS full pad vs single whisker OMI	fig leg	0.34	fig leg		
+	-	Supp 5	unpaired t test	fig legend	12 vs 53	9 mice, 1 recording session each	fig leg	L5 FS full pad vs single whisker OMI	fig leg	0.69	fig leg		
+	-	results para 12	2-way ANOVA	results para 12	75	9 mice, 1 recording session each	results para 12	Fano Factor, control vs light	results para 12	0.45	results para 12	f(1) = 0.69	
+	-	supp fig 10	2-way ANOVA	Direct translaminar para 6	75	7 mice for DRD3, 1 recording session each	methods para 6	mean rate change	Direct translaminar para 6	0.7	fig legend	f(1) = 0.144	
+	-	supp 5	2-way anova	fig legend	24	3 mice, 1 session each	fig leg	L5 RS mean rate change	fig leg	1.3e-4	fig leg		
+	-	supp 5	2-way anova	fig legend	12	3 mice, 1 session each	fig leg	L5 RS mean rate change	fig leg	0.002	fig leg		
+	-	para 10	Wilcoxon sign rank	para 10	59	11 mice, 1 recording each	para 10	L4 RS mean rate change V1	para 10	7.3828e-09	para 10	z = 5.8	
+	-	para 10	Wilcoxon sign rank	para 10	23	4 mice, 1 recording each	para 10	L5RS mean rate change V1 control mice	para 10	0.8195	para 10	z = 0.23	
+	-	para 10	Wilcoxon sign rank	para 10	24	3 mice, 1 recording each	para 10	L5 RS mean rate change V1 ChR2 mice	para 10	1.8126e-05	para 10	z = 4.3	

+ -	Supp 11A, para 30	Fisher's exact test	Results Para 30	12 versus 18	55 connections tested onto 12 PV+ cells, recorded in 10 slices taken from 4 mice; 52 connections tested onto 18 GIN cells recorded in 11 slices taken from 3 mice. Contingency table defined as: 5 Connected PV cells, 7 Unconnected PV cells; 0 Connected GIN cells, 18 Unconnected GIN cells	Para 30	Exact numbers reported	Para 25, 30	0.0056	para 30	DF=1	
+ -	Supp 8e-i			31	31 FS cells recorded in 26 slices taken from 13 mice	supp fig 8 legend	Mean, standard error	supp fig 8 legend				
+ -	Fig 5h			31	31 FS cells recorded in 26 slices taken from 13 mice	fig5 legend	Mean	fig5 legend				
+ -	Supp 8a-d			22	22 ChR2+ cells recorded in 12 slices taken from 5 mice	supp fig 8 legend	Mean, standard error	supp fig 8 legend				
+ -	Supp 9 a,b,e			16	16 pyramidal cells recorded in 9 slices taken from 4 mice	supp fig 9 legend	Mean, standard error	supp fig 9 legend				
+ -	Supp 9 c,d			19	19 ChR2+ cells recorded in 11 slices taken from 5 mice	supp fig 9 legend	Mean, standard error	supp fig 9 legend				
+ -	Supp 9 e			4	4 PV+ cells recorded in 3 slices taken from 2 mice	supp fig 9 legend	Mean	supp fig 9 legend				
+ -	6d right			15	15 L5 pyramidal neurons, recorded in 12 slices from 3 mice	fig 6 legend	Mean, standard error					
+ -	6d left			7	7 L5 FS cells in 7 slices from 3 mice	fig 6 legend	mean, standard error					
+ -	6g	t-test	results para 26	7	7 FS-PC pairs in 5 slices from 3 mice. variable number of IPSC measurements for each pair (range 12-31 trials)	fig 6 legend	mean		variable (range: 10^-12- 0.21)	fig 6 legend	variable (range: 12.19 through -1.50)	
+ -	Supp 5g	Kruskal-wallis	fig legend	125	125 neurons across 4 animals	fig 5H	distribution of preferred positions	fig legend	2.65e-7	fig leg		
+ -	Supp 7g			42 cells in vitro	42 neurons recorded in 36 slices from 17 mice	supp fig 7 legend	Mean, standard error	supp fig 7 legend				
+ -	11b	Wilcoxon	fig leg	75	9 mice, 1 session each	11b	fraction of HF spikes	fig leg	0.46	fig leg		
+ -	11c	Wilcoxon	fig leg	75	9 mice, 1 session each	11c	CV of interspike intervals	fig leg	0.22	fig leg		
+ -	11d	Wilcoxon	fig leg	75	9 mice, 1 session each	11d	Change in Burst rate	fig leg	0.67	fig leg		

