nature portfolio

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Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our Editorial Policies and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the 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
☐	☒	A statement on 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 statistical parameters 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

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	All data were collected as JSON Session Format from Medtronic clinical tablet (Samsung). All JSON files were processed and stored with the Brain Recording Visualization and Analysis Online (BRAVO) Platform developed by University of Florida (Cagle et. al., 2023).
Data analysis	Data were analyzed in Python 3.10 on Windows 10 Desktop. All analysis scripts were custom made.

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 and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio 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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

All data can be made available via reasonable request to the data owner at University of Florida INFORM Database. Original JSON files containing Protect Health Information and additional recordings not specific to the published data may not be made available at the time, but minimally cleaned data specific to the results published can be made available.

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	The results were reported on both sex (biological attribute). The sex and gender were not part of the inclusion nor exclusion criteria for the study. The sex was reported by the patient as part of the clinical chart documentation. There were no sex/ gender based analysis because we intend to describe the circadian rhythm in a population level comparison between neural targets. There were no difference between proportion of male/female in either of the basal ganglia target for DBS, therefore, we did not analyze the difference between sex.
Reporting on race, ethnicity, or other socially relevant groupings	We did not use race, ethnicity, or other socially relevant grouping information for the proposed study.
Population characteristics	All patients recruited in the study consisted of patients with Parkinson's disease who underwent deep brain stimulation therapy.
Recruitment	This retrospective study was performed at the Norman Fixel Institute for Neurological Diseases at the University of Florida (UF). All subjects included (119) provided informed consent, in accordance with the Declaration of Helsinki, to participate in the UF INFORM Database, a clinical-research database that hosts subjects' clinical records and neural recordings. The study was approved by UF Institutional Review Board (IRB) to request and process data from UF INFORM Database. The inclusion criteria were individuals diagnosed with PD by a movement disorders-trained neurologist and who received DBS therapy with the sensing-enabled Medtronic Percept PC neurostimulator with unilateral or bilateral electrode implanted in the GPi or STN.
Ethics oversight	University of Florida Institutional Review Board, and University of Florida INFORM Database Committee.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is 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/documents/nr-reporting-summary-flat.pdf

Life sciences study design

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

Sample size	The total sample size for the study included 165 unique hemispherical recordings from 119 unique patients. As a retrospective study, we requested all data collected at University of Florida since the use of Medtronic Percept neurostimulator.
Data exclusions	We did not exclude any patients from our initial sample size of 119 who received DBS therapy with the sensing-enabled Medtronic Percept PC neurostimulator with unilateral or bilateral electrode implanted in the GPi or STN.
Replication	The process of circadian rhythm identification is replicated within the database. The group-level results and analysis were not replicated due to the requirement of accessing other center's DBS database.
Randomization	There is no randomization in this study because it is a retrospective observational study.
Blinding	The researchers were not blinded because it is not an interventional study.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒ ☐	Antibodies
☒ ☐	Eukaryotic cell lines
☒ ☐	Palaeontology and archaeology
☒ ☐	Animals and other organisms
☒ ☐	Clinical data
☒ ☐	Dual use research of concern
☒ ☐	Plants

Methods

n/a	Involved in the study
☒ ☐	ChIP-seq
☒ ☐	Flow cytometry
☒ ☐	MRI-based neuroimaging

Plants

Seed stocks	*Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.*
Novel plant genotypes	*Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.*
Authentication	*Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.*