

Reporting Summary

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Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. figure legend, table legend, main text, or Methods section).

n/a Confirmed

- The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
- An indication of whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- The statistical test(s) used AND whether they are one- or two-sided
Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- A description of all covariates tested
- A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- A full description of the statistics including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
Give P values as exact values whenever suitable.
- For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated
- Clearly defined error bars
State explicitly what error bars represent (e.g. SD, SE, CI)

Our web collection on [statistics for biologists](#) may be useful.

Software and code

Policy information about [availability of computer code](#)

Data collection

We used the "Coherence Software" from Neurolite to detect orofacial movements in the digital audio and video recordings and to mark the timepoints of the respective event onset in the synchronously recorded ECoG.

Data analysis

For data pre-processing and data analysis we used Matlab (version 2017a) and the anatomy toolbox version 18 of SPM8. For the hierarchical anatomical assignment of electrode contacts to cortical brain areas we used a custom Matlab-based algorithm. Custom code is available from the corresponding author upon request.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

No unique materials were used.

Field-specific reporting

Please select the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

Life sciences Behavioural & social sciences Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/authors/policies/ReportingSummary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size

Since we used data from non-experimental behavior, the sample size of each orofacial movement class was determined by the amount of suitable events from the respective participant. Participants were patients undergoing evaluation for epilepsy surgery and thus, we could only use data from patients with grid electrode contacts over the mouth motor cortex in the time window of evaluation. We think that the sample sizes are sufficient for the kind of analysis we did, especially since we adapted our methods to address the issue of possible small sample sizes.

Data exclusions

We excluded orofacial movements accompanied by clear movements of other body parts or, in the case of the nonspeech events by speaking in the time period from two seconds before to two seconds after movement onset from the analysis to avoid influences of confounding movement-, or speech-related brain activity.
We also excluded one electrode contact in P1 from the further analysis. At this electrode contact lips motor responses were observed during ESM, but this contact was located close to the midline remote from all other precentral mouth motor responses. At this contact, no significant brain activity was recorded during any orofacial movement class investigated. We assume that this contact covers another anatomical area, possibly the supplementary motor area, and thus, we dropped it from the following analyses.

Replication

Our basic findings were reproducible across all six investigated participants.

Randomization

Since we used orofacial movements-related ECoG data during non-experimental, real-life conditions, no randomization was used. Orofacial movements within each investigated participant were arranged chronologically in their order of appearance in the ongoing ECoG recordings.

Blinding

Since we did not allocate patients to different groups, no blinding was necessary.

Reporting for specific materials, systems and methods

Materials & experimental systems

- | | |
|-------------------------------------|---|
| n/a | Involvement in the study |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Unique biological materials |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Antibodies |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Eukaryotic cell lines |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Palaeontology |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Animals and other organisms |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> Human research participants |

Methods

- | | |
|-------------------------------------|---|
| n/a | Involvement in the study |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> ChIP-seq |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Flow cytometry |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> MRI-based neuroimaging |

Human research participants

Policy information about [studies involving human research participants](#)

Population characteristics

We analyzed ECoG data of 6 participants (4 male, 2 female), aged between 22 and 57, who were diagnosed with pharmaco-resistant epilepsy and thus, were undergoing pre-neurosurgical evaluation with ECoG. The ESM-defined mouth motor cortex on

the left hemisphere was at least partially covered in all participants investigated. The seizure onset zone was located outside of the investigated mouth motor cortex in all participants, except in P4 where one electrode contact was located within the seizure onset zone, but did not show any movement-related effect.

Recruitment

We collected all data retrospectively with the help of digital audio and video data after the neurosurgical procedures were completed. Thus, we have chosen participants whose mouth motor cortex was at least partially covered by an electrode grid due to the pre-surgical diagnosis. We have no information about the genotype or the current diagnosis of these participants. Participant details are provided in Supplementary Table 1.