## 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.

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<td>Results para 6</td>
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<td>ANOVA: p &lt; 0.0001 for all comparisons post test: medial: E9 ctr mt: p=0.6554 E10 ctr mt: p=0.0001 E9 E10 ctr: p=0.0002 E9 E10 mt: p=0.9908 lateral: E9 ctr mt: p=0.5069 E10 ctr mt: p=0.0001 E9 E10 ctr: p=0.0001 E9 E10 mt: p=0.0005 Lmx1a: E9 ctr mt: p=0.9639 E10 ctr mt: p=0.0001 E9 E10 ctr: p=0.0001 E9 E10 mt: p=0.0005</td>
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<td>bin ( 0-600: p = 0.002 ) ( 600-1200: p = 0.0062 ) &gt;1200: ( p = 0.0011 )</td>
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<td>n=5 cells of 5 slices of 4 animals, n=7 cells of 7 slices of 5 animals</td>
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<td>5, 6</td>
<td>mice from 3 litters per group</td>
<td>Methods, SupFig legend</td>
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<td>Methods, SupFig legend</td>
<td>error bars are mean +/- SEM</td>
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<td>Methods, SupFig legend</td>
<td>error bars are mean +/- SEM</td>
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<td>( p = 0.244 ) ( p = 0.376 ) ( p = 0.597 )</td>
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<td>5, 6</td>
<td>mice from 3 litters per group</td>
<td>Methods, SupFig legend</td>
<td>error bars are mean +/- SEM</td>
<td>SupFig legend</td>
<td>( p = 0.795 ) ( p = 0.111 ) ( p = 0.104 )</td>
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### Table 1: Statistical Tests and Results

| *S9e* repeated measures ANOVA | SupFig. legend | 5, 6 mice form 3 litters per group | SupFig. legend | error bars are mean +/- SEM | SupFig. legend | p = 0.228 | p = 0.454 | p = 0.465 | p = 0.480 | p = 0.147 | p = 0.769 | p = 0.193 | p = 0.999 | p = 0.986 | p = 0.223 | p = 0.230 | p = 0.351 | F(1,9) = 1.67 | F(3,32) = 0.92 | F(3,32) = 0.90 | F(1,9) = 0.54 | F(2,18) = 0.147 | F(2,18) = 0.27 | F(1,9) = 1.97 | F(4,36) = 0.02 | F(4,36) = 0.08 | F(1,9) = 1.71 | F(11,11) = 1.64 | F(1,11) = 1.03 |
| *S9f* repeated measures ANOVA | SupFig. legend | 5, 6 mice form 3 litters per group | SupFig. legend | error bars are mean +/- SEM | SupFig. legend | p = 0.187 | p = 0.323 | p = 0.864 | p = 0.349 | p = 0.399 | p = 0.262 | p = 0.436 | p = 0.054 | p = 0.958 | p = 0.067 | p = 0.430 | p = 0.876 | F(1,9) = 2.03 | F(3,31) = 1.21 | F(3,31) = 0.28 | F(1,9) = 0.97 | F(4,36) = 1.04 | F(4,36) = 1.37 | F(1,9) = 0.66 | F(4,36) = 2.57 | F(4,36) = 0.15 | F(1,9) = 4.32 | F(4,36) = 0.98 | F(4,36) = 0.30 |
| *S10a* unpaired t-test | SupFig. legend | 5, 6 mice form 3 litters per group | SupFig. legend | error bars are mean +/- SEM | SupFig. legend | p=0.369 | 
| *S10b* unpaired t-test | SupFig. legend | 5, 6 mice form 3 litters per group | SupFig. legend | error bars are mean +/- SEM | SupFig. legend | p=0.024 | t(9)=3.725 | 
| *S10d* paired t-test | SupFig. legend | 11, 12 mice form 4 litters per group | SupFig. legend | error bars are mean +/- SEM | SupFig. legend | p = 0.047 | p = 0.004 | p = 0.64 | t(10)=3.2 | t(11)=3.7 |
| *S10e* paired t-test | SupFig. legend | 11, 12 mice form 4 litters per group | SupFig. legend | error bars are mean +/- SEM | SupFig. legend | p = 0.047 | p = 0.004 | p = 0.64 | t(10)=3.2 | t(11)=3.7 |
| *Sup Tab2* unpaired t-test | Tab legend | 5, 5 wt: n=5 neurons, 4 brain slices, 3 mice mutant: n=5, 3 brain slices, 2 mice | Tab legend | mean +/- SEM | Tab legend | 0.230 | 0.096 | 0.766 | 0.163 | 0.392 | 0.026 | 0.537 | 0.877 | 0.630 | t=1.301 df=8 | t=1.883 df=8 | t=0.307 df=8 | t=0.167 df=7 | t=3.181 df=8 | t=2.083 df=8 | t=6.678 df=9 | t=0.167 df=9 | t=2.818 df=8 | t=4.358 df=9 | t=7.288 df=10 | t=0.500 df=8 | t=0.161 df=7 |
| *Sup Tab5* unpaired t-test | Tab legend | 5, 7 n=12 neurons from 9 mice | Tab legend | mean +/- SEM | Tab legend | 0.0112 | 0.0669 | 0.0001 | 0.8709 | 0.0201 | 0.00038 | 0.0028 | 0.0198 | Table | t=3.181 df=9 | t=2.083 df=8 | t=6.678 df=9 | t=0.167 df=9 | t=2.818 df=8 | t=4.358 df=9 | t=7.288 df=10 | na/ df=10 | t=2.770 df=10 |
| *resul ts, p.4* unpaired t-test | 3, 3 2 controls and 3 mutants from one litter, 1 control from separate litter | Methods, p.4 | error bars are mean +/- SEM | Methods | p=0.0053 | p(4)=5.502 | p.4 |
| *resul ts, p.6* unpaired t-test | 3, 3 3 controls and 3 mutants from one litter | Methods, p.6 | error bars are mean +/- SEM | Methods | p=0.0102 | t(4)=4.574 | p.6 |
| *resul ts, p.8* unpaired t-test with Welch’s correction | 3, 3 3 controls from one litter, 2 mutants each from separate litter | Methods, p.8 | error bars are mean +/- SEM | Methods | p=0.0455 | p(8)=4.56 | p.8 |

