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# Main Figures: 4

# Supplementary Figures: 9

# 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 | |
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| | FIGURE NUMBER | WHICH TEST? | SECTION & PARAGRAPH # | EXACT VALUE | DEFINED? | SECTION & PARAGRAPH # | REPORTED? | SECTION & PARAGRAPH # | EXACT VALUE | SECTION & PARAGRAPH # | VALUE | SECTION & PARAGRAPH # |
| + - | 2a | two-tailed paired t-test | Fig. legend, Results para 4 | 1370 | Number of responsive neurons from S1 sessions | Fig. legend | Error bars are mean +/- SEM across 5 mice, Hit-Miss: mean +/- 95% CI FA-CR: mean +/- 95% CI | Results para 4, Methods, statistics | p=1.17e-57 for Hit vs Miss p=0.130 for FA vs CR | Fig. legend | t(1369)=16.79 for Hit vs Miss t(1369)=1.512 for FA vs CR | Fig. legend |
| + - | 2b | two-tailed paired t-test | Fig. legend, Results para 4 | 607 | Number of responsive neurons from S2 sessions | Fig. legend | Error bars are mean +/- SEM across 5 mice, Hit-Miss: mean +/- 95% CI FA-CR: mean +/- 95% CI | Results para 4, Methods, statistics | p=2.22e-70 for Hit vs Miss p=5.33e-5 for FA vs CR | Fig. legend | t(606)=20.32 for Hit vs Miss t(606)=4.07 for FA vs CR | Fig. legend |
| + - | 2c | two-tailed Wilcoxon signed-rank test | Fig. legend | 1370, 607 | Number of responsive neurons from S1 and S2 sessions | Fig. legend | Errorbars are mean +/- SEM across 5 mice | Methods, statistics | p=1.73e-110 for hit vs miss in S1, p=3.76e-79 for hit vs miss in S2 | Fig. legend | S1: z=22.33 S2:z=18.84 | Fig. legend |
| + - | 2c | two-tailed Wilcoxon rank sum test | Fig. legend | 1370, 607 | Number of responsive neurons from S1 and S2 sessions | Fig. legend | Errorbars are mean +/- SEM across 5 mice | Results para 4, Methods, statistics | p = 8.38e-14 for normalized miss in S1 vs normalized miss in S2 | Fig. legend | z = 7.46 | Fig. legend |
| + - | 2d left | two-tailed K-S test | Fig. legend | 2490, 1471 | Number of neurons from S1 and S2 sessions | Fig. legend | All data points are plotted in fig., median in legend | Results para 5, Fig. legend | p=0.0013 | Fig. legend | K-S stat = 0.063 | Fig. legend |
| + - | 2d middle | two-tailed K-S test | Fig. legend | 2490, 1471 | Number of neurons from S1 and S2 sessions | Fig. legend | All data points are plotted in fig., median in legend | Results para 5, Fig. legend | p=0.056 | Fig. legend | K-S stat = 0.044 | Fig. legend |
| + - | 2d right | two-tailed K-S test | Fig. legend | 2490, 1471 | Number of neurons from S1 and S2 sessions | Fig. legend | All data points are plotted in fig., median in legend | Results para 5, Fig. legend | p=1.96e-7 | Fig. legend | K-S stat = 0.093 | Fig. legend |
| + - | 2g | bootstrap test | Fig. legend ,Methods | 26898 (SP), 12387 (DP), 431962 (All) | Number of pairwise distances for SP, DP and all neurons | Fig. legend | All data points are plotted in fig., medians in text. | Results para 5, Fig. legend | p<5e-5 (20,000 bootstrap iterations) | Fig. legend | NA | NA |
| + - | 2i | ANCOVA | Fig. legend | 5 / 78 | Number of mice/ number of binned values | Fig. legend | Errorbars are mean +/- SEM across mice | Fig. legend | p=1.711e-10 (test of zero slope) p=0.062 (difference between SP vs DP) | Fig. legend | F(1,74)=54.84 (slope) F(1,74)=3.58 (difference between SP and DP slopes) | Fig. legend |
| + - | 2j | ANCOVA | Fig. legend | 5 / 58 | Number of mice/ number of binned values | Fig. legend | Errorbars are mean +/- SEM across mice | Fig. legend | p=0.08 (test of zero slope) p=0.34 (difference between SP vs DP) | Fig. legend | F(1,54)=3.11 (slope) F(1,54)=0.92 (difference between SP and DP slopes) | Fig. legend |

