

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	Sequencing platforms used to generate the raw data are listed as followed: PacBio SMRT, Oxford Nanopore, Illumina HiSeq, NovaSeq.
Data analysis	The softwares used in this manuscript include Hifiasm v0.19.5-r587, RagTag v1.0.1, Juicer v1.5, 3D-DNA v201008, Juicebox v1.11.08, NextDenovo v2.5.0, Minimap2 v2.26, Integrative Genomics Viewer v2.13.1, BUSCOs v5.2.2, kmc v3.2.2, GenomeScope2.0 v1.0.0, Hisat2 v2.10.2, StringTie v1.3.0, Braker v3.0.2, PASA v2.5.1, MAKER v 3.01.03, AUGUSTUS v3.4.0, RepeatModeler v2.0.4, EDTA v2.0.1, RepeatMasker v4.1.2, TIDK v0.2.0, Tandem Repeats Finder v4.09, SyRI v1.6.3, Plotsr v1.0.0, Orthofinder v2.5.2, Minigraph-Cactus v2.6.11, PanGenome Graph Builder v0.5.4, SVIM-asm v1.0.3, Truvari v4.1.0, PanGenie v2.1.0, vg v1.51.0, GTX v2.2.1, PLINK v3.31, PopLDdecay v3.26, IQ-TREE v1.6.619, ADMIXTURE v1.3, phateR v1.0.7, selscan v2.0.0, vcftools v0.1.13, PermGWAS v2023.05, LDAK v5.2, LDpred2 v1.12.4, STAR v2.4.2, featureCounts v2.0.2, clusterProfiler v4.0, calc_switchErr v1.0, Yak v0.1, WhatShap v2.0, CD-HIT v4.8.1, PHATE v1.0.11, BWA v0.7.17, seqkit v2.2.0, odgi v0.8.4, vcfbub v0.1.0, bedtools v2.30.0, SAMtools v1.3.1.

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 long-read and Hi-C sequencing data have been deposited in the National Center for Biotechnology Information (NCBI) database under the accession code BioProject: PRJNA1048106. All re-sequencing data generated have been deposited in the NCBI database under the accession codes BioProject: PRJNA994294. All assemblies have been deposited under the accession codes BioProject: PRJNA1018808, PRJNA1018809, PRJNA1029477, PRJNA1029478, PRJNA1029479, PRJNA1029480, PRJNA1130629, PRJNA1130630, PRJNA1130639, PRJNA1130641, PRJNA1130642, PRJNA1130643, PRJNA1130644, PRJNA1130647, PRJNA1130648, PRJNA1130649, PRJNA1130650, PRJNA1130651. These data are also available at the National Genomics Data Center (NGDC) Genome Sequence Archive (GSA) (<https://ngdc.cncb.ac.cn/gsa/>) with BioProject codes PRJCA024688 and PRJCA024753. The Grapepan v1.0, all assembled genome sequences, and annotations have been deposited to Zenodo with the following DOIs: <https://doi.org/10.5281/zenodo.10851547>, <https://doi.org/10.5281/zenodo.10846425>.

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	No specific statistical methods were used to determine sample size for the experiments. 466 grape varieties representing the full range of phenotypic diversity and geographic distribution of grapes worldwide were collected, including varieties from China, Germany, France, Canada, Japan, the United States, and other countries. All of these genotypes fully reflect grape genetic diversity, were chosen for our main study. We selected 9 representative accessions including all different Vitis morphotypes and some wild types for pan-genome construction. All detailed information was provided with supplemental dataset and figures.
Data exclusions	No data were excluded from the analyses.
Replication	All experiments were performed once with at least three independent biological replicates. All replications were successful and were used.
Randomization	For each grape accession, the sampling process for genome DNA/RNA sequencing was randomly conducted
Blinding	Blinding is not necessary for genome sequencing and assembly, since the investigators know which grape accessions they were handling.

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 and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☐	☒ Plants

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

Plants

Seed stocks	We collected all modern cultivars of <i>V. vinifera</i> ssp. <i>vinifera</i> from the experimental orchard of Zhengzhou Fruit Research Institute of the Chinese Academy of Agricultural Sciences (Zhengzhou, China).
Novel plant genotypes	No novel plant genotypes
Authentication	Each plant stock has authentication by Zhengzhou Fruit Research Institute of the Chinese Academy of Agricultural Sciences.