**Methods:**
- *S9e* and *S9f*: Mice were divided into groups of 5, with 3 litters per group.
- *S10a* and *S10b*: Unpaired t-test was used to compare two independent groups.
- *S10d* and *S10e*: Paired t-test was used for matched samples.
- *Sup Tab2* and *Sup Tab5*: Additional statistical tests were performed with the specified sample sizes and conditions.
### 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?

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<table>
<thead>
<tr>
<th>Table of results, p.9</th>
<th>paired t-test</th>
<th>p.9</th>
<th>3</th>
<th>n=3 slices of 3 mice</th>
<th>p.9</th>
<th>mean ± SEM</th>
<th>p=0.1827</th>
<th>p.9</th>
<th>t=2.014 df=2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Table of results, p.9</td>
<td>paired t-test</td>
<td>p.9</td>
<td>3</td>
<td>n=3 slices of 3 mice</td>
<td>p.9</td>
<td>mean ± SEM</td>
<td>p=0.0285</td>
<td>p.9</td>
<td>t=5.795 df=2</td>
</tr>
</tbody>
</table>
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 #)?

Fig.1-3,5: independent biological samples, assumption: normal distribution (N=3 too small for normality test), most comparisons: distributions not significantly different between groups. Significant differences in distribution between groups: t-test with Welch’s correction
Fig.4g: N≥5, NAc passed normality test, PFC (Gli2 mt) significantly non-normal tested using Kolmogorow-Smirnow test--> non-parametric test
Fig.6h: Friedman test, control condition significantly non-normal tested using Kolmogorow-Smirnow test--> non-parametric test
Fig.7c: unpaired t-test with Welch’s correction, P value for F test to compare variances 0.0022, variances are significantly different
Fig.7h: one-way ANOVA /w Dunnett’s multiple comparison test, passed normality test
Fig.7j: repeated measures ANOVA /w Dunnett’s multiple comparison test
Fig.8c,d: unpaired t-test with Welch’s correction, passed normality test
Fig.8e,f: repeated measures ANOVA, passed normality test
Fig.51: independent biological samples, assumption: normal distribution (N=3 too small for normality test) one-way ANOVA /w Tukey’s multiple comparison test
Fig.52,53: independent biological samples, assumption: normal distribution (N too small for normality test), most comparisons: distributions not significantly different between groups. Significant differences in distribution between groups: t-test with Welch’s correction
S5a: most comparisons: distributions not significantly different between groups. Significant differences in distribution between groups: t-test with Welch’s correction
Fig.55d: N=5, passed normality test
Fig.55e,f: N≥5, passed normality test; significant differences in distribution between groups: t-test with Welch’s correction
Fig. S6a,b: did not pass normality test, Mann Whitney test
Fig.S9, S10: passed normality test

