

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	NanoFilt IsoSeq v3 pipeline (v3.8.0, https://github.com/PacificBiosciences/IsoSeq) fastp (v0.23.4)
Data analysis	Hifiasm (v334) HiCanu (v2.2) Minimap2 Jellyfish (v2.1.3), GenomeScope (v2.0) Winnowmap2 (v2.03) DEGseq Purge_Dups (v1.2.6) Juicer (v1.6), 3D-DNA pipelines (v2.20) Juicebox (v2.20) Bandage (v0.8.1) GraphAligner (v1.0.17) Minimap2 SVision TRF (v4.09.1) MARS, MAFFT (v7.505), EMBOSS (version 6.6.0) KaryoploteR (v1.28.0), StainedGlass (v0.6) srf (https://github.com/lh3/srf)

Mercury, Compleasm (v0.2.5)
 TBtools (v2.096)
 HISAT2 (v2.2.1)
 StringTie (v2.1.7), TACO
 Iso-seq3 workflow (<https://github.com/PacificBiosciences/pbbioconda>)
 TransDecoder (v5.5.0)
 GenomeThreader (v1.7.1)
 GffRead (v0.12.7)
 Augustus (v3.4.0)
 BLASTP (v2.12.0)
 KofamKOALA web server (KEGG release v110)
 InterProScan (v 5.55-88.0)
 clusterProfiler package (v4.10.1)
 DeepTMHMM (v1.0.8)
 DESeq2
 bwa-mem2 (v2.2.1)
 MACS2 (v2.2.9.1)
 Repbase (v26.11), EDTA (v2.0.1), RepeatModeler2 (v2.0.2a), CD-HIT (v4.8.1)
 PASTECClassifier, DeepTE, RepeatMasker
 nucmer (v4.0.0rc1)
 MAFFT (v7.487)
 PhyML (v3.3.20190909)
 Crossmap workflow (https://github.com/soybase/crossmap_workflow)
 transanno (v0.4.0)
 CrossMap (v0.6.5), TBtools-II (v2.096)
 OrthoFinder (v2.5.4), MAFFT (v 7.490), IQ-TREE118 (v2.3.3), MMseqs2 (v13.45111), WGD (v0.6.5), GENESPACE package (v1.3.1)
 gRNA-Cas9-AI
 EAGpro (v2.0), GraphPad Prism (v 9.5.0)

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 data supporting the findings of this study are available within the Article and its Supplementary Data files. The raw sequence data generated in this study have been deposited in the Genome Sequence Archive (GSA) database under accession id CRA027090 [<https://ngdc.cncb.ac.cn/gsa/browse/CRA027090>], CRA027091 [<https://ngdc.cncb.ac.cn/gsa/browse/CRA027091>], CRA027092 [<https://ngdc.cncb.ac.cn/gsa/browse/CRA027092>], CRA027178 [<https://ngdc.cncb.ac.cn/gsa/browse/CRA027178>] and CRA027308 [<https://ngdc.cncb.ac.cn/gsa/browse/CRA027308>]. The whole genome assembly reported in this paper have been deposited in the Genome Warehouse (GWH) database under accession GWHFHGK000000000.1 [<https://ngdc.cncb.ac.cn/gwh/Assembly/86355/show>]. All data was cataloged under the umbrella project accession number PRJCA031569 [<https://ngdc.cncb.ac.cn/bioproject/browse/PRJCA031569>].

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

Reporting on race, ethnicity, or other socially relevant groupings

Population characteristics

Recruitment

Ethics oversight

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	For DNA samples, such as those used in HiFi-CCS, HiC, and ONT, or RNA samples used in RNA-seq and iso-seq, the required amount is calculated based on the minimum sequencing requirements. For behavioral and electrophysiological studies typically determine sample requirements based on experiential values within the field.
Data exclusions	No data were excluded.
Replication	all attempts at replication were successful.
Randomization	Samples were allocated to control and experimental groups based on their genotypes.
Blinding	Blinding is impossible because animals with different genotypes showed visible distinct phenotypes.

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	Bactrocera dorsalis, lab-reared strains, embryos, larvae, pupae and adults.
Wild animals	This study did not involve wild animals.
Reporting on sex	For PacBio HiFi low-input library construction, a single 12-day-old male adult and a female adult were selected from the F1 generation. The Hi-C library was prepared from the cross-linked chromatin of mixed larvae (mixed sex) using a standard Hi-C protocol. For the Oxford Nanopore ultralong library, long DNA fragments from mixed larvae (mixed sex) were size-selected and processed using the Ligation Sequencing SQK-ULK001 Kit (Oxford Nanopore Technologies, Oxford, UK) according to the manufacturer's instructions. Samples from different organ parts were collected for RNA extraction and RNA-seq, the sex of the sample were listed in Table S17. For behavior test and electro-physiology test, only male were used since the those study was focused on male lures.
Field-collected samples	The study did not involve samples collected from the field.
Ethics oversight	No ethical approval or guidance was required for the study involving pests

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

Plants

Seed stocks	n/a
Novel plant genotypes	n/a
Authentication	n/a