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* You should state whether an appropriate sample size was computed when the study was being designed
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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:

We present proof-of-concept validation of our analysis pipeline based on previously published sample size. The relevant information can be found in main text where figures 15-20 are described.

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* You should report how often each experiment was performed
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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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The focus of this manuscript is to describe analysis pipeline, so we only present proof-of-concept validation and so biological replication is not applicable. There are no explicit exclusion criteria of the data/subject used for validation. The inclusion criteria of place cells can be found in main text.

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* Statistical analysis methods should be described and justified
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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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To validate extracted neural activities and cross-session cell registration of the presented pipeline, we generated all the null distributions by either shuffling extracted neural activities or cell mappings. All p-values reported in the submission are based on these bootstrap distributions. The relevant details can be found in main text.

(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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* 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
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There are no experimental groups used in this manuscript.

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

The source data for all validation figures (15-20) are uploaded alongside this submission.

In addition, all the code used to generate figures in the submission can be found on github. The repo for figure 1-14 and figure 20 can be found at <https://github.com/denisecailab/minian_paper_data>. The repo for figure 15-19 can be found at <https://github.com/denisecailab/minian-validation>.

All the source data (raw recordings) are downloadable through Figshare at <https://doi.org/10.6084/m9.figshare.c.5987038.v1>.

We have also included convenient scripts in github repo to automatically download necessary data and reproduce folder structure.