variances were estimated, if variances were not similar between groups t-test with Welch’s correction was used
Fig.6, Fig. S9a-f: when variances were not similar a Greenhouse Geisser correction was used (see statistical analysis section)

yes, two-sided t-test (Methods)

ANOVA with multiple comparison tests as indicated

Histological analysis and behavioral tests: N/A
Electrophysiology:
- Only cells which were visible over the course of the entire experiment were included for analysis of fluorescence intensity after calcium imaging experiments. See methods.
- (Suppl. Methods, p.8)
- Fig. S6g-i: Two mutants were excluded because they did not explore at all.

3. Are criteria for excluding data points reported?

Was this criterion established prior to data collection?

Where is this described (section, paragraph #)?

Histological analysis and behavioral tests: N/A
Electrophysiology:
- Only cells which were visible over the course of the entire experiment were included for analysis of fluorescence intensity after calcium imaging experiments. See methods.
- (Suppl. Methods, p.8)
- Fig. S6g-i: Two mutants were excluded because they did not explore at all.
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 #)?

Complete blinding was not possible, since mutants presented a phenotype. Attentional tasks: The experimenter was informed of the genotype of the groups only after data collection.

yes (Methods)

6. For experiments in live vertebrates, is a statement of compliance with ethical guidelines/regulations included?
   Where (section, paragraph #)?

yes (Methods)

7. Is the species of the animals used reported?
   Where (section, paragraph #)?

yes (Methods)

8. Is the strain of the animals (including background strains of KO/transgenic animals used) reported?
   Where (section, paragraph #)?

yes (Methods)

9. Is the sex of the animals/subjects used reported?
   Where (section, paragraph #)?

yes for behavioral tests (Methods)

10. Is the age of the animals/subjects reported?
    Where (section, paragraph #)?

yes (Methods)

11. For animals housed in a vivarium, is the light/dark cycle reported?
    Where (section, paragraph #)?

yes (Methods)

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

yes (Methods)

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

yes (Methods)

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 #)?

Yes (Methods)

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

Where (section, paragraph #)?

N/A

see point 3, not reported

a. How were the criteria for exclusion defined?

Where is this described (section, paragraph #)?

N/A, low exploration level, see point 3

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 #)?

N/A

**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 #)?

      yes (Methods)

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

      Where does this appear (section, paragraph #)?

      all antibodies are well established, yes (Methods)

2. Cell line identity

   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 #)?

      N/A

   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

   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 #)?

      N/A
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?
   Where (section, paragraph #)?
   N/A

Computer code/software

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

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

2. If computer code was used to generate results that are central to the paper’s conclusions, include a statement in the Methods section under "Code availability" to indicate whether and how the code can be accessed. Include version information as necessary and any restrictions on availability.
   N/A

Human subjects

1. Which IRB approved the protocol?
   Where is this stated (section, paragraph #)?
   N/A

2. Is demographic information on all subjects provided?
   Where (section, paragraph #)?
   N/A

3. Is the number of human subjects, their age and sex clearly defined?
   Where (section, paragraph #)?
   N/A

4. Are the inclusion and exclusion criteria (if any) clearly specified?
   Where (section, paragraph #)?
   N/A
5. How well were the groups matched?
   Where is this information described (section, paragraph #)?
   
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?
      
   N/A
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? 
      N/A
   b. How were the ROI’s defined (functional vs anatomical localization)?
      N/A

21. Is there correction for multiple comparisons within each voxel?
    N/A

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

### Additional comments

Additional Comments

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Nature Neuroscience: doi:10.1038/nn.4020