nature neuroscience

Corresponding Author:	Golding	# Main Figures:	8
Manuscript Number:	NN-A52568A	# Supplementary Figures:	7
Manuscript Type:	Article	# 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		TEST USED n		DESCRIPTIVE S (AVERAGE, VARI,		P VALL	JE	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 #
+ -	lf	Unpaired t- test with Welch's correction	Fig. 1f legend , Results para. 1	46 and 12	46 (bIV spectrin) and 12 (PanNav) axons from 3 gerbils	Fig. 1f legend, Results para. 1	error bars are mean +/- SEM	Fig. 1f legen d, Result s para. 1	AIS length: BIV spectrin vs. PanNav: p = 0.2196	Fig. 1f legend, Results para. 1	t=1.267 df = 20	Fig. 1f legend, Results para. 1
+	lf	Unpaired t- test with Welch's correction	Fig. 1f legend , Results para. 1	22	22 (Nav1.6) axons from 3 gerbils	Fig. 1f legend, Results para. 1	error bars are mean +/- SEM	Fig. 1f legen d, Result s para. 1	AIS length: BIV spectrin vs Nav 1.6: p= 0.0062 Pan Nav vs. Nav 1.6: p=0.0016	Fig. 1f legend, Results para. 1	bIV vs Nav1.6 t=2.904,df =37 PanNav vs Nav1.6 t=3.474, df=29	Fig. 1f legend, Results para. 1
+ -	2e	Unpaired two-tailed Students t- test	Fig. 2e, legend , Results para. 2	6 and 6	slices from 6 gerbils each for AIS and soma comparisons	Fig. 2e legend, Results para. 2	error bars are mean +/- SEM	Fig. 2e legen d, Result s para. 2	AIS vs. Soma: Ih V1/2: p=0.74 Ih slope: p=0.27	Fig. 2e legend, Results para. 2	t(10) = 0.34 t(10) = 1.16	Fig. 2e legend, Results para. 2
+ -	2f	Unpaired two-tailed Students t- test	Fig. 2f, Results para. 2	6 and 6	slices from 6 gerbils each for AIS and soma comparisons	Fig. 2f, Results para. 2	error bars are mean +/- SEM	Fig. 2f, Result s para. 2	(tfast, p = 0.56; tslow, p = 0.33; [Afast/ (Afast +Aslow)], p = 0.08	Fig. 2f, Results para. 2	t(10) = 0.60 t(10) = 1.05 t(10) = -1.98	Fig. 2f, Results para. 2
+ -	Зc	Paired two- tailed Students t- test	Fig 3c legend , Results para. 3	9	slices from 9 gerbils	Fig 3c legend, Results para. 3	error bars are mean +/- SEM	Fig 3c legen d, Result s para. 3	p=0.00028 for AIS, p=4.72E-07 for Soma, and p=0.00013 for Cell	Fig 3c legend, Results para. 3	t(8) = 6.12 t(8) = 14.61 t(8) = 6.88	Fig 3c legend, Results para. 3
+ -	Зc	Paired two- tailed Students t- test	Fig 3c legend , Results para. 3	6	slices from 6 gerbils	Fig 3c legend, Results para. 3	error bars are mean +/- SEM	Fig 3c legen d, Result s para. 3	ZD internal: p=0.07 and 0.66 for Cell and AIS	Fig 3c legend, Results para. 3	t(5) = -2.29 t(5) = 0.46	Fig 3c legend, Results para. 3
+ -	Зc	Paired two- tailed Students' t- test	Fig 3c legend , Results para. 3	5	slices from 5 gerbils	Fig 3c legend, Results para. 3	error bars are mean +/- SEM	Fig 3c legen d, Result s para. 3	ZD7288 "Bath": p=0.012 for Cell at 380 nm, p = 0.86 for Cell, and p = 0.08 for AIS	Fig 3c legend, Results para. 3	t(4) = -4.39 t(4) = 2.38 t(4) = -0.18	Fig 3c legend, Results para. 3
+ -	3c	Paired 2- tailed Students' t- test	Fig 3c legend , Results para. 3	6	slices from 6 gerbils	Fig 3c legend, Results para. 3	error bars are mean +/- SEM	Fig 3c legen d, Result s para. 3	Cs+ "Bath": p=0.00012 for Cell at 380 nm, p = 0.13 and 0.24 for Cell and AIS	Fig 3c legend, Results para. 3	t(5) = 10.76 t(5) = -1.78 t(5) = -1.32	Fig 3c legend, Results para. 3

