

Corresponding Author: Mark Nelson

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Main Figures: 5

Supplementary Figures: 13

Supplementary Tables: 2

Supplementary Videos: 3

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 | |
| + - 1f | unpaired t-test | fig legend | 8, 7 | cells from 8 and 7 mice | Fig legend | error bars are mean +/- SEM | Meth ods | 0.0005 | Fig legend | t = 4.587 df = 13 | Fig legend | |

| | | 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 # | |
| + - | 1i | unpaired t-test | fig legend | 5, 6 | cells from 3 and 4 mice | fig legend | error bars are mean +/- SEM | Meth ods page 25 | Fig legend | 0.0253 | t=2.678 df=9 | Fig legend |
| + - | 1i | unpaired t-test | fig legend | 7, 5 | cells from 2 and 4 mice | fig legend | error bars are mean +/- SEM | Meth ods | Fig legend | 0.0011 | t=4.548 df=10 | Fig legend |
| + - | 1i | one-way ANOVA | fig legend | 5, 7, 5 | cells from 3, 2 and 2 mice | fig legend | error bars are mean +/- SEM | Meth ods | Fig legend | 0.251 | F (DFn, DFd) = 1.528 (2, 14) | Fig legend |
| + - | 2f | one-way ANOVA | fig legend | 6, 6, 5 | experiments from 6, 6, and 5 mice | fig legend | error bars are mean +/- SEM | Meth ods | Fig legend | < 0.0001 | F (DFn, DFd) = 154.8 (2, 14) | Fig legend |
| + - | 2h | paired t-test | fig legend | 5 | experiments from 5 mice | fig legend | error bars are mean +/- SEM | Meth ods | Fig legend | 0.0002 | t=12.94 df=4 | Fig legend |
| + - | 2j | paired t-test | fig legend | 6 | experiments from 6 mice | fig legend | error bars are mean +/- SEM | Meth ods | Fig legend | 0.1128, 0.4984, 0.3908, 0.2580 | t=1.921 df=5, t=0.7296 df=5, t=0.9390 df=5, t=1.276 df=5 | Fig legend |
| + - | 3g | paired t-test | fig legend | 11 | experiments, 11 mice | fig legend | error bars are mean +/- SEM | Meth ods | Fig legend | 0.0038 | t=3.75 df=10 | Fig legend |
| + - | 3h | paired t-test | fig legend | 9 | experiments, 9 mice | fig legend | error bars are mean +/- SEM | Meth ods | Fig legend | 0.8265 | t=0.2265 df=8 | Fig legend |
| + - | 3i | paired t-test | fig legend | 6 | experiments, 6 mice | fig legend | error bars are mean +/- SEM | Meth ods | Fig legend | >0.9999 | t=0 df=5 | Fig legend |
| + - | 3j | one-way ANOVA | fig legend | 11, 9, 6 | experiments from 11, 9 and 6 mice | fig legend | error bars are mean +/- SEM | Meth ods | Fig legend | 0.0160 | F (DFn, DFd) = 4.974 (2,23) | Fig legend |
| + - | 4d | paired t-test | fig legend | 8 | experiments from 7 mice | fig legend | error bars are mean +/- SEM | Meth ods | Fig legend | <0.0001 | t=10.86 df=7 | Fig legend |
| + - | 4e | paired t-test | fig legend | 18 | capillaries from 7 mice | fig legend | error bars are mean +/- SEM | Meth ods | Fig legend | 0.6014 | t=0.5324 df=17 | Fig legend |
| + - | 5a | Two-way ANOVA | fig legend | 6, 5 | experiments from 6 and 5 mice | fig legend | error bars are mean +/- SEM | Meth ods | Fig legend | <0.0001 | q = 9.033 DF = 18 | Fig legend |
| + - | 5c | Two-way ANOVA | fig legend | 7, 6 | experiments from 7 and 6 mice | fig legend | error bars are mean +/- SEM | Meth ods | Fig legend | <0.0001 | q = 14.3 DF = 22 | Fig legend |
| + - | s1 | unpaired t test | fig legend | 5,6 | capillaries from 5 and 6 mice | fig legend | error bars are mean +/- SEM | Meth ods | Fig legend | 0.0108 | t=3.204 df=9 | Fig legend |
| + - | s2c | unpaired t test | fig legend | 14, 14 | cells from 3 and 4 mice | fig legend | error bars are mean +/- SEM | Meth ods | Fig legend | 0.5176 | t=0.6564 df=25 | Fig legend |
| + - | s2d | unpaired t test | fig legend | 14, 14 | cells from 3 and 4 mice | fig legend | error bars are mean +/- SEM | Meth ods | Fig legend | 0.2002 | t=1.316 df=25 | Fig legend |
| + - | s4b | paired t test | fig legend | 7 | experiments from 7 mice | fig legend | error bars are mean +/- SEM | Meth ods | Fig legend | 0.7549 | t=0.3268 df=6 | Fig legend |
| + - | s4b | paired t test | fig legend | 7 | experiments from 7 mice | fig legend | error bars are mean +/- SEM | Meth ods | Fig legend | 0.5995 | t=0.5542 df=6 | Fig legend |
| + - | s4b | paired t test | fig legend | 7 | experiments from 7 mice | fig legend | error bars are mean +/- SEM | Meth ods | Fig legend | 0.2616 | t=1.239 df=6 | Fig legend |
| + - | s4b | paired t test | fig legend | 7 | experiments from 7 mice | fig legend | error bars are mean +/- SEM | Meth ods | Fig legend | 0.7666 | t=0.3107 df=6 | Fig legend |
| + - | s7b | unpaired t test | fig legend | 7, 8 | experiments from 7, and 8 mice | fig legend | error bars are mean +/- SEM | Meth ods | Fig legend | 0.2580 | t=1.183 df=13 | Fig legend |
| + - | s7b | unpaired t test | fig legend | 7, 8 | experiments from 7, and 8 mice | fig legend | error bars are mean +/- SEM | Meth ods | Fig legend | 0.7969 | t=0.2627 df=13 | Fig legend |