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| + - | 2k | one-tailed Wilcoxon rank sum test | Fig. legend | 7 (S1), 9 (S2) | Number of sessions | Fig. legend | Errorbars are mean +/- SEM across mice | Fig. legend | p=0.045 | Fig. legend | ranksum = 76 | Fig. legend |
| + - | 2l | one-tailed Wilcoxon rank sum test | Fig. legend | 7 (S1), 9 (S2) | Number of sessions | Fig. legend | Errorbars are mean +/- SEM across mice | Fig. legend | p=0.021 | Fig. legend | ranksum=40 | Fig. legend |
| + - | 2m | two-tailed permutation test | Fig. legend | 1370 (S1), 607 (S2) | Number of responsive neurons | Fig. legend | All data points are plotted in fig., mean +/- SEM across mice in text | Fig. legend, Results para 9 | p<5e-5 (20,000 bootstrap iterations) | Fig. legend | NA | NA |
| + - | 2m | two-tailed permutation test | Fig. legend | 536 (S1), 287 (S2) | Number of significant SP neurons | Fig. legend | All data points are plotted in fig. | Fig. legend | p<5e-5 (20,000 bootstrap iterations) | Fig. legend | NA | NA |
| + - | 2m | two-tailed permutation test | Fig. legend | 338 (S1), 259 (S2) | Number of significant DP neurons | Fig. legend | All data points are plotted in fig. | Fig. legend | p<5e-5 (20,000 bootstrap iterations) | Fig. legend | NA | NA |
| + - | 3f | two-tailed Wilcoxon signed-rank test | Fig. legend | 88 (s2p), 648 (unlabelled) | Number of responsive neurons from 3 mice | Fig. legend | Errorbars are mean +/- SEM across mice | Results para 12 | s2p: p=7.43e-11 unlabeled: p=2.11e-43 | Fig. legend,Results para 12 | s2p: z=6.511, unlabeled: z=13.81 | Fig. legend |
| + - | 3f | two-tailed permutation test | Fig. legend | 88 (s2p), 648 (unlabeled) | Number of responsive neurons from 3 mice | Fig. legend | Errorbars are mean +/- SEM across mice | Fig. legend | p=0.031 | Fig. legend | NA | NA |
| + - | 3g | two-tailed permutation test | Fig. legend | 133 (s2p), 1134 (unlabeled) | Number of neurons from 3 mice | Fig. legend | All data points are plotted in fig. Medians in legend | Fig. legend | p<5e-5 (20,000 bootstrap iterations) | Fig. legend | NA | NA |
| + - | 3h | two-tailed permutation test | Fig. legend | 133 (s2p), 1134 (unlabeled) | Number of neurons from 3 mice | Fig. legend | All data points are plotted in fig. Medians in legend | Fig. legend | p<5e-5 (20,000 bootstrap iterations) | Fig. legend | NA | NA |
| + - | 3i | one-tailed Wilcoxon signed-rank test | Fig. legend | 8 | Number of sessions | Fig. legend | Errorbars are mean +/- SEM across mice | Fig. legend | p=0.012 | Fig. legend | signedrank=34 | Fig. legend |
| + - | 3j | one-tailed Wilcoxon signed-rank test | Fig. legend | 8 | Number of sessions | Fig. legend | Errorbars are mean +/- SEM across mice | Fig. legend | p=0.055 | Fig. legend | signedrank=30 | Fig. legend |
| + - | 3k | two-tailed permutation test | Fig. legend | 88 (s2p), 648 (unlabeled) | Number of responsive neurons from 3 mice | Fig. legend | Errorbars are mean +/- SEM across sessions | Fig. legend,Results para 13 | p<5e-5 (20,000 bootstrap iterations) | Fig. legend | NA | NA |
| + - | 4e | two-tailed paired t-test | Fig. legend,Results para 15 | 160 | Number of axons from 4 mice | Fig. legend | Errorbars are mean +/- SEM across mice, text gives Hit-Miss mean +/- 95% CI | Fig. legend,Results para 15 | p=0.0014 | Fig. legend,Results para 15 | t(159) = 3.249 | Fig. legend |
| + - | 4f | two-tailed paired t-test | Fig. legend,Results para 15 | 440 | Number of axons from 4 mice | Fig. legend | Errorbars are mean +/- SEM across mice, text gives Hit-Miss mean +/- 95% CI | Fig. legend,Rsults para 15 | p = 0.0019 | Fig. legend,Results para 15 | t(439) = 3.127 | Fig. legend |

