DATA NOTE

The genome sequence of the Gold Spangle, *Autographa bractea* (Denis & Schiffermüller), 1775 (Lepidoptera: Noctuidae)

[version 1; peer review: 2 approved]

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Abstract

We present a genome assembly from a male specimen of *Autographa bractea* (Gold Spangle; Arthropoda; Insecta; Lepidoptera; Noctuidae). The assembly contains two haplotypes with total lengths of 412.45 megabases and 412.70 megabases. Most of haplotype 1 (99.7%) is scaffolded into 31 chromosomal pseudomolecules, including the Z sex chromosome. Haplotype 2 was assembled to scaffold level. The mitochondrial genome has also been assembled, with a length of 15.31 kilobases. Gene annotation of this assembly on Ensembl identified 13 179 protein-coding genes. This work is part of Project Psyche, a collaborative programme generating genomes for European butterflies and moths.

Keywords

Autographa bractea; Gold Spangle; genome sequence; chromosomal; Lepidoptera

Open Peer Review

Approval Status ✓ ✓

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This article is included in the Tree of Life gateway.

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Species taxonomy

Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Endopterygota; Amphiesmenoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Obtectomera; Noctuoidea; Noctuidae; Plusiinae; *Autographa*; *Autographa bractea* (Denis & Schiffermüller), 1775 (NCBI:txid987891)

Background

The Gold Spangle, *Autographa bractea* (Denis & Schiffermüller), is a noctuid moth occurring in Europe, western Siberia, northern Turkey and northern Iran (Goater *et al.*, 2003; Macek *et al.*, 2009). The thorax and head are grey-brown, while the abdomen is light brown with a pale brown brush on the first three abdominal segments (Goater *et al.*, 2003). The forewings are light brown with a reddish median area. The antemedian line is narrow and white, straight from the dorsum to the cell; the postmedian line is slightly curved and curves out next to the large median metallic spot (Goater *et al.*, 2003). Hindwings are yellowish with a greyish terminal area. The morphology of the male and female genitalia is illustrated in Nowacki (1998). The gold spangle is mainly nocturnal with a wandering tendencies (Goater *et al.*, 2003).

It is a univoltine species with adults flying from June to August, with the exception of the Southern Alps, where it is locally bivoltine (Macek *et al.*, 2009). It inhabits mountainous, mesophilous and hygrophilous habitats such as wet woodland edges, forest clearings and wet meadows. The larvae are polyphagous and feed on various herbaceous plants, including *Crepis*, *Hieracium*, *Plantago*, *Stachys* and *Taraxacum* (Macek *et al.*, 2009). The larvae of the early instar overwinter (Goater *et al.*, 2003). We present a chromosome-level, haplotype-resolved genome sequence of the Gold Spangle, *Autographa bractea*, sequenced as part of Project Psyche. The sequence data were derived from a male specimen (Figure 1) collected from Brochwald, Meiringen, Switzerland.

Methods

Sample acquisition

The specimen used for genome sequencing was an adult male *Autographa bractea* (specimen ID SAN28000084, ToLID ilAutBrac1; Figure 1), collected from Brochwald, Meiringen, Switzerland (latitude 46.6743, longitude 8.1334; elevation 1 470 m) on 2023-07-09. The specimen was collected and identified by Camille Cornet (University of Neuchâtel).

Nucleic acid extraction

Protocols for high molecular weight (HMW) DNA extraction developed at the Wellcome Sanger Institute (WSI) Tree of Life Core Laboratory are available on protocols.io (Howard *et al.*, 2025). The ilAutBrac1 sample was weighed and triaged to determine the appropriate extraction protocol. Tissue from the thorax was homogenised by powermashing using a PowerMasher II tissue disruptor.

Figure 1. Voucher photograph of the *Autographa bractea* (ilAutBrac1) specimen used for genome sequencing.

HMW DNA was extracted in the WSI Scientific Operations core using the Automated MagAttract v2 protocol. DNA was sheared into an average fragment size of 12–20 kb following the Megaruptor®3 for LI PacBio protocol. Sheared DNA was purified by automated SPRI (solid-phase reversible immobilisation). The concentration of the sheared and purified DNA was assessed using a Nanodrop spectrophotometer and Qubit Fluorometer using the Qubit dsDNA High Sensitivity Assay kit. Fragment size distribution was evaluated by running the sample on the FemtoPulse system. For this sample, the final post-shearing DNA had a Qubit concentration of 43.98 ng/μL and a yield of 2 067.06 ng, with a fragment size of 12.3 kb.

