***eLife’s* transparent reporting form**

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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
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* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

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This information can be found in the figures and legends.

**Replicates**

* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
* The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
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* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

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All experiments were performed at least twice with appropriate sample sizes. Replicates of in vivo experiments are reported as the number of mice. This part of information can be found in the section of ’Mice’ in ‘Methods’. Replicates of *in vitro* experiments are reported in Methods. For Ca2+ imaging in cultured cortical neurons, the representative experiment is shown in the main figure, and other replicates are shown in the supplementary figures when necessary.

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* Statistical analysis methods should be described and justified
* Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
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* Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

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Statistical analysis methods and statistical details can be found in each figure legend and section of ‘Data analysis and statistics’ in Methods. Raw data are presented as scatter plot graphs when possible. Criteria of significance: \* *p*<0.05, \*\* *p*<0.01, \*\*\* *p*<0.001, were calculated when applicable, and most of the key questions were based on *p*<0.01 (\*\*) or *p*<0.001 (\*\*\*).

(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

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Source data associated with Figures 1-7 have been uploaded to Dryad.