

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 (<i>n</i>) 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 <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
☒	☐ 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
☒	☐ 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 <i>d</i> , Pearson's <i>r</i>), 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 for data collection
Data analysis	Software and algorithms used in this study: FASTQC v0.11.8 – quality control of sequencing reads, Trimmomatic v0.39 – read trimming, STAR v2.7.11a – read alignment, FeatureCounts v2.0.1 – read quantification, DESeq2 v2.11.40.8 – differential expression analysis, Blast2GO v6.0.3 – functional annotation, CD-HIT v4.8.1 – sequence clustering, deepTools v3.2.1 (bamCoverage) – coverage visualization, Bedtools v2.31.0 (getfasta) – genomic interval extraction, MEME Suite v5.5.8 – motif discovery, Circos v0.69.8 – genome visualization, HMMER v3.3.2 (jackhmmer, hmmscan) – HMM-based searches, BLASTp v2.10.1 – protein sequence similarity searches, Pfam-A database – protein family annotation, AlphaFold3 server – structural prediction, ChimeraX v1.8 – structural visualization, MAFFT v7 – multiple sequence alignment, OrthoFinder v2.5.5 – orthology inference, R v4.3.2 (RStudio) – statistical analyses, Python 3.10 including NumPy v1.26.3, Pandas v2.2.0, Matplotlib v3.8.3, Seaborn v0.13.2. Custom code developed to process and handle the data was created specifically for this study and is available on GitHub (https://doi.org/10.5281/zenodo.17662492).

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](#)

The raw sequence data that support the findings of this study have been submitted to the Gene Expression Omnibus (GEO) under the accession number GSE293402. Source data are provided with this paper.

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	Not applicable because the study does not involve human, vertebrate animals, or cell lines
Reporting on race, ethnicity, or other socially relevant groupings	Not applicable because the study does not involve human, vertebrate animals, or cell lines
Population characteristics	Not applicable because the study does not involve human, vertebrate animals, or cell lines
Recruitment	Not applicable because the study does not involve human, vertebrate animals, or cell lines
Ethics oversight	Not applicable because the study does not involve human, vertebrate animals, or cell lines

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](https://www.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	When conducting both phenotypic and genomic/transcriptomic analyses, we used the sample size following standard procedures from previous publications. Sample sizes were as large as practicable for observations of phenotypes. No statistical methods were used to predetermine sample sizes.
Data exclusions	No data was excluded for the analyses
Replication	RNA-seq samples were triplicated. For phenotypic analyses, samples were taken by replicates, and all attempts of replication were successful. Results are expressed by mean and SD.
Randomization	The experimental groups were allocated based on the genotype, using appropriate controls for each experiment. Within each experiment group, the samples was randomly selected for statistic analysis.
Blinding	Blinding during data collection was not relevant to most of the experiments conducted. Given that the investigators needed to be aware of both control and treated groups, blinding was not feasible.

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	Involvement 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	Involvement in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Plants

Seed stocks

The study did not involve plants

Novel plant genotypes

The study did not involve plants

Authentication

The study did not involve plants