

Reporting Summary

Nature Research 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 Research policies, see [Authors & Referees](#) 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
<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. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P 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 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 to collect data.
Data analysis	Genome assembly: soap (version 2.04), SPAdes (version 3.5.0), Redundans (version 0.12c), SMRT Analysis software (version 2.3), FALCON (version 3.0), Quiver (version 2.1.0), bwa (v0.7.12), SAMtools (not known) Gene annotation: Augustus (version 3.0), glimmer (version 3.0.3), snap (version 2013-11-29), scipio(not known), EVM (version 2012-06-25), BUSCO (version 3), RepeatMasker (version 4.0.7), dnaPipeTE (version 1.3). Orthologs/Phylogeny: OrthoFinder (version 1.1.4), agriGO (version 2.0), PartitionFinder (not known), RAxML (not known), ASTRAL (5.6.3), BEAST (2.5.1), Tracer (1.7.1) Misc: MCL (version 14-137), R library "e1071"(version 1.7-0), ImageJ (not known), R library "caper" (version 1.0.1), BS-Seeker2 (version 2.0.8)

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. 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

All sequencing data, assemblies and gene annotations generated in this project can be found in the European Nucleotide Archive under the project accession number PRJEB26555. We requested publishing of the data on June 11, 2019.

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	Sample size of the association mapping is 48. Small size was chosen as a pragmatic compromise between maximizing species number and feasibility. Simulations on such associations and the results of the association should that the size was sufficient for this study.
Data exclusions	No data was excluded from the study.
Replication	Replications were performed for the analysis of the DNA methylomes of 10 species. For each species the replication was highly successful.
Randomization	Samples were not selected randomly, but according to their phylogenetic placements. This has been taken care of in the association study by correcting for the expected covariation due to different relatedness.
Blinding	Blinding was not performed. The assessment of the phenotypes happens before the association. As the association are complex there is no chance to known on the influence of the assessed values. In this sense blinding was immanent in the experiment.

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

Methods

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

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