nature portfolio

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Last updated by author(s): Aug 23, 2025

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	No software was used for data collection.
Data analysis	Software used for data analysis are described in methods, including Jellyfish(v2.2.10), hifiasm(v0.19), BUSCO(v5.2.1), BWA(V0.7.17), Minimap2(v2.26), samtools(v1.15), Augustus(v3.1.0), SNAP(2006-07-28), GeMoMa(v1.7), Hisat(v2.1.0), Stringtie(v2.1.4), GenemarkS-T(v5.1), Trinity(v2.11), PASA(v2.4.1), gmap(2020-06-30), EVM(v1.1.1), HiC-Pro(v2.8.1), MCScanX(version not specified), JCVI(v0.9.13), RepeatModeler2(v2.0.1), RECON(v1.0.8), RepeatScout(v1.0.6), Dfam(v3.5), LTR retriever(v2.9.0), LTRharvest(v1.5.10), RepeatMasker(v4.1.2), tRNAscan-SE(v1.3.1), barrnap(v0.9), Rfam(v14.5), Infernal(v1.1),HISAT2(v2.1.0), edgeR(v3.28.1), clusterProfiler(v3.6.1), isoseq3 pipeline(v3.8.2), CCS(v6.4.0), Lima(v2.7.1), pigeon(v1.0.0), OrthoFinder(v2.5.4), MUSCLE(v3.6), IQ-TREE(v2.2.0-beta), MAFFT(v7.505), FastTree(v2.1.11), PhyloPYPruner(v1.2.4), MitoZ(v2.3), GATK4(v4.1.2.0), bcftools(v1.9),MEGA11. Reference or link of each software is given.

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 assemblies and annotations generated in this study are available at GenBank with project ID: PRJNA1133666. The genome sequence and annotation data are also provided in figshare via a private link (https://figshare.com/s/6fdb414c8744e1e532b8) for manuscript review.

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.
Reporting on race, ethnicity, or other socially relevant groupings	not applicable.
Population characteristics	not applicable.
Recruitment	not applicable.
Ethics oversight	not applicable.

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	Ninety adult ticks from the same mother were used for genome sequencing.
Data exclusions	No data were excluded.
Replication	No sample was resequenced, this is not required by the state of the art of genomics.
Randomization	Randomization is not required for genome sequencing by the state of the art of genomics.
Blinding	No blinding was necessary as we used all data for the genome assembly and analyses thereof.

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 fed on the New Zealand white rabbit ear until engorged and were maintained in an incubator at 26°C ± 1°C under 75% ± 5% relative humidity.
Wild animals	No animals were collected from the wild.
Reporting on sex	The ticks used parthenogenetic adults and bisexual adult females of Haemaphysalis longicornis
Field-collected samples	The parthenogenetic and bisexual Haemaphysalis longicornis were collected by flag-dragging and 50ml ventilated centrifuge tube from Cangxi County (31◦ 44′ 35″ N, 105◦ 49′ 04″ E), Sichuan Province, and Yu County (40◦ 03′ 03″ N, 115◦ 23′ 15″ E), Hebei Province, China.
Ethics oversight	All experimental procedures in this study were approved by the Animal Ethics Committee of the Hebei Normal University (Protocol Number: IACUC-193212).

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

Plants

Seed stocks	not applicable.
Novel plant genotypes	not applicable.
Authentication	not applicable.

Flow Cytometry

Plots

Confirm that:

☐ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☒ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☐ All plots are contour plots with outliers or pseudocolor plots.

☒ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	The heads of adult ticks from parthenogenetic and bisexual Haemaphysalis longicornis were carefully severed, and the visceral tissues were dissected using fine forceps. The tissues were placed in a plastic dish containing 500 µl of CyStain UV Ploidy reagent and finely minced using a sharp blade to fully release the nuclei, and soaked for 1 min. The resulting suspension was filtered through a 50 µm CellTrics filter into a sample tube. Subsequently, 2 ml of CyStain UV Ploidy reagent was added and incubated in the dark for 2 min. The nuclei suspension was then analyzed using the CyFlow Space Flow Cytometer (Sysmex Partec, Germany) and the corresponding FloMax software.

Instrument	CyFlow Space Flow Cytometer.
Software	FloMax software.
Cell population abundance	500 cells were extracted and examined.
Gating strategy	not applicable.

☒ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.