***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/%20)), life science research (see the [BioSharing Information Resource](https://biosharing.org/%22%20%5Ct%20%22_blank)), or the [ARRIVE guidelines](http://www.plosbiology.org/article/info%3Adoi/10.1371/journal.pbio.1000412) for reporting work involving animal research. Where applicable, authors should refer to any relevant reporting standards documents in this 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:

In non-human primate research, it is a common standard to use 2 animals. We recorded 535 neurons in total from 2 monkeys, 292 in monkey A and 243 in monkey B. This information can be found in ‘Single-cell mapping of curve and corner selective neurons reveals they are spatially clustered’ section.

**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:

In the experiments, each visual stimulus was repeated for multiple times, depending on how long the animals can keep performing. For 4x imaging, n = 18 for monkey A and n = 10 for monkey B. (see ‘Cortical mapping of curve-biased and corner-biased regions in V4’ section). For 16x imaging and contour feature stimuli, n = 10 for both monkeys (see ‘Single-cell mapping of curve and corner selective neurons reveals they are spatially clustered’ section). For 16x imaging and grating stimuli, n = 11 for monkey A and n = 8 for monkey B. No data is excluded in the analysis.

**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:

One-way ANOVA tests were performed to compare cortical responses (see ‘Cortical mapping of curve-biased and corner-biased regions in V4’ and ‘Curve and corner domains’ in the method section), as well as single neuron responses (see ‘Single-cell mapping of curve and corner selective neurons reveals they are spatially clustered’). Bonferroni correction was applied whenever multiple comparisons are made. Pearson correlations were given in Figure 3-5.

(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:

No apriori allocation of neurons was applied. In Figure 3, neurons were grouped according to their spatial locations (inside or outside the curve/corner domains which were determined by 4x imaging). In Figure S4, neurons were grouped according to the results of K-Means clustering.

**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 and code in this study can be found in Github (https://github.com/RJiang1994/macaque-v4-2P).