+ -	3e	One-way repeated measures ANOVA	Fig. 3f legend , Results para 4	5	slices from 5 gerbils	Fig. 3f legend, Results para 4	error bars aremean±SEM	Fig. 3f legen d, Result s para 4	Delta Vrest: 0-30 μm: p=0.0007; 30-60 μm, p=0.28; 60-90 μm, p=0.52	Fig. 3f legend, Results para 4	F(2,4) = 25.23 R square = 0.86, F(2,4) = 1.53 R square = 0.28, F(2,4) = 0.54 R square = 0.12	Fig. 3f legend, Results para 4
+ -		Paired 2- tailed Students' t- test	Result s para. 5	4 and 4	slices from 4 gerbils each (4 for AIS block and 4 for soma block)	Results para. 5	error bars aremean±SEM	Result s para. 5	delta dV/dt; AIS block; p=0.03, Soma block: p=0.06; delta Vthreshold: AIS block: p=0.03 Soma block: p=0.24	Results para. 5	t(3) = -3.5, t(3) = -2.94 t(3) = 3.66 t(3) = 1.44	Results para. 5
+ -	5d	Paired 2- tailed Students' t- test	Fig. 5d legend , Results para. 6	3,5	AIS; slices from 3 and 5 gerbils for vehicle and ZD7288	Fig. 5d legend, Results para. 6	error bars aremean±SEM	Fig. 5d legen d, Result s para. 6	AIS; delta Vrest: Vehicle: p=0.77 for Veh and p=0.007 for ZD; delta threshold: p=0.88 for Veh and p=0.008 for ZD; delta dV/dt: p=0.51 for Veh and p= 0.01 for ZD	Fig. 5d legend, Results para. 6	t(2) = 0.34 t(4) = 5.08 t(2) = 0.17 t(4) = 4.94 t(2) = 0.79 t(4) = -4.09	Fig. 5d legend, Results para. 6
+	5d	Paired 2- tailed Students' t- test	Fig. 5d legend , Results para. 6	5	Soma; slices from 5 gerbils	Fig. 5d legend, Results para. 6	error bars aremean±SEM	Fig. 5d legen d, Result s para. 6	Soma; delta Vrest: p=0.01 delta threshold: p=0.08 delta dVdt: p=0.71	Fig. 5d legend, Results para. 6	t(4) = 4.57 t(4) = -2.38 t(4) = 0.40	Fig. 5d legend, Results para. 6
+ -	6g,h	Paired 2- tailed Students' t- test	Fig. 6g,h legend , Results para. 7	6 and 7	slices from 6 gerbils for 5-HT and slices from 7 gerbils for 5-HT (WAY)	Fig. 6g,h legend, Results para. 7	error bars aremean±SEM	Fig. 6g,h legen d, Result s para. 7	5-HT; Vhalf: p=1.8E-05, Max Ih: p=0.02, I_leak: p=0.77 5-HT (WAY); Vhalf: p=0.07, Max Ih: p=0.74, I_leak: p=0.45	Fig. 6g,h legend, Results para. 7	5-HT: t(5) = 15.94 t(5) = -3.03 t(5) = -0.31 5-HT (WAY) t(6) = 2.25 t(6) = 0.35 t(6) = -0.80	Fig. 6g,h legend, Results para. 7