+ -	Supp 1d	Wilcoxon	para 32	14	14 L5 pyramidal cells from 14 slices from 5 animals	suppl fig 1d legend	Reduction in currents	suppl fig 1d legend	1.2*10 ⁻⁴ (IPSCs) & 1.2*10 ⁻⁴ (EPSCs)	N/A	z=3.28	
+ -	Supp 10e	Wilcoxon	para 24	13	13 L5 pyramidal cells from 8 slices from 4 animals	suppl fig 10e legend	Reduction in currents	suppl fig 10e legend	2.4*10 ⁻⁴ (IPSCs) & 2.4*10 ⁻⁴ (EPSCs)	suppl fig 10e legend	z=3.16	
+ -	Supp 2e left			5	5 L2/3-L4 layer boundaries from 2 Drd3 and 3 Scnn mice	supp fig 2 legend	Mean, std error	supp fig 2 legend				
+ -	Supp 2e middle			8	8 L4-L5 layer boundaries from 2 Drd3, 3 Scnn, 2 Rbp4, and 1 Ntsr1 mice	supp fig 2 legend	Mean, std error	supp fig 2 legend				
+ -	Supp 2e right			3	3 L5-L6 layer boundaries from 2 Rbp4 and 1 Ntsr1	supp fig 2 legend	Mean, std error	supp fig 2 legend				
+ -	Supp 11e	Wilcoxon signed rank	fig leg	123	11 mice, 1 recording each	supp fig 11e	change in burst rate V1	supp figure 11e	0.6950	supp fig 11e	z = 0.39	
+ -	Supp 11f	Wilcoxon signed rank	fig leg	123	11 mice, 1 recording each	supp fig 11f	CV of interspike intervals V1	supp figure 11f	0.6443	supp fig 11f	z = -0.46	
+ -	Supp 11g	Wilcoxon signed rank	fig leg	130	13 mice, 1-3 recordings each	supp fig 11g	change in burst rate V1 SOM	supp figure 11g	6.2169e-04	supp fig 11g	z = -3.42	
+ -	Supp 11h	Wilcoxon signed rank	fig leg	130	13 mice, 1-3 recordings each	supp fig 11h	CV of interspike intervals V1 SOM	supp figure 11h	1.4699e-06	supp fig 11h	z = -4.82	
+ -	V1 para graph h	Wilcoxon signed rank	paragr aph 13?	59	11 mice, 1 recording each	V1 paragrap h	reduction of L4 RS firing rate	para 13	7.3828e-09	para 13	z=5.78	
+ -	V1 para graph h	Wilcoxon signed rank	paragr aph 13?	23	4 mice, 1 recording each	V1 paragrap h	change in L5 RS firing rate in control mice	para 13	0.8195	para 13	z=-0.23	
+ -	V1 para graph h	Wilcoxon signed rank	paragr aph 13	24	3 mice, 1 recording each	V1 paragrap h	change in reduced L5 RS firing rate in scnn Chr2 mice	para 13	1.8126e-05	para 13	z=4.29	
+ -	Supp 1e			8 cells	4 slices from 3 mice	Supp fig 1 legend						

► Representative figures

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

If so, what figure(s)?

Yes, figure 1 and 6, and supplemental figure 1 and 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 #)?

Virally induced opsin expression in SCNN mice was repeated 18 times for this experiment. There is no challenge in repeatability using the described protocol.

GAD67 co-localization was performed in 1 mouse and analyzed across two separate section of the barrel cortex, totaling 5 barrel columns.

► 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.

Sample size was not explicitly chosen and we collected data from as many cells as possible. In each case, a specific number of mice were available, they were recorded from, and the data was analyzed. Based on prior experience with multi-channel recordings, we knew that 3 - 6 mice would provide enough cells for statistics.

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?

Yes, each figure legend states the test used for the given p value

- 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 #)?

All data where a wilcoxon sign-rank test were used failed the test for normality.

- 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 #)?

Differences in variance within and between groups was performed by the ANOVA.

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

all t-tests and sign-rank tests were paired

- e. Are there adjustments for multiple comparisons?

no multiple comparisons were performed

3. Are criteria for excluding data points reported?

Was this criterion established prior to data collection?

Where is this described (section, paragraph #)?

Yes

Yes

Methods: Analysis of multi-electrode neural data, paragraph 3

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 assignment was necessary. Each animal served as its own control.

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 done.

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

Where (section, paragraph #)?

Yes. 1st sentence of methods.

7. Is the species of the animals used reported?

Where (section, paragraph #)?

yes, 1st paragraph of methods

8. Is the strain of the animals (including background strains of KO/transgenic animals used) reported?

Where (section, paragraph #)?

yes, 1st paragraph of methods

9. Is the sex of the animals/subjects used reported?

Where (section, paragraph #)?

no, both sexes were used indiscriminately

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

Where (section, paragraph #)?

yes, 1st paragraph of methods

11. For animals housed in a vivarium, is the light/dark cycle reported?

Where (section, paragraph #)?

yes, 1st paragraph of methods

12. For animals housed in a vivarium, is the housing group (i.e. number of animals per cage) reported?

Where (section, paragraph #)?

yes, 1st paragraph of methods

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

Where (section, paragraph #)?

yes, 1st paragraph of methods

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

Where (section, paragraph #)?

No history

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

Where (section, paragraph #)?

N/A

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

Where (section, paragraph #)?

no exclusions

- 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)?

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

N/A

Where (section, paragraph #)?

- a. Were they recently authenticated?

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

► 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.

1. Are accession codes for deposit dates provided?

N/A

Where (section, paragraph #)?

▶ 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.

UltraMegaSort is custom spike sorting software that is available from the author.
Custom software written in MATLAB was used for the acquisition and analysis of whole cell recording data.

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 #)?

N/A

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?

▶ Additional comments

Additional Comments