

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
<input type="checkbox"/>	<input checked="" type="checkbox"/> The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
<input type="checkbox"/>	<input checked="" type="checkbox"/> A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
<input type="checkbox"/>	<input checked="" type="checkbox"/> 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>
<input checked="" type="checkbox"/>	<input type="checkbox"/> A description of all covariates tested
<input type="checkbox"/>	<input checked="" type="checkbox"/> A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
<input type="checkbox"/>	<input checked="" type="checkbox"/> 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)
<input type="checkbox"/>	<input checked="" type="checkbox"/> 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>
<input checked="" type="checkbox"/>	<input type="checkbox"/> For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
<input checked="" type="checkbox"/>	<input type="checkbox"/> For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
<input type="checkbox"/>	<input checked="" type="checkbox"/> 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	The long reads for 16 RMAs were generated using Single Molecule Real Time (SMRT) sequencing technology with the Sequel II platform. The Hi-C data and RNA-seq data was generated on DNBSEQ-T7 platform.
Data analysis	Tools and software use in this study are Hifiasm (v0.16.1-r375); BUSCO (v5.4.3); LTR_retriever (v2.9.0); 3D-DNA (v170123); Juicerbox (v1.5.2); RepeatModeler (v2.0.3); RepeatMasker (v4.1.2); Trimmomatic (v0.38); HISAT2 (v2.1.0); Augustus (v3.4.0); GETA (v2.5.5); pbmm2 (v1.5.0); DeepVariant (v1.4.0); Whatshap (v1.1); MUMmer4 (v4.0.0rc1); bwa (v0.7.17); BLAST (v2.9.0+); minimap2 (v2.24-r1122); StringTie (v1.3.5); DESeq2 (v1.34.0); svim-asm (v1.0.2); DeepVariant (v1.4.0); BCFtools (v1.9); cuteSV (v1.0.13); Ngmlr (v0.2.7); sniffles (v1.0.12); pbsv (v2.8.0); svim-asm (v1.0.2); Assemblytics (v1.2.1); BEDtools (v2-2.25.0); vg (v1.38); LEA (v3.6.0); ADMIXTURE (v1.3.0); gradientForest (v0.1.34); vegan (v2.6.4); pyRona (v0.36); The customized codes used in this study have been deposited in GitHub [https://github.com/ZhaoGroupLab/moso-bamboo-pangenome] and Zenodo [https://doi.org/10.5281/zenodo.12794412].

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](#)

For the 427 resequenced accessions from our previous study, the sequencing data have been deposited in the National Center for Biotechnology Information (NCBI) Sequence Read Archive (SRA) under accession number PRJNA755164 [<https://www.ncbi.nlm.nih.gov/bioproject/PRJNA755164>] and the China National GenBank (CNGB) under accession number CNP0001535 [<https://db.cngb.org/search/project/CNP0001535>].

For the 16 representative moso bamboo accessions and 186 RNA-seq samples generated in this study, the sequencing data have been deposited in the Genome Sequence Archive (GSA) under accession numbers CRA014344 [<https://ngdc.cncb.ac.cn/gsa/browse/CRA014344>]. The reference genome used in this study are available in the GSA database under BioProject code PRJCA022610 [<https://ngdc.cncb.ac.cn/bioproject/browse/PRJCA022610>].

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	<input type="text" value="This study does not contain human data."/>
Reporting on race, ethnicity, or other socially relevant groupings	<input type="text" value="This study does not contain human data."/>
Population characteristics	<input type="text" value="This study does not contain human data."/>
Recruitment	<input type="text" value="This study does not contain human data."/>
Ethics oversight	<input type="text" value="This study does not contain human data."/>

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	<input type="text" value="We selected 16 representative moso bamboo accessions based on a previous phylogenetic study that identified 16 distinct geographic areas encompassing most of the species' range in China."/>
Data exclusions	<input type="text" value="No samples were excluded in this study, all 16 accessions were used in analysis. Some specific filter to low-quality sequencing were already described in the Methods section."/>
Replication	<input type="text" value="These samples were selected for DNA sequencing, Blinding is not necessary for sample collection. Three biological replicates for RNA-seq were used in ASE analyses."/>
Randomization	<input type="text" value="These samples were selected for DNA sequencing, Blinding is not necessary for sample collection."/>
Blinding	<input type="text" value="These samples were selected for DNA sequencing, Blinding is not necessary for sample collection."/>

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
<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 and archaeology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern
<input type="checkbox"/>	<input checked="" type="checkbox"/> Plants

Methods

n/a	Involvement
<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

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
<input checked="" type="checkbox"/>	<input type="checkbox"/> Public health
<input checked="" type="checkbox"/>	<input type="checkbox"/> National security
<input checked="" type="checkbox"/>	<input type="checkbox"/> Crops and/or livestock
<input checked="" type="checkbox"/>	<input type="checkbox"/> Ecosystems
<input checked="" type="checkbox"/>	<input type="checkbox"/> Any other significant area

Experiments of concern

Does the work involve any of these experiments of concern:

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

Plants

Seed stocks

All samples in this study were taken in the field. The location were already described in the supplementary.

Novel plant genotypes

not novel plant genotypes were produced.

Authentication

Not relevant to this study.