PacBio HiFi library preparation and sequencing

Library preparation and sequencing were performed at the WSI Scientific Operations core. Libraries were prepared using the SMRTbell Prep Kit 3.0 (Pacific Biosciences, California, USA), according to the manufacturer's instructions. The kit includes reagents for end repair/A-tailing, adapter ligation, post-ligation SMRTbell bead clean-up, and nuclease treatment. Size selection and clean-up were performed using diluted AMPure PB beads (Pacific Biosciences). DNA concentration was quantified using a Qubit Fluorometer v4.0 (ThermoFisher Scientific) and the Qubit 1X dsDNA HS assay kit. Final library fragment size was assessed with the Agilent Femto Pulse Automated Pulsed Field CE Instrument (Agilent Technologies) using the gDNA 55 kb BAC analysis kit.

The sample was sequenced on a Revio instrument (Pacific Biosciences). The prepared library was normalised to 2 nM, and 15 μL was used for making complexes. Primers were annealed and polymerases bound to generate circularised complexes, following the manufacturer's instructions. Complexes were purified using 1.2X SMRTbell beads, then diluted to the Revio loading concentration (200–300 pM) and

spiked with a Revio sequencing internal control. The sample was sequenced on a Revio 25M SMRT cell. The SMRT Link software (Pacific Biosciences), a web-based workflow manager, was used to configure and monitor the run and to carry out primary and secondary data analysis. Specimen details, sequencing platforms, and data yields are summarised in Table 1.

Hi-C

Sample preparation and crosslinking

The Hi-C sample was prepared from 20–50 mg of frozen tissue from the head of the ilAutBrac1 sample using the Arima-HiC v2 kit (Arima Genomics). Following the manufacturer's instructions, tissue was fixed and DNA crosslinked using TC buffer to a final formaldehyde concentration of 2%. The tissue was homogenised using the Diagnocine Power Masher-II. Crosslinked DNA was digested with a restriction enzyme master mix, biotinylated, and ligated. Clean-up was performed with SPRISelect beads before library preparation. DNA concentration was measured with the Qubit Fluorometer (Thermo Fisher Scientific) and Qubit HS Assay Kit. The biotinylation percentage was estimated using the Arima-HiC v2 QC beads.

Hi-C library preparation and sequencing

Biotinylated DNA constructs were fragmented using a Covaris E220 sonicator and size selected to 400–600 bp using SPRISelect beads. DNA was enriched with Arima-HiC v2 kit Enrichment beads. End repair, A-tailing, and adapter ligation were carried out with the NEBNext Ultra II DNA Library Prep Kit (New England Biolabs), following a modified protocol where library preparation occurs while DNA remains bound to the Enrichment beads. Library amplification was performed using KAPA HiFi HotStart mix and a custom Unique Dual Index (UDI) barcode set (Integrated DNA Technologies). Depending on sample concentration and biotinylation percentage determined at the crosslinking stage, libraries were amplified with 10–16 PCR cycles. Post-PCR clean-up was performed with SPRISelect beads. Libraries were quantified using the AccuClear Ultra High Sensitivity dsDNA Standards Assay Kit (Biotium) and a FLUOstar Omega plate reader (BMG Labtech).

Prior to sequencing, libraries were normalised to 10 ng/μL. Normalised libraries were quantified again to create equimolar and/or weighted 2.8 nM pools. Pool concentrations were checked using the Agilent 4200 TapeStation (Agilent) with High Sensitivity D500 reagents before sequencing. Sequencing was performed using paired-end 150 bp reads on the Illumina NovaSeq X. Specimen details, sequencing platforms, and data yields are summarised in Table 1.

Genome assembly

Prior to assembly of the PacBio HiFi reads, a database of *k*-mer counts ($k = 31$) was generated from the filtered reads using FastK. GenomeScope2 (Ranallo-Benavidez *et al.*, 2020) was used to analyse the *k*-mer frequency distributions, providing estimates of genome size, heterozygosity, and repeat content.

The HiFi reads were assembled using Hifiasm in Hi-C phasing mode (Cheng *et al.*, 2021; Cheng *et al.*, 2022), producing two haplotypes. Hi-C reads (Rao *et al.*, 2014) were mapped to the primary contigs using bwa-mem2 (Vasimuddin *et al.*, 2019). Contigs were further scaffolded with Hi-C data in YaHS (Zhou *et al.*, 2023), using the --break option for handling potential misassemblies. The scaffolded assemblies were evaluated using Gfastats (Formenti *et al.*, 2022), BUSCO (Manni *et al.*, 2021) and MERQURY.FK (Rhie *et al.*, 2020). The mitochondrial genome was assembled using MitoHiFi (Uliano-Silva *et al.*, 2023), which runs MitoFinder (Allio *et al.*, 2020) and uses these annotations to select the final mitochondrial contig and to ensure the general quality of the sequence.