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| + - | 4g | two-tailed sign test | Fig. legend | 160(S1 axons), 440 (S2 axons) | Number of axons from 4 mice each | Fig. legend | Errorbars are mean +/- SEM across mice | Fig. legend | p=0.0034 (S1 axons), p=1.15e-18 (S2 axons) | Fig. legend | sign=99 (S1 axons), sign=313 (S2 axons) | Fig. legend |
| + - | 4g | two-tailed Wilcoxon rank sum test | Fig. legend | 160(S1 axons), 440 (S2 axons) | Number of axons from 4 mice each | Fig. legend | Errorbars are mean +/- SEM across mice | Fig. legend | p=1.33e-4 | Fig. legend | z=3.821 | Fig. legend |
| + - | 4h | two-tailed Wilcoxon rank sum test | Fig. legend | 7(S1 axons), 10(S2 axons) | Number of sessions from 4 mice each | Fig. legend | Errorbars are mean +/- SEM across mice | Fig. legend | p=0.044 | Fig. legend | z=2.05 | Fig. legend |
| + - | 4i | two-tailed Wilcoxon rank sum test | Fig. legend | 7(S1 axons), 10(S2 axons) | Number of sessions from 4 mice each | Fig. legend | Errorbars are mean +/- SEM across mice | Fig. legend | p=0.109 | Fig. legend | z=-1.47 | Fig. legend |
| + - | 4m | two-tailed paired t-test | Fig. legend | 12(S1), 15(S2), 12(Cntl) | Number of sessions from S1, S2 and control experiments | Fig. legend | Errorbars are mean +/- SEM across 4 mice | Fig. legend | p=9.22e-7 (S1) p=2.00e-5 (S2) p=0.023 (Cntl) | Fig. legend | t(11)=9.781 (S1) t(14)=6.286 (S2) t(11)=2.651 (Control) | Fig. legend |
| + - | 4m | two-tailed Wilcoxon rank sum test | Fig. legend | 12(S1), 15(S2), 12(Cntl) | Number of sessions from S1, S2 and control experiments | Fig. legend | Errorbars are mean +/- SEM across 4 mice | Fig. legend | p=0.421 (S1 vs S2) p=0.001 (S2 vs Control) | Fig. legend | z=-0.805 (S1 vs S2) z=-3.270 (S2 vs Control) | Fig. legend |
| + - | S1c | two-tailed K-S test | Fig. legend | 338(S1), 502(S2) | Number of first-lick times from S1 and S2 sessions | Fig. legend | All data points are plotted in fig. | Fig. legend | p=0.436 | results para 2, fig. legend | K-S stat=0.0597 | Fig. legend |
| + - | S3e left | two-tailed paired t-test | Fig. legend | 226 | Number of S1 neurons from 4 mice | Fig. legend | Errorbars are mean +/- SEM across 4 mice | Fig. legend | p=1.53e-21 | Fig. legend | t(225)=10.60 | Fig. legend |
| + - | S3e right | two-tailed paired t-test | Fig. legend | 214 | Number of S2 neurons from 4 mice | Fig. legend | Errorbars are mean +/- SEM across 4 mice | Fig. legend | p=3.50e-13 | Fig. legend | t(213)=7.76 | Fig. legend |
| + - | S3f | two-tailed Wilcoxon rank sum test | Fig. legend | 226(S1), 214(S2) | Number of S1 and S2 neurons from 4 mice | Fig. legend | Errorbars are mean +/- SEM across 4 mice | Fig. legend | p=0.006 | Fig. legend | z=2.721 | Fig. legend |
| + - | S3h | two-tailed permutation test | results para 11, fig. legend | 4910 | Number of mean noise correlations between S1 and S2 neurons | Fig. legend | Errorbars are mean +/- SEM across sessions | Fig. legend | p<2e-5 (20,000 bootstrap iterations) | Fig. legend | NA | NA |
| + - | S3i left<br>S3i middle<br>S3i right | two-tailed permutation tests | Fig. legend | 226(S1), 214(S2) | Number of S1 and S2 neurons from 4 mice | Fig. legend | All data points are plotted in fig. median and 3rd quartile in legend. | Fig. legend | p=0.003<br>p=0.392<br>p=0.023 | Fig. legend | NA | NA |
| + - | S3j | one-tailed Wilcoxon sign rank test | Fig. legend | 9 | Number of sessions | Fig. legend | Error bars are mean +/- SEM across 3 mice | Fig. legend | p=0.037 (S1&S2 combined vs S1)<br>p=0.005 (S1&S2 combined vs S2) | Fig. legend | signrank=7<br>signrank=2 | Fig. legend |