+	Gi	Paired 2- tailed Students' t- test	Fig. 6i legend , Results para. 7	6 and 7	slices from 6 gerbils for 5-HT and slices from 7 gerbils for 5-HT (WAY)	Fig. 6i legend, Results para. 7	error bars aremean±SEM	Fig. 6i legen d, Result s para. 7	τfast: CTL vs. 5-HT, p = 0.01; CTL vs. 5-HT/ WAY, p = 0.0006; TSIOW: CTL vs. 5-HT, p = 0.003; CTL vs. 5-HT/ WAY, p = 0.16; [Afast/(Afast +ASIOW)]: CTL vs. 5-HT, p = 0.0005; CTL vs. 5-HT/ WAY, p = 0.21	Fig. 6i legend, Results para. 7	t(5) = -3.98 t(6) = -7.77 t(5) = -1.83 t(6) = -1.66 t(5) = 5.89 t(6) = 1.45	Fig. 6i legend, Results para. 7
+ -	7d	Paired 2- tailed Students' t- test	Fig. 7d legend , Results para. 8	7	slices from 7 gerbils	Fig. 7d legend, Results para. 8	error bars aremean±SEM	Fig. 7d legen d, Result s para. 8	5-HT Vrest: p=0.001 threshold: p=0.002 dV/dt: p=0.002	Fig. 7d legend, Results para. 8	t(6) = 5.46 t(6) = 5.19 t(6) = -5.10	Fig. 7d legend, Results para. 8
+	7d	Paired 2- tailed Students' t- test	Fig. 7d legend , Results para. 8	5	slices from 5 gerbils	Fig. 7d legend, Results para. 8	error bars aremean±SEM	Fig. 7d legen d, Result s para. 8	5-HT in ZD7288: Vrest: p=0.82 threshold: p=0.78 dV/dt: p=0.92	Fig. 7d legend, Results para. 8	t(4) = 0.24 t(4) = 0.36 t(4) = 0.10	Fig. 7d legend, Results para. 8
+	7d	Paired 2- tailed Students' t- test	Fig. 7d legend , Results para. 8	6	slices from 6 gerbils	Fig. 7d legend, Results para. 8	error bars aremean±SEM	Fig. 7d legen d, Result s para. 8	soma 5-HT Vrest: p=0.0004 threshold: p=0.10 dV/dt: p=0.29	Fig. 7d legend, Results para. 8	t(5) = 8.16 t(5) = 1.98 t(5) = -1.19	Fig. 7d legend, Results para. 8
+	8b	Paired 2- tailed Students' t- test	Fig. 8b legend , Results para. 9	6	slices from 6 gerbils	Fig. 8b legend, Results para. 9	error bars aremean±SEM	Fig. 8b legen d, Result s para. 9	granisetron: p=1.9E-05	Fig. 8b legend, Results para. 9	t(5) = 17.25	Fig. 8b legend, Results para. 9
+	8c, d	Paired 2- tailed Students' t- test	Fig. 8c,d legend , Results para. 9	8	slices from 8 gerbils	Fig. 8c,d legend, Results para. 9	error bars aremean±SEM	Fig. 8c,d legen d, Result s para. 9	WAY: Vrest: p=0.0039 threshold: p=0.81	Fig. 8c,d legend, Results para. 9	t(7) = 4.21 t(7) = -0.26	Fig. 8c,d legend, Results para. 9
+	8c,d	Paired 2- tailed Students' t- test	Fig. 8c,d legend , Results para. 9	8	slices from 8 gerbils	Fig. 8c,d legend, Results para. 9	error bars aremean±SEM	Fig. 8c,d legen d, Result s para. 9	ZD: Vrest: p=0.4 threshold: p-0.56	Fig. 8c,d legend, Results para. 9	t(7) = 0.95 t(7) =0.63	Fig. 8c,d legend, Results para. 9