Table 1. Specimen and sequencing data for BioProject PRJEB78792.

Platform	PacBio HiFi	Hi-C
ToLID	ilAutBrac1	ilAutBrac1
Specimen ID	SAN28000084	SAN28000084
BioSample (source individual)	SAMEA115109800	SAMEA115109800
BioSample (tissue)	SAMEA115109818	SAMEA115109819
Tissue	thorax	head
Instrument	Revio	Illumina NovaSeq X
Run accessions	ERR13485742	ERR13493999
Read count total	2.24 million	764.18 million
Base count total	22.05 Gb	115.39 Gb

Assembly curation

The assembly was decontaminated using the Assembly Screen for Cobionts and Contaminants (ASCC) pipeline. TreeVal was used to generate the flat files and maps for use in curation. Manual curation was conducted primarily in PretextView and HiGlass (Kerpedjiev *et al.*, 2018). Scaffolds were visually inspected and corrected as described by Howe *et al.* (2021). Manual corrections included 17 breaks and 114 joins. This reduced the scaffold count by 41.4% and increased scaffold N50 by 2.3%. The curation process is described at https://gitlab.com/wtsi-grit/rapid-curation. PretextSnapshot was used to generate a Hi-C contact map of the final assembly.

Assembly quality assessment

The Merqury.FK tool (Rhie *et al.*, 2020), run in a Singularity container (Kurtzer *et al.*, 2017), was used to evaluate *k*-mer completeness and assembly quality for both haplotypes using the *k*-mer database ($k = 31$) computed prior to genome assembly. The analysis outputs included assembly QV scores and completeness statistics.

The genome was analysed using the BlobToolKit pipeline, a Nextflow (Di Tommaso *et al.*, 2017) implementation of the earlier Snakemake version (Challis *et al.*, 2020). The pipeline aligns PacBio reads using minimap2 (Li, 2018) and SAMtools (Danecek *et al.*, 2021) to generate coverage tracks. It runs BUSCO (Manni *et al.*, 2021) using lineages identified from the NCBI Taxonomy (Schoch *et al.*, 2020). For the three domain-level lineages, BUSCO genes are aligned to the UniProt Reference Proteomes database (Bateman *et al.*, 2023) using DIAMOND blastp (Buchfink *et al.*, 2021). The genome is divided into chunks based on the density of BUSCO genes from the closest taxonomic lineage, and each chunk is aligned to the UniProt Reference Proteomes database with DIAMOND blastx. Sequences without hits are chunked using seqtk and aligned to the NT database with blastn (Altschul *et al.*, 1990). The BlobToolKit suite consolidates all outputs into a blobdir for visualisation. The BlobToolKit pipeline was developed using nf-core tooling (Ewels *et al.*, 2020) and MultiQC (Ewels *et al.*, 2016), with containerisation through Docker (Merkel, 2014) and Singularity (Kurtzer *et al.*, 2017).

We used lep_busco_painter to paint Merian elements along chromosomes (Wright *et al.*, 2024). Merian elements represent the 32 ancestral linkage groups in Lepidoptera. The painting process utilised BUSCO gene locations from the lepidoptera_odb10 set (Kriventseva *et al.*, 2019) and chromosome lengths from NCBI Datasets. Each complete BUSCO gene (both single-copy and duplicated) was assigned to a Merian element based on a reference database, then plotted along chromosomes drawn to scale.

Genome sequence report

Sequence data

PacBio sequencing of the *Autographa bractea* specimen generated 22.05 Gb (gigabases) from 2.24 million reads, which were used to assemble the genome. GenomeScope2.0 analysis estimated the haploid genome size at 419.50 Mb, with a heterozygosity of 2.35% and repeat content of 29.92% (Figure 2). These estimates guided expectations for the assembly. Based on the estimated genome size, the sequencing