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| + - | S3k | one-tailed Wilcoxon sign rank test | Fig. legend | 9 | Number of sessions | Fig. legend | Error bars are mean +/- SEM across 3 mice | Fig. legend | p=0.014 (S1 vs S2)<br><br>p=0.037 (S1&S2 combined vs S1)<br><br>p=0.010 (S1&S2 combined vs S2) | Fig. legend | signrank=41<br>signrank=7<br>signrank=3 | Fig. legend |
| + - | S9a row 1 | two-tailed K-S test | Fig. legend | 2490(S1), 1471(S2) | Number of neurons from S1 and S2 sessions | Fig. legend | All data points are plotted in fig. | NA | p=2.20e-4<br>p=0.060<br>p=0.002 | Fig. legend | K-S stat=0.070<br>K-S stat=0.044<br>K-S stat=0.060 | Fig. legend |
| + - | S9a row 2 | two-tailed K-S test | Fig. legend | 2490(S1), 1471(S2) | Number of neurons from S1 and S2 sessions | Fig. legend | All data points are plotted in fig. | NA | p=5.14e-7<br>p=0.060<br>p=0.002 | Fig. legend | K-S stat=0.090<br>K-S stat=0.044<br>K-S stat=0.060 | Fig. legend |
| + - | S9a row 3 | two-tailed K-S test | Fig. legend | 2490(S1), 1471(S2) | Number of neurons from S1 and S2 sessions | Fig. legend | All data points are plotted in fig. | NA | p=9.76e-6<br>p=0.041<br>p=7.15e-5 | Fig. legend | K-S stat=0.081<br>K-S stat=0.046<br>K-S stat=0.074 | Fig. legend |
| + - | S9a row 4 | two-tailed K-S test | Fig. legend | 2490(S1), 1471(S2) | Number of neurons from S1 and S2 sessions | Fig. legend | All data points are plotted in fig. | NA | p=8.17e-8<br>p=0.051<br>p=1.76e-4 | Fig. legend | K-S stat=0.096<br>K-S stat=0.045<br>K-S stat=0.071 | Fig. legend |
| + - | 3d | two-tailed paired t-test | Fig. legend | 88 | Number of responsive S2p neurons from 3 mice | Fig. legend | Error bars are mean +/- SEM across mice | Fig. legend | p=9.24e-7 | Fig. legend | t(87)=5.284 | Fig. legend |
| + - | 3e | two-tailed paired t-test | Fig. legend | 648 | Number of responsive unlabeled neurons from 3 mice | Fig. legend | Error bars are mean +/- SEM across mice | Fig. legend | p=2.43e-35 | Fig. legend | t(647)=13.187 | Fig. legend |

## Representative figures

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

   If so, what figure(s)?

   Fig. 1e-g; Fig. 3b,c; Fig. 4b,d; Supp. Fig. 3a-d; Supp. Fig. 4c; Supp. Fig. 8a,b.

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 #)?

   Images are example traces or schematics for experiments whose N values are reported in the legends and methods.

## 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 predetermine sample sizes. Sample sizes are similar to what have been reported in the field. This is described in the Methods section titled "Statistics".

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

   Where (section, paragraph #)?

   Statistical tests are justified as appropriate in multiple subsections of the Methods.

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

Yes, in the Methods section titled "Statistics".

b. Do the data meet the assumptions of the specific statistical test you chose (e.g. normality for a parametric test)?

Where is this described (section, paragraph #)?

Yes, this is described in the Methods section titled "Statistics".

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 #)?

Yes, all data are reported with standard error of the mean or median with interquartile range. The variance is similar between groups. Dispersion is reported directly with the data. This is described in "data analysis" subsections of the Methods.

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

Yes. In Methods and throughout.

e. Are there adjustments for multiple comparisons?

No.

3. To promote transparency, *Nature Neuroscience* has stopped allowing bar graphs to report statistics in the papers it publishes. If you have bar graphs in your paper, please make sure to switch them to dot-plots (with central and dispersion statistics displayed) or to box-and-whisker plots to show data distributions.

We now show dot-plots instead (superimposed on bar graphs).

4. Are criteria for excluding data points reported?

Was this criterion established prior to data collection?

Where is this described (section, paragraph #)?

Yes. This is described in multiple subsections titled "data analysis" under Methods.

5. 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 #)?

Assignment was not randomized, as described in Methods section titled "Statistics".

6. 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, as described in Methods section titled "Statistics".

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

Where (section, paragraph #)?

Yes, reported in first line of Methods section.

8. Is the species of the animals used reported?

Where (section, paragraph #)?

Yes, in Methods section titled "Mice".

