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	no software was used.
Data analysis	Guppy v2.0, seqtk v1.2, WTDBG2 v2.2, minimap2 v0.2, Racon v1.3.1, Pilon v1.18, Purge Haplotigs v1.0.0, bwa mem v0.7.17, SAMtools v1.3, Juicer v1.6, 3D-DNA v170123, fastp v0.20.0, TransDecoder v5.5.0, CDSKIT v0.9.1, RepeatMasker v4.0.9, RepeatModeler v2.0, EDTA v2.1.0, pyGenomeTracks v3.6, StainedGlass v0.4, HiGlass v0.10.1, StringTie v2.1.4, HiSat2 v2.1.0, Trinity v2.8.5, TransAbyss v2.0.1, EvidentialGene v2022.01.20, PASA v2.3.3, GeneMark-ES v4.65, Braker v2.1.2, STAR v2.7.2b, Augustus v3.3.2, GeMoMa v1.6.1, EVidenceModeler v1.1.1, BUSCO v5.3.2, Trinotate v3.2.1, SignalP v4.1, TMHMM v2.0c, RPS-BLAST v2.9.0, JCVI v1.2.7, WGDdetector v1.1, bwa mem v0.7.17-r1188, SAMtools v1.12, bedtools v2.30.0, KMC v3.1.0, AMALGKIT v0.6.8.0, kallisto v0.48.0, edgeR v3.36.0, SeqKit v2.3.1, MEME Suite v5.4.1, MAFFT v7.475, ClipKIT v1.3.0, CDSKIT v0.10.2, IQ-TREE v2.2.0.3, ASTRAL v.5.7.3, catfasta2phyml v2018-09-28, NWKIT v0.11.2, MCMCTREE in PAML v4.9, OrthoFinder v2.5.4, GeneRax v2.0.4, RADTE v0.2.0, mapnh v2, CSUBST v.1.1.0, ggtree v3.2.0, matplotlib v3.6.1, seaborn v0.12.0, ggplot2 v3.3.5, Open-Source PyMOL v2.4.0, SubPhaser v1.2.5, Custom codes available at https://doi.org/10.5061/dryad.xsj3tx9mj

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](#)

Raw data and results are available at Dryad (https://doi.org/10.5061/dryad.xsj3tx9mj). The N. gracilis genome assembly and gene models are available from the DNA Data Bank of Japan (DDBJ) with the accession numbers BSYO01000001 to BSYO01000176 The N. gracilis genome assemblies are also available on CoGe (https://genomevolution.org/coge/) (genome ID: male assembly, 61566; female Hi-C assembly, 61892; female syntenic path assembly, 61931) and Dryad (https://doi.org/10.5061/dryad.xsj3tx9mj). DNA and mRNA sequencing reads were deposited to DDBJ (PRJDB15224, PRJDB15738, PRJDB15742, and PRJDB15737) and EBI (PRJEB20488), and the accession numbers are shown in Supplementary Table 1 and Supplementary Table 4. In this study, data were sourced from the following publicly accessible databases: DDBJ (https://www.ddbj.nig.ac.jp/index-e.html), JASPAR (https://jaspar.genereg.net/), NCBI (https://www.ncbi.nlm.nih.gov/), OrthoDB (https://www.orthodb.org/), Pfam (https://www.ebi.ac.uk/interpro/), and UniProt (https://www.uniprot.org/).

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	N/A
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	N/A
Recruitment	N/A
Ethics oversight	N/A

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	Differential expression analysis of RNA-seq data was performed with triplicate samples (or more) to meet the accepted standards in the field (Conesa et al., 2016, https://doi.org/10.1186/s13059-016-0881-8).
Data exclusions	In the heterologous RNA-seq mapping analysis of flower samples, one sample (DRR461757) was excluded from the analysis due to its low mapping rate of 4.7% (see Supplementary Table 4).
Replication	A single RNA-seq experiment was performed for each analysis, and it included a minimum of three biological replicates.
Randomization	In the feeding experiments, individuals of Nepenthes gracilis were randomly assigned to either the control group or the feeding treatment group. In the flower RNA-seq experiments, no randomization was performed because we collected all available flowers that were spontaneously produced by cultivated plants.
Blinding	Blinding was not implemented in this study due to the nature of the interventions and the logistical constraints involved in executing them.

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

Dual use research of concern

Policy information about dual use research of concern

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

No	Yes	
☒	☐	Public health
☒	☐	National security
☒	☐	Crops and/or livestock
☒	☐	Ecosystems
☒	☐	Any other significant area

Experiments of concern

Does the work involve any of these experiments of concern:

No	Yes	
☒	☐	Demonstrate how to render a vaccine ineffective
☒	☐	Confer resistance to therapeutically useful antibiotics or antiviral agents
☒	☐	Enhance the virulence of a pathogen or render a nonpathogen virulent
☒	☐	Increase transmissibility of a pathogen
☒	☐	Alter the host range of a pathogen
☒	☐	Enable evasion of diagnostic/detection modalities
☒	☐	Enable the weaponization of a biological agent or toxin
☒	☐	Any other potentially harmful combination of experiments and agents