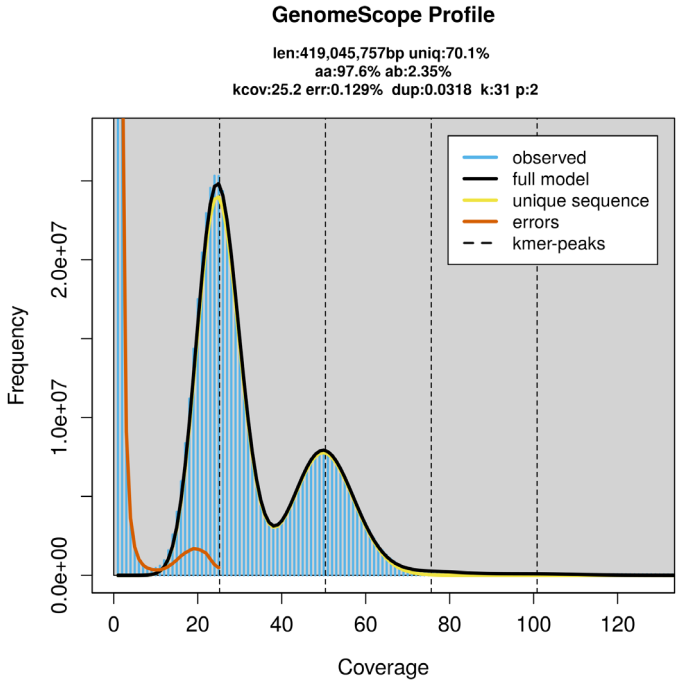

Figure 2. Frequency distribution of *k*-mers generated using GenomeScope2. The plot shows observed and modelled *k*-mer spectra, providing estimates of genome size, heterozygosity, and repeat content based on unassembled sequencing reads.

data provided approximately 50× coverage. Hi-C sequencing produced 115.39 Gb from 764.18 million reads, which were used to scaffold the assembly. Table 1 summarises the specimen and sequencing details.

Assembly statistics

The genome was assembled into two haplotypes using Hi-C phasing. Haplotype 1 was curated to chromosome level, while haplotype 2 was assembled to scaffold level. The final assembly has a total length of 412.45 Mb in 81 scaffolds, with 135 gaps, and a scaffold N50 of 13.65 Mb (Table 2).

Most of the assembly sequence (99.7%) was assigned to 31 chromosomal-level scaffolds, representing 30 autosomes and the Z sex chromosome. These chromosome-level scaffolds, confirmed by Hi-C data, are named according to size (Figure 3; Table 3). Chromosome painting with Merian elements illustrates the distribution of orthologues along chromosomes and highlights patterns of chromosomal evolution relative to Lepidopteran ancestral linkage groups (Figure 4). The sex chromosome Z was identified by homology to the genome of *Autographa pulchrina* (GCA_905475315.1) (Boyes *et al.*, 2023).

The mitochondrial genome was also assembled (length 15.31 kb, OZ182405.1). This sequence is included as a contig in the multifasta file of the genome submission and as a standalone record.

Assembly quality metrics

For haplotype 1, the estimated QV is 65.5, and for haplotype 2, 66.1. When the two haplotypes are combined, the assembly achieves an estimated QV of 65.8. The *k*-mer completeness is 65.54% for haplotype 1, 65.62% for haplotype 2, and 99.43% for the combined haplotypes (Figure 5).

BUSCO analysis using the lepidoptera_odb10 reference set (n = 5 286) identified 98.9% of the expected gene set (single = 98.4%, duplicated = 0.5%) in haplotype 1. For haplotype 2, BUSCO analysis identified 98.8% of the expected gene set (single = 98.2%, duplicated = 0.6%). The snail plot in Figure 6 summarises the scaffold length distribution and other assembly statistics for haplotype 1. The blob plot in Figure 7 shows the distribution of scaffolds by GC proportion and coverage for haplotype 1.

Table 4 lists the assembly metric benchmarks adapted from Rhie *et al.* (2021) and the Earth BioGenome Project Report on Assembly Standards September 2024. The EBP metric, calculated for the haplotype 1, is **6.C.Q65**, meeting the recommended reference standard.

Genome annotation report

The *Autographa bractea* genome assembly (GCA_964264225.1) was annotated by Ensembl at the European Bioinformatics Institute (EBI). This annotation includes 26 947 transcribed mRNAs from 13 179 protein-coding and 4 087 non-coding genes. The average transcript length is 15 118.18 bp, with an average of 1.56 coding transcripts per gene and 7.24 exons per transcript. For further information, please refer to the Ensembl annotation page.

Wellcome Sanger Institute – Legal and Governance

The materials that have contributed to this genome note have been supplied by a Tree of Life collaborator. The Wellcome Sanger Institute employs a process whereby due diligence

Table 2. Genome assembly statistics.