+ -	52	One-way repeated measures ANOVA	Fig. S2 legend	3	slices from 3 gerbils	Fig. S2 legend	error bars aremean±SEM	Fig. S2 legend	Spike probability: p=0.002 and 0.53 for soma and soma/DC; Vrest: p=0.01 and 0.40; Max dV/dt: p=0.19 and 0.76; spike threshold: p=0.73 and 0.19	Fig. S2 legend	Spike probability: F(2,2) = 24.97 R square = 0.93, F(2,2) = 0.32 R square = 0.14 Vrest F(2,2) = 20.44 R square = 0.91, F(2,2) = 0.88 R square = 0.30 MaxdV/dt F(2,2) = 2.49 R square = 0.55, F(2,2) = 0.11 R square = 0.05 Spike threshold F(2,2) = 0.14 R square = 0.06, F(2,2) = 2.54 R square = 0.93	Fig. S2 legend
+ -	S3d	One-way repeated measures ANOVA	Fig. S3 legend	6	slices from 6 gerbils	Fig. S3 legend	error bars aremean±SEM	Fig. S3 legend	2mv, p=0.004 4mv, p=0.037 6mv, p=0.002 8mv, p=0.009 10mV, p=0.0008	Fig. S3 legend	$\begin{array}{l} F(2,5) = 14.13 \\ R \; square = 0.12 \\ F(2,5) = 5.76 \\ R \; square = 0.19 \\ F(2,5) = 16.63 \\ R \; square = 0.10 \\ F(2,5) = 22.17 \\ R \; square = 0.816 \end{array}$	Fig. S3 legend
+ -	S3e	One-way repeated measures ANOVA	Fig. S3 legend	6	slices from 6 gerbils	Fig. S3 legend	error bars aremean±SEM	Fig. S3 legend	2mv, p=0.07 4mv, p=0.08 6mv, p=0.008 8mv, p=0.0007 10mV, p=0.03	Fig. S3 legend	$\begin{array}{l} F(2,5) = 2.22\\ R \; square = 0.96\\ F(2,5) = 5.50\\ R \; square = 0.96\\ F(2,5) = 10.82\\ R \; square = 0.91\\ F(2,5) = 16.32\\ R \; square = 0.71\\ F(2,5) = 6.05\\ R \; square = 0.55\\ \end{array}$	Fig. S3 legend
+ -	S3f	One-way repeated measures ANOVA	Fig. S3 legend	6	slices from 6 gerbils	Fig. S3 legend	error bars aremean±SEM	Fig. S3 legend	2mv, p=0.06 4mv, p=0.12 6mv, p=0.003 8mv, p=0.0001 10mV, p=0.02	Fig. S3 legend	$\begin{array}{l} F(2,5) = 1.66\\ R \ square = 0.99\\ F(2,5) = 2.54\\ R \ square = 0.34\\ F(2,5) = 17.47\\ R \ square = 0.98\\ F(2,5) = 4.15\\ R \ square = 0.92\\ F(2,5) = 5.15\\ R \ square = 0.92 \end{array}$	Fig. S3 legend
+	S5	Paired 2- tailed Students' t- test	Fig. S5 legend	3	slices from 3 gerbils	Fig. S5 legend	error bars aremean±SEM	Fig. S5 legend	Max Ih, p = 0.029; inst leak, p=0.73; V1/2, p=0.017	Fig. S5 legend	t(2) = 5.67 t(2) = 0.4 t(2) = -7.49	Fig. S5 legend
+	S6	One-way repeated measures ANOVA	Fig. S6 legend	5	slices from 5 gerbils	Fig. S6 legend	error bars aremean±SEM	Fig. S6 legend	AP probability: AIS, p=0.88 soma, p=0.56	Fig. S6 legend	F(2,4) = 0.18 R square = 0.99 F(2,4) = 0.53 R square = 0.99	Fig. S6 legend
+ -	S6	One-way repeated measures ANOVA	Fig. S6 legend	5	slices from 5 gerbils	Fig. S6 legend	error bars aremean±SEM	Fig. S6 legend	Vrest: AIS, p=0.08 soma, p=0.98	Fig. S6 legend	F(2,4) = 0.96 R square = 0.99 F(2,4) = 0.29 R square = 0.99	Fig. S6 legend
+	S6	One-way repeated measures ANOVA	Fig. S6 legend	5	slices from 5 gerbils	Fig. S6 legend	error bars aremean±SEM	Fig. S6 legend	spike threshold: AIS, p=0.91 soma, p=0.22	Fig. S6 legend	F(2,4) = 3.19 R square = 0.99 F(2,4) = 0.18 R square =0.99	Fig. S6 legend