| | | | | | | | | | | | | |
|--------|------|---------------|------------|------|-------------------------------|------------|-----------------------------|----------|---------|------------|-------------------|------------|
| + - | s9e | paired t test | fig legend | 11 | experiments from 11 mice | fig legend | error bars are mean +/- SEM | Meth ods | 0.0004 | Fig legend | t=5.244 df=10 | Fig legend |
| + - | s9f | paired t test | fig legend | 9 | experiments from 9 mice | fig legend | error bars are mean +/- SEM | Meth ods | 0.8800 | Fig legend | t=0.1558 df=8 | Fig legend |
| + - | s9g | paired t test | fig legend | 6 | experiments from 6 mice | fig legend | error bars are mean +/- SEM | Meth ods | 0.4367 | Fig legend | t=0.8448 df=5 | Fig legend |
| + - | s10c | paired t test | fig legend | 6 | experiments from 6 mice | fig legend | error bars are mean +/- SEM | Meth ods | 0.5464 | Fig legend | t=0.6466 df=5 | Fig legend |
| + - | s10d | paired t test | fig legend | 6 | experiments from 6 mice | fig legend | error bars are mean +/- SEM | Meth ods | 0.9199 | Fig legend | t=0.1057 df=5 | Fig legend |
| + - | s11d | paired t test | fig legend | 5 | experiments from 5 mice | fig legend | error bars are mean +/- SEM | Meth ods | 0.0354 | Fig legend | t=3.123 df=4 | Fig legend |
| + - | 5a | Two-way ANOVA | fig legend | 6, 5 | experiments from 6 and 5 mice | fig legend | error bars are mean +/- SEM | Meth ods | 0.0083 | Fig legend | q = 5.214 DF = 18 | Fig legend |
| + - | 5a | Two-way ANOVA | fig legend | 6, 5 | experiments from 6 and 5 mice | fig legend | error bars are mean +/- SEM | Meth ods | 0.0187 | Fig legend | q = 4.676 DF = 18 | Fig legend |
| + - | 5c | Two-way ANOVA | fig legend | 7, 6 | experiments from 7 and 6 mice | fig legend | error bars are mean +/- SEM | Meth ods | <0.0001 | Fig legend | q = 8.396 DF = 22 | Fig legend |
| + - | 5c | Two-way ANOVA | fig legend | 7, 6 | experiments from 7 and 6 mice | fig legend | error bars are mean +/- SEM | Meth ods | 0.0238 | Fig legend | q = 4.413 DF = 22 | Fig legend |
| + - | s12g | paired t test | fig legend | 5 | experiments from 5 mice | fig legend | error bars are mean +/- SEM | Meth ods | 0.5627 | Fig legend | t=0.6303 df=4 | Fig legend |
| + - | s12h | paired t test | fig legend | 5 | experiments from 5 mice | fig legend | error bars are mean +/- SEM | Meth ods | 0.1202 | Fig legend | t=1.969 df=4 | Fig legend |
| + - | s5b | paired t test | fig legend | 5 | experiments from 5 mice | fig legend | error bars are mean +/- SEM | Meth ods | 0.0005 | Fig legend | t=10.48 df=4 | Fig legend |
| + - | s5b | paired t test | fig legend | 5 | experiments from 5 mice | fig legend | error bars are mean +/- SEM | Meth ods | 0.0385 | Fig legend | t=3.038 df=4 | Fig legend |
| + - | s5b | paired t test | fig legend | 5 | experiments from 5 mice | fig legend | error bars are mean +/- SEM | Meth ods | 0.0330 | Fig legend | t=3.196 df=4 | Fig legend |
| + - | s5b | paired t test | fig legend | 5 | experiments from 5 mice | fig legend | error bars are mean +/- SEM | Meth ods | 0.0538 | Fig legend | t=2.706 df=4 | Fig legend |
| + - | s12e | paired t test | fig legend | 5 | experiments from 5 mice | fig legend | error bars are mean +/- SEM | Meth ods | 0.3778 | Fig legend | t=0.991 df=4 | Fig legend |
| + - | s12f | paired t test | fig legend | 5 | experiments from 5 mice | fig legend | error bars are mean +/- SEM | Meth ods | 0.4804 | Fig legend | t=0.7773 df=4 | Fig legend |
| + - | s12i | paired t test | fig legend | 5 | experiments from 5 mice | fig legend | error bars are mean +/- SEM | Meth ods | 0.7554 | Fig legend | t=0.3337 df=4 | Fig legend |
| + - | s12j | paired t test | fig legend | 4 | experiments from 4 mice | fig legend | error bars are mean +/- SEM | Meth ods | 0.9096 | Fig legend | t=0.1233 df=3 | Fig legend |