Assembly name	ilAutBrac1.hap1.1	ilAutBrac1.hap2.1
Assembly accession	GCA_964264225.1	GCA_964264215.1
Assembly level	chromosome	scaffold
Span (Mb)	412.45	412.70
Number of chromosomes	31	scaffold-level
Number of contigs	216	188
Contig N50	5.9 Mb	5.59 Mb
Number of scaffolds	81	65
Scaffold N50	13.65 Mb	13.72 Mb
Longest scaffold length (Mb)	38.89	-
Sex chromosomes	Z	-
Organelles	Mitochondrion: 15.31 kb	-

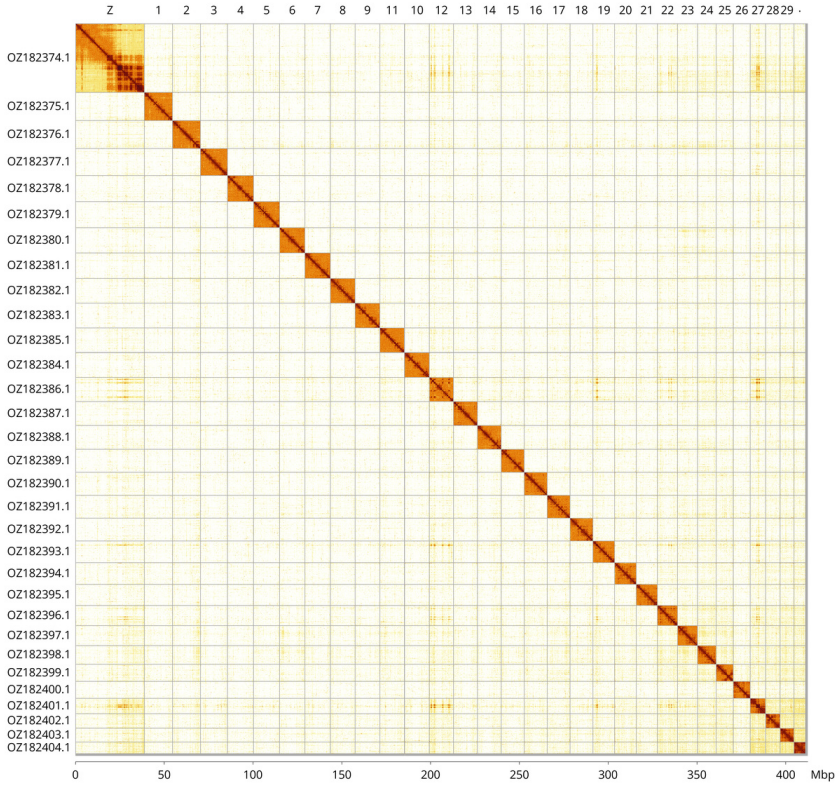

Figure 3. Hi-C contact map of the *Autographa bractea* genome assembly. Assembled chromosomes are shown in order of size and labelled along the axes, with a megabase scale shown below. The plot was generated using PretextSnapshot.

Table 3. Chromosomal pseudomolecules in the haplotype 1 genome assembly of *Autographa bractea* ilAutBrac1.

INSDC accession	Molecule	Length (Mb)	GC%	Assigned Merian elements
OZ182375.1	1	15.83	35.50	M2
OZ182376.1	2	15.69	36	M17;M20
OZ182377.1	3	15.26	36	M1
OZ182378.1	4	14.71	35.50	M3
OZ182379.1	5	14.63	35	M9
OZ182380.1	6	14.28	35	M8
OZ182381.1	7	14.26	35	M5
OZ182382.1	8	13.96	35	M7
OZ182383.1	9	13.96	34.50	M12
OZ182384.1	10	13.89	35	M18
OZ182385.1	11	13.94	35	M16
OZ182386.1	12	13.65	35.50	M23
OZ182387.1	13	13.44	35.50	M4
OZ182388.1	14	13.42	35.50	M6
OZ182389.1	15	13	35	M21
OZ182390.1	16	12.92	35.50	M10
OZ182391.1	17	12.89	35	M22
OZ182392.1	18	12.79	35.50	M15
OZ182393.1	19	12.28	35	M13
OZ182394.1	20	12.22	36	M14
OZ182395.1	21	11.85	36	M11
OZ182396.1	22	11.36	36	M19
OZ182397.1	23	11.19	35	M24
OZ182398.1	24	10.57	35	M26
OZ182399.1	25	9.66	35.50	M27
OZ182400.1	26	9.44	35.50	M28
OZ182401.1	27	8.69	38	M30
OZ182402.1	28	8.12	36	M25
OZ182403.1	29	7.87	36.50	M29
OZ182404.1	30	6.56	37	M31
OZ182374.1	Z	38.89	36.50	MZ

