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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	We generated all data by ourselves, including genome sequencing, population resequencing, RNAseq (see 'data availability').
Data analysis	All softwares used in this study have been listed in the Method section with the version numbers and original citations, mainly including: Hifiasm (v0.16.1), BWA (v0.7.17), HiC-Pro (v3.0.0), Juicer-box (v1.91), ALLHiC (v0.9.13), RepeatModeler (v2.0.1), RepeatMasker (v4.1.2), GeneWise (v2.4.1), AUGUSTUS (v3.2.2), Jcvi (v1.1.18), MUMmer (v4.0), SyRI (v1.4), DIAMOND (v0.9.24), OrthoFinder (v2.5.5), CAFE (v2.1), HMMER3 (v3.3), Omicverse (v1.5.3), DESeq2 (v1.18), Samtools (v1.11), GATK (v4.3,) GCTA (v1.94.1), ADMIXTURE (v1.3.0), VCFtools (v0.1.16), XP-CLR (v1.0), PopLDdecay (v3.42), PLINK (v1.9), and Bcftools (v1.19).

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 genome sequences, genome assembly, transcriptome sequencing data and population genome variations (including SNPs and InDels) have been deposited at the National Genomics Data Center (CNGB) under project number PRJCA047272. The assembly information is available under the accession number GWHGQOW00000000.1, GWHGQOX00000000.1 and GWHGRZP00000000.1. All other datasets generated and analyzed during the present study are available in the Supplementary table.

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	*Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design; whether sex and/or gender was determined based on self-reporting or assigned and methods used. Provide in the source data disaggregated sex and gender data, where this information has been collected, and if consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected. Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.*
Reporting on race, ethnicity, or other socially relevant groupings	*Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status). Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.) Please provide details about how you controlled for confounding variables in your analyses.*
Population characteristics	*Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."*
Recruitment	*Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.*
Ethics oversight	*Identify the organization(s) that approved the study protocol.*

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

Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	We report reference-quality, haplotype-resolved genome assemblies of the parthenogenetic Haemaphysalis longicornis and two reference-quality genomes of the bisexual H. longicornis. Comparative genomic analysis revealed high collinearity between the parthenogenetic and bisexual genomes, with a stable chromosomal architecture maintained among the three haplotypes of parthenogenetic strain. The parthenogenetic genome exhibited a major expansion in cell cycle-related gene families, including the inhibitor of apoptosis protein (IAP) family. Population resequencing revealed chromosome 7 harboring high genetic differentiation and several genes likely associated with parthenogenesis. The knockdown of the BIRC5 gene of the IAP family suppressed oviposition in both strains, but the parthenogenetic strain exhibited milder adverse effects. Overall, our results reveal the genomic and evolutionary features associated with polyploid parthenogenesis in H. longicornis.

Research sample	All samples are described in the material and methods and supplemental tables.
Sampling strategy	To generate whole-genome assemblies, we sequenced and assembled the genomes of parthenogenetic and bisexual H. longicornis, respectively. For population genetic analysis, we re-sequenced 69 parthenogenetic H. longicornis and 110 bisexual H. longicornis.
Data collection	The collection of genomic data and transcriptomic data has been described in the Methods.
Timing and spatial scale	For genomic data collection, H. longicornis individuals were collected in 2021 and subjected to genomic sequencing in 2022. For population genomic data, H. longicornis were collected from May to Aug 2023 and sent out for whole-genome resequencing. For the RNAi experiment, phenotypic experimental observations were conducted from Oct 2024 to Apr 2025, and transcriptomic sequencing data were acquired during the same period. Relevant detailed information was provided in the Methods section.
Data exclusions	No data were excluded. Whenever a subset of the data was analysed, it was disclosed in the description of methods.
Reproducibility	All codes and data have been made publicly available and therefore the study can be reproduced. Detailed information on experimental conditions and the number of sample replicates has been described in the Methods section. All experimental results can be well reproduced.
Randomization	Tick species identification was conducted on 1-10 randomly selected ticks from each sampling site, with resequencing conducted on 179 samples covering four provinces. During the experiment, H. longicornis ticks in both the experimental and control groups were randomly assigned to RNAi interference, as detailed in the Methods section.
Blinding	Blinding was applied when conducting species identification of H. longicornis population samples.

Did the study involve field work? ☒ Yes ☐ No

Field work, collection and transport

Field conditions	Sampling was conducted by randomly collecting ticks that were biting domestic animals in Shandong, Henan, Hubei, and Anhui provinces. In this study, temperature and rainfall had no impact on the research results.
Location	Locations are described as above mentioned and in Supplementary file of this manuscript.
Access & import/export	erformed under permit as described in the manuscript.
Disturbance	Minimal

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

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals	The ticks were maintained in small cloth bags and allowed to bite to engorgement on the ears of New Zealand white rabbits (each weighing 2 kg).
Wild animals	None.

Reporting on sex	Parthenogenetic and bisexual female H. longicornis were distinguished by a common thymine (T) deletion at position 8,497 in the mitochondrial genome. Bisexual male H. longicornis was confirmed by amplifying the mitochondrial COX1 gene.
Field-collected samples	For resequencing study, tick samples were collected and placed in cryovials, quickly immersed with liquid nitrogen, and later transferred to a -80°C freezer upon returning to the laboratory.
Ethics oversight	All experiments were performed in accordance with the ethics and guidelines approved by the Animal Ethics Committee of Shandong First Medical University, as stated in the Methods section of the manuscript.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Plants

Seed stocks	*Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.*
Novel plant genotypes	*Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.*
Authentication	*Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.*