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| 9. Is the strain of the animals (including background strains of KO/ transgenic animals used) reported?<br>Where (section, paragraph #)? | Yes, in Methods section titled "Mice" and in Supp. Fig. 6. |
| 10. Is the sex of the animals/subjects used reported?<br>Where (section, paragraph #)? | Yes, in Methods section titled "Mice" and in Supp. Fig. 6. |
| 11. Is the age of the animals/subjects reported?<br>Where (section, paragraph #)? | Yes, in Methods section titled "Mice". |
| 12. For animals housed in a vivarium, is the light/dark cycle reported?<br>Where (section, paragraph #)? | Yes, in Methods section titled "Mice". |
| 13. For animals housed in a vivarium, is the housing group (i.e. number of animals per cage) reported?<br>Where (section, paragraph #)? | Yes, in Methods section titled "Mice". |
| 14. For behavioral experiments, is the time of day reported (e.g. light or dark cycle)?<br>Where (section, paragraph #)? | Yes, in Methods section titled "Mice". |
| 15. Is the previous history of the animals/subjects (e.g. prior drug administration, surgery, behavioral testing) reported?<br>Where (section, paragraph #)? | Mice were only used for the experiments reported here, as described in the Methods. |
| a. If multiple behavioral tests were conducted in the same group of animals, is this reported?<br>Where (section, paragraph #)? | Behavioral testing is described fully in the Methods section titled "Behavioral task." |
| 16. If any animals/subjects were excluded from analysis, is this reported?<br>Where (section, paragraph #)? | No animals were excluded. |
| a. How were the criteria for exclusion defined?<br>Where is this described (section, paragraph #)? | N/A |
| b. Specify reasons for any discrepancy between the number of animals at the beginning and end of the study.<br>Where is this described (section, paragraph #)? | N/A |

## Reagents

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

   N/A. No antibodies were used.

   a. Is antibody catalog number given?

      Where does this appear (section, paragraph #)?

      N/A

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

      Where does this appear (section, paragraph #)?

      N/A

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. No cell lines were used.

   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

Provide a Data availability statement in the Methods section under "Data availability", which should include, where applicable:

- Accession codes for deposited data
- Other unique identifiers (such as DOIs and hyperlinks for any other datasets)
- At a minimum, a statement confirming that all relevant data are available from the authors
- Formal citations of datasets that are assigned DOIs
- A statement regarding data available in the manuscript as source data
- A statement regarding data available with restrictions

See our data availability and data citations policy page for more information.

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.

Where is the Data Availability statement provided (section, paragraph #)?

Data availability is described in Methods section titled "Data availability".

## 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 #)?

   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?

   N/A

   a. If yes, is the number rejected and reasons for rejection described?

      Where (section, paragraph #)?

      N/A

2. Is the number of blocks, trials or experimental units per session and/or subjects specified?

   Where (section, paragraph #)?

   N/A

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

   N/A

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.

   N/A

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| 5. Is the task design clearly described?<br>Where (section, paragraph #)? | N/A |
| 6. How was behavioral performance measured? | N/A |
| 7. Is an ANOVA or factorial design being used? | N/A |
| 8. For data acquisition, is a whole brain scan used?<br>If not, state area of acquisition. | N/A |
| a. How was this region determined? | N/A |
| 9. Is the field strength (in Tesla) of the MRI system stated? | N/A |
| a. Is the pulse sequence type (gradient/spin echo, EPI/spiral) stated? | N/A |
| b. Are the field-of-view, matrix size, slice thickness, and TE/TR/ flip angle clearly stated? | N/A |
| 10. Are the software and specific parameters (model/functions, smoothing kernel size if applicable, etc.) used for data processing and pre-processing clearly stated? | N/A |
| 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 #)? | N/A |
| 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 #)? | N/A |
| 13. How were anatomical locations determined, e.g., via an automated labeling algorithm (AAL), standardized coordinate database (Talairach daemon), probabilistic atlases, etc.? | N/A |
| 14. Were any additional regressors (behavioral covariates, motion etc) used? | N/A |
| 15. Is the contrast construction clearly defined? | N/A |
| 16. Is a mixed/random effects or fixed inference used? | N/A |
| a. If fixed effects inference used, is this justified? | N/A |
| 17. Were repeated measures used (multiple measurements per subject)? | N/A |

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|---|---|
| a. If so, are the method to account for within subject correlation and the assumptions made about variance clearly stated? | N/A |
| 18. If the threshold used for inference and visualization in figures varies, is this clearly stated? | N/A |
| 19. Are statistical inferences corrected for multiple comparisons? | N/A |
| a. If not, is this labeled as uncorrected? | N/A |
| 20. Are the results based on an ROI (region of interest) analysis? | N/A |
| 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

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|---|---|
| Additional Comments | |