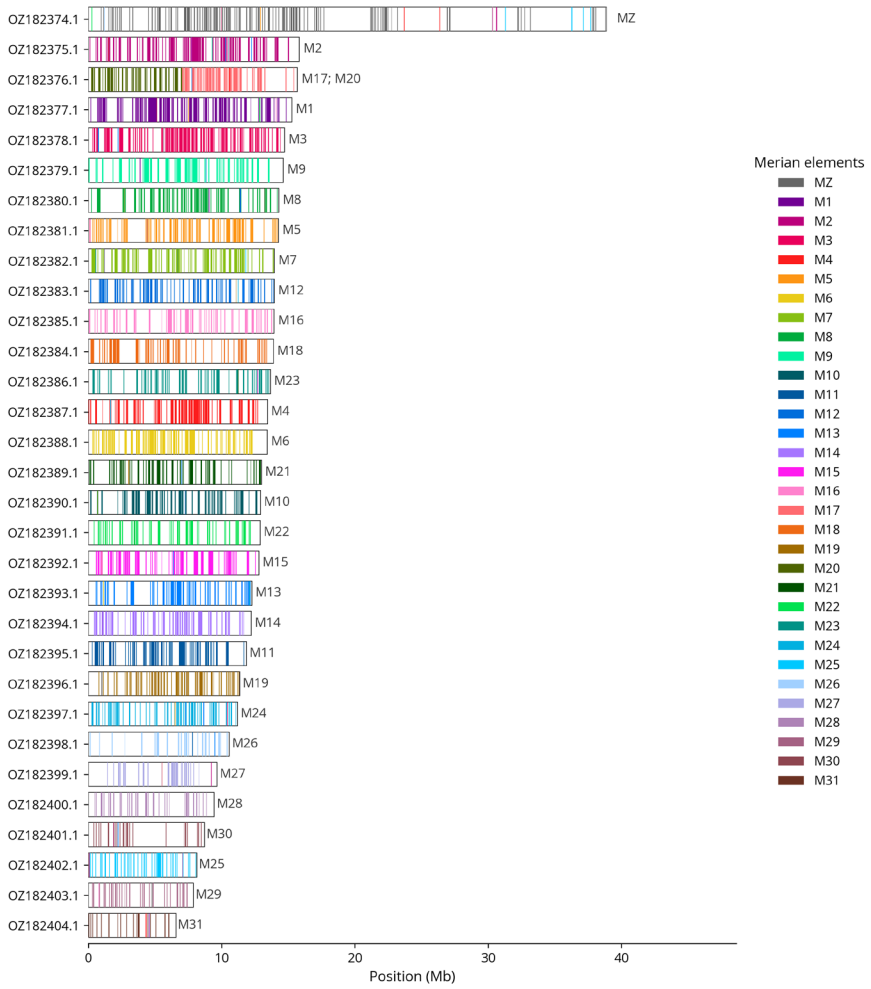

Figure 4. Merian elements painted across chromosomes in the ilAutBrac1.hap1.1 assembly of *Autographa bractea*. Chromosomes are drawn to scale, with the positions of orthologues shown as coloured bars. Each orthologue is coloured by the Merian element that it belongs to. All orthologues which could be assigned to Merian elements are shown.

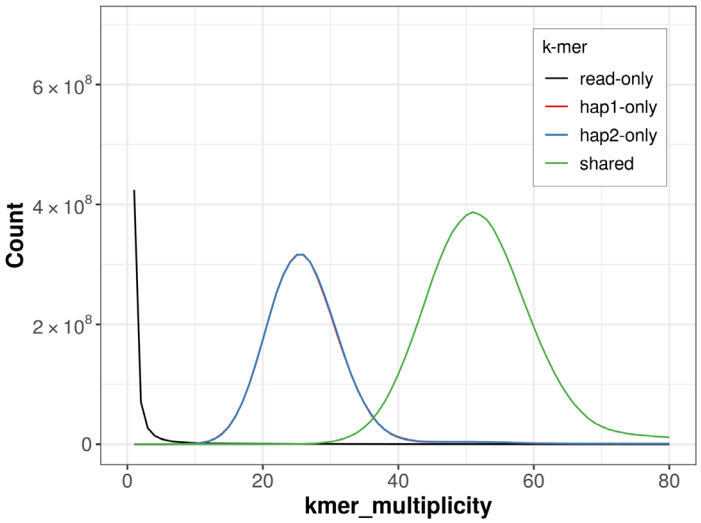

Figure 5. Evaluation of *k*-mer completeness using MerquryFK. This plot illustrates the recovery of *k*-mers from the original read data in the final assemblies. The horizontal axis represents *k*-mer multiplicity, and the vertical axis shows the number of *k*-mers. The black curve represents *k*-mers that appear in the reads but are not assembled. The green curve (the homozygous peak) corresponds to *k*-mers shared by both haplotypes and the red and blue curves (the heterozygous peaks) show *k*-mers found only in one of the haplotypes.

