**eLife’s transparent reporting form**

We encourage authors to provide detailed information *within their submission* to facilitate the interpretation and replication of experiments. Authors can upload supporting documentation to indicate the use of appropriate reporting guidelines for health-related research (see [EQUATOR Network](http://www.equator-network.org)), life science research (see the [BioSharing Information Resource](http://www.biosharingsoftware.org)), or the [ARRIVE guidelines](http://www.arriveguidelines.org) for reporting work involving animal research. Where applicable, authors should refer to any relevant reporting standards documents in this form.

If you have any questions, please consult our Journal Policies and/or contact us: editorial@elifesciences.org.

**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:

> Our study focuses on fluorescence signals obtained in vivo, from awake, behaving mice performing a novel task. As such, the distribution of data (response magnitudes) was not known before, therefore precise estimation of sample size was not possible. However, response measurements from a total of 353 neurons (5 mice) should constitute a reasonable sample size, for example in the estimation of proportion (proportion of neurons that were modulated), according to Dell, Holleran and Ramakrishnan (2002), ILAR J, 43(4):207.

**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:
Information about replicates can be found at the following locations:

Main text:
Page 2, line 26
Page 2, line 46
Page 3, line 16
Page 3, line 18-19
Page 3, line 24-25

Figure legends:
Figure 1 b,c,e,g
Figure 2 e,f,g
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:

Statistics with appropriate sample size declarations and test statistics are reported in the following locations:
Page 2, lines 44-46
Page 2, line 47 – page 3, line 1
Page 3, lines 14-17
Page 3, lines 19-20
Page 3, lines 23-25

(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:

Most comparisons were within session and within animals.

In the supplementary figure 5, we split the analysis according to the behavioural performance. In this case, the definitions of our groups are clearly indicated by the behavioural performance measure displayed in the figure (Supp fig. 5d)

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:
