***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
* You should state the statistical method of sample size computation and any required assumptions
* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

Power calculations for the number of animals and cell collected for in vitro electrophysiology were performed as part of the initial experimental design as required by UK Home Office project license (Methods) and our funders: MRC (MR/K004387/1) and BBSRC (BB/P003796/1). Our power analysis assumes normal data, 2 sided t-test, significance level of 5%, statistical power 80-90% and an effect size derived from previous experiments (e.g. LSPS mapping of GABAergic input in neonates: d, 8.26; r, 0.97 for P10-15; Cohen 1988), plus an estimate of standard deviation from previous data. Such analysis return minimum sample sizes for experiments of 6 – 14 recordings. This information is not included at present in the manuscript.

**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
* If you encountered any outliers, you should describe how these were handled
* Criteria for exclusion/inclusion of data should be clearly stated
* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

The number of replicates obtained for each experiments are reported in the main text and/or figure legends:

Figure 1: figure legend;

Figure 2: main text and figure legend

Figure 3: main text and above panels 3c-h;

Figure 4: counts are reported in the main text and figure legend.

Figure 5 replicates (n-numbers) are clearly reported alongside the data in panel 5c-h and in the main text lines;

Figure 6: main text and panels 6e,f.

Figure 7: the number of replicates is reported in the text.

A statement of biological versus technical replication is not included as data is obtained from individual mice as identified (material and methods).

All data were included in the analysis, see for example figure 1d-i.

**Statistical reporting**

* 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)
* For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
* 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.

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

Statistical analysis methods are reported in the methods

Further details are provided for individual tests:

Figure 1, ANOVA and Kruskal-Wallis tests reported in legend.

Figure 2c, Mann-Whitney test reported in legend.

Figure 4, 2-tailed t-tests reported in legend.

Figure 6c, Kolmogorov-Smirnov test is reported in legend.

Figure 7c, two-tailed t-test outcome is reported in main text.

Figure 7e, K-means cluster analysis reported in legend.

(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.)

**Group allocation**

* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
* Indicate if masking was used during group allocation, data collection and/or data analysis

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

Samples were not allocated to groups. *Post hoc* analysis revealed the presence of two distinct subplate population as discussed in the main text.

**Additional data files (“source data”)**

* We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* Include model definition files including the full list of parameters used
* Include code used for data analysis (e.g., R, MatLab)
* Avoid stating that data files are “available upon request”

Please indicate the figures or tables for which source data files have been provided:

Data files and analysis will be released via the University of Oxford research database (ora.ox.ac.uk) in line with University and funder open access policies.

The customized Matlab script for data analysis of optogenetic experiments will be release via Github.