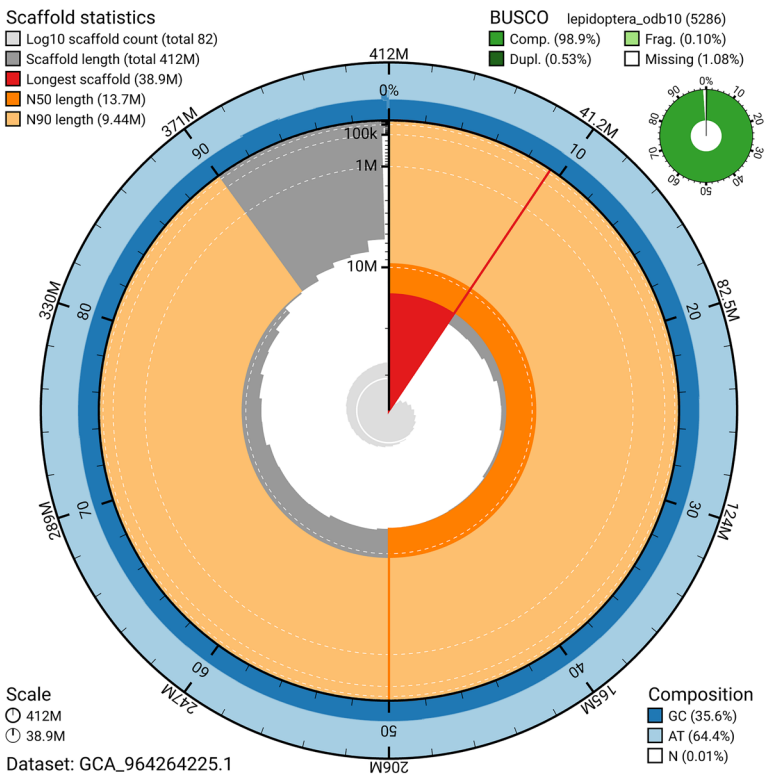

Figure 6. Assembly metrics for ilAutBrac1.hap1.1. The BlobToolKit snail plot provides an overview of assembly metrics and BUSCO gene completeness. The circumference represents the length of the whole genome sequence, and the main plot is divided into 1,000 bins around the circumference. The outermost blue tracks display the distribution of GC, AT, and N percentages across the bins. Scaffolds are arranged clockwise from longest to shortest and are depicted in dark grey. The longest scaffold is indicated by the red arc, and the deeper orange and pale orange arcs represent the N50 and N90 lengths. A light grey spiral at the centre shows the cumulative scaffold count on a logarithmic scale. A summary of complete, fragmented, duplicated, and missing BUSCO genes in the set is presented at the top right. An interactive version of this figure can be accessed on the BlobToolKit viewer.

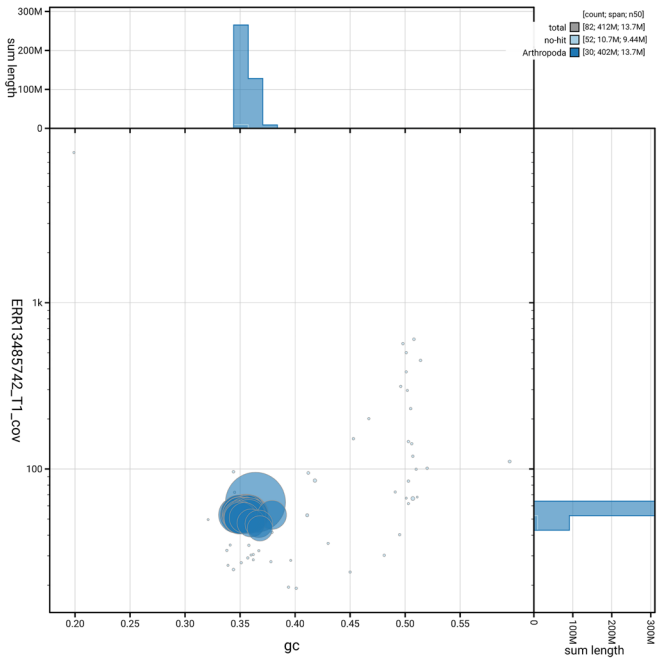

Figure 7. BlobToolKit GC-coverage plot for ilAutBrac1.hap1.1. Blob plot showing sequence coverage (vertical axis) and GC content (horizontal axis). The circles represent scaffolds, with the size proportional to scaffold length and the colour representing phylum membership. The histograms along the axes display the total length of sequences distributed across different levels of coverage and GC content. An interactive version of this figure is available on the BlobToolKit viewer.

Table 4. Earth Biogenome Project summary metrics for the *Autographa bractea* assembly.