April 2015

+ -	S6	One-way repeated measures ANOVA	Fig. S6 legend	5	slices from 5 gerbils	Fig. S6 legend	error bars aremean±SEM	Fig. S6 legend	dV/dt: AIS, p=0.18 soma, p=0.83	Fig. S6 legend	F(2,4) = 2.02 R square = 0.38 F(2,4) = 0.32 R square = 0.77	Fig. S6 legend
+ -		Paired 2- tailed Students' t- test	Results para. 3	6	slices from 6 gerbils	Results para. 3	error bars aremean±SEM	Result s para. 3	(XE-001) Vrest: p=0.21	Results para. 3	t(5) = 1.50	Results para. 3
+		Paired 2- tailed Students' t- test	Results para. 7	4	slices from 4 gerbils	Results para. 7	error bars aremean±SEM	Result s para. 7	(Ketanserin) Vhalf: p=0.013, Max Ih: p=0.002	Results para. 7	t(3) = 5.29 t(4) = -10.05	Results para. 7

Representative figures

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

If so, what figure(s)?

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 #)?

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.

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?
- 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 #)?

c. Is there any estimate of variance within each group of data?

Is the variance similar between groups that are being statistically compared?

Yes, Fig. 1

Yes, sample sizes are reported for every experiment and statistical test throughout the Results section.

For immunolabeling, Results, paragraph 1.

No. Selected sample sizes are standard to the field.

Yes

Yes, the section is called "Data analysis and statistics."

Normality was assumed but not tested. This is stated in the Methods under the "Data analysis and statistics" section.

Yes, SEM is reported for each statistical comparison throughout the Results section.

- d. Are tests specified as one- or two-sided?
- e. Are there adjustments for multiple comparisons?
- 3. Are criteria for excluding data points reported?

Was this criterion established prior to data collection?

Where is this described (section, paragraph #)?

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 #)?

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 #)?

6. For experiments in live vertebrates, is a statement of compliance with Yes, Methods, paragraph 1 ethical guidelines/regulations included?

Where (section, paragraph #)?

7. Is the species of the animals used reported?

Where (section, paragraph #)?

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

Where (section, paragraph #)?

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

Where (section, paragraph #)?

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

Where (section, paragraph #)?

- 11. For animals housed in a vivarium, is the light/dark cycle reported? Where (section, paragraph #)?
- 12. For animals housed in a vivarium, is the housing group (i.e. number of animals per cage) reported?

Where (section, paragraph #)?

Two sided Yes n/a n/a

n/a

Results, paragraph 1 and Methods, paragraph 2

Methods, paragraph 2

Methods, paragraph 2

Methods, paragraph 2

Not reported: animals' light dark cycle was standard and not critical to be reported.

No

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

Where (section, paragraph #)?

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

Where (section, paragraph #)?

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 #)?

- 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)?
 - a. Is antibody catalog number given?

Where does this appear (section, paragraph #)?

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

Where does this appear (section, paragraph #)?

- 2. Cell line identity
 - Are any cell lines used in this paper listed in the database of commonly misidentified cell lines maintained by <u>ICLAC</u> and <u>NCBI Biosample</u>?

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. n/a n/a

n/a

n/a

n/a

Yes; Methods, Immunostaining section.

No

n/a

Yes

Yes

.

Yes

- c. For each cell line, include in the Methods section a statement that specifies:
 - the source of the cell lines
 - have the cell lines been authenticated? If so, by which method?
 - have the cell lines been tested for mycoplasma
 - contamination?
- Where (section, paragraph #)?

Data 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?

n/a

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.
- 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 #)?

Specified in Methods ("Current clamp electrophysiology with AAQ")

n/a

- Is the number of human subjects, their age and sex clearly defined?
 Where (section, paragraph #)?
- 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?
- 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