► Representative figures

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

If so, what figure(s)?

F1, F2, F3, F4, F5, S2, S3, S4, S5, S6, S7, S8, S9, S10, S11, S12

- 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 #)?

Yes. All data on experimental repetitions is provided in figure legends and discussed in the online methods 'Statistics' section.

► 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 sample size calculation was performed. Our approach is justified in the online methods 'Statistics' section.

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

Where (section, paragraph #)?

Yes. Statistical tests are noted in the figure legends and justified in the online methods 'Statistics' section.

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

Yes. Statistical tests are noted in the figure legends and discussed in the online methods 'Statistics' section.

- 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 online methods 'Statistics' section.

- 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, standard error of the mean was used. Described in online methods 'Statistics' section.

Variance is similar between all groups, as evidenced in the error bars presented with all summary data in each Figure.

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

Yes. Described in online methods 'Statistics' section.

- e. Are there adjustments for multiple comparisons?

Yes, described in the post-hoc tests noted in the figure legends.

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.

To conform to this requirement, we have presented all data individual data points collected in dot plots (with a connecting line where appropriate for paired experiments), along with mean and standard error in summary data.

4. Are criteria for excluding data points reported?

Was this criterion established prior to data collection?

Where is this described (section, paragraph #)?

No exclusions were made.

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 #)?

Randomization was not necessary.

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 #)?
- Blinding was not performed. This is stated in the online methods 'Statistics' section.
7. For experiments in live vertebrates, is a statement of compliance with ethical guidelines/regulations included?
Where (section, paragraph #)?
- Yes. Online methods 'Animal Husbandry' section.
8. Is the species of the animals used reported?
Where (section, paragraph #)?
- Yes. Online methods 'Animal Husbandry' section.
9. Is the strain of the animals (including background strains of KO/transgenic animals used) reported?
Where (section, paragraph #)?
- Yes. Online methods 'Animal Husbandry' and 'Generation of EC Kir2.1-/- mice' sections.
10. Is the sex of the animals/subjects used reported?
Where (section, paragraph #)?
- Yes. Online methods 'Animal Husbandry' section.
11. Is the age of the animals/subjects reported?
Where (section, paragraph #)?
- Yes. Online methods 'Animal Husbandry' section.
12. For animals housed in a vivarium, is the light/dark cycle reported?
Where (section, paragraph #)?
- Yes. Online methods 'Animal Husbandry' section.
13. For animals housed in a vivarium, is the housing group (i.e. number of animals per cage) reported?
Where (section, paragraph #)?
- Yes. Group housing was used and this is noted in the online methods 'Animal Husbandry' section.
14. For behavioral experiments, is the time of day reported (e.g. light or dark cycle)?
Where (section, paragraph #)?
- Not applicable.
15. Is the previous history of the animals/subjects (e.g. prior drug administration, surgery, behavioral testing) reported?
Where (section, paragraph #)?
- Not applicable.
- a. If multiple behavioral tests were conducted in the same group of animals, is this reported?
Where (section, paragraph #)?
- Not applicable.
16. If any animals/subjects were excluded from analysis, is this reported?
Where (section, paragraph #)?
- No exclusions were made.

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)?

Antibodies were not used.

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

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 #)?

Cell lines were not 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.

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 availability

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:

- 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.

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

Data availability statements are present in the online methods under the heading '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.

Not applicable.

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.

Not applicable.

► 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 #)?
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.

- 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