Measure	Value	Benchmark
EBP summary (haplotype 1)	6.C.Q65	6.C.Q40
Contig N50 length	5.90 Mb	≥ 1 Mb
Scaffold N50 length	13.65 Mb	= chromosome N50
Consensus quality (QV)	Haplotype 1: 65.5; haplotype 2: 66.1; combined: 65.8	≥ 40
k-mer completeness	Haplotype 1: 65.54%; Haplotype 2: 65.62%; combined: 99.43%	≥ 95%
BUSCO (haplotype 1)	C:98.9% [S:98.4%; D:0.5%]; F:0.1%; M:1.0%; n:5 286	S > 90%; D < 5%
Percentage of assembly assigned to chromosomes	99.70%	≥ 90%

Notes: EBP summary uses log10(Contig N50); chromosome-level (C) or log10(Scaffold N50); Q (Merqury QV). BUSCO: C=complete; S=single-copy; D=duplicated; F=fragmented; M=missing; n=orthologues

is carried out proportionate to the nature of the materials themselves, and the circumstances under which they have been/are to be collected and provided for use. The purpose of this is to address and mitigate any potential legal and/or ethical implications of receipt and use of the materials as part of the research project, and to ensure that in doing so, we align with best practice wherever possible. The overarching areas of consideration are:

- Ethical review of provenance and sourcing of the material
- Legality of collection, transfer and use (national and international).

Each transfer of samples is undertaken according to a Research Collaboration Agreement or Material Transfer Agreement entered into by the Tree of Life collaborator, Genome Research Limited (operating as the Wellcome Sanger Institute), and in some circumstances, other Tree of Life collaborators.

Data availability

European Nucleotide Archive: Autographa bractea (gold spangle). Accession number PRJEB78792. The genome sequence is released openly for reuse. The *Autographa bractea* genome sequencing initiative is part of the Sanger Institute Tree of Life Programme (PRJEB43745) and Project Psyche (PRJEB71705). All raw sequence data and the assembly have been deposited in INSDC databases. Raw data and assembly accession identifiers are reported in Table 1 and Table 2.

Pipelines used for genome assembly at the WSI Tree of Life are available at https://pipelines.tol.sanger.ac.uk/pipelines. Table 5 lists software versions used in this study.

Author information

Contributors are listed at the following links:

- Members of the Wellcome Sanger Institute Tree of Life Management, Samples and Laboratory team
- Members of Wellcome Sanger Institute Scientific Operations – Sequencing Operations
- Members of the Wellcome Sanger Institute Tree of Life Core Informatics team
- Members of the Tree of Life Core Informatics collective
- Members of the Project Psyche Community

Table 5. Software versions and sources.

Software	Version	Source
BEDTools	2.30.0	https://github.com/arq5x/bedtools2
BLAST	2.14.0	ftp://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/

Software	Version	Source
BlobToolKit	4.3.9	https://github.com/blobtoolkit/blobtoolkit
BUSCO	5.5.0	https://gitlab.com/ezlab/busco
bwa-mem2	2.2.1	https://github.com/bwa-mem2/bwa-mem2
Cooler	0.8.11	https://github.com/open2c/cooler
DIAMOND	2.1.8	https://github.com/bbuchfink/diamond
fasta_windows	0.2.4	https://github.com/tolkit/fasta_windows
FastK	1.1	https://github.com/thegenemyers/FASTK
GenomeScope2.0	2.0.1	https://github.com/tbenavi1/genomescope2.0
Gfastats	1.3.6	https://github.com/vgl-hub/gfastats
Hifiasm	0.19.8-r603	https://github.com/chhylp123/hifiasm
HiGlass	1.13.4	https://github.com/higlass/higlass
lep_busco_painter	1.0.0	https://github.com/charlottewright/lep_busco_painter
MerquryFK	1.1.2	https://github.com/thegenemyers/MERQURY.FK
Minimap2	2.24-r1122	https://github.com/lh3/minimap2
MitoHiFi	3	https://github.com/marcelauliano/MitoHiFi
MultiQC	1.14; 1.17 and 1.18	https://github.com/MultiQC/MultiQC
Nextflow	23.10.0	https://github.com/nextflow-io/nextflow
PretextSnapshot	0.0.5	https://github.com/sanger-tol/PretextSnapshot
PretextView	1.0.3	https://github.com/sanger-tol/PretextView
samtools	1.19.2	https://github.com/samtools/samtools
sanger-tol/ascc	0.1.0	https://github.com/sanger-tol/ascc
sanger-tol/blobtoolkit	0.6.0	https://github.com/sanger-tol/blobtoolkit
sanger-tol/curationpretext	1.4.2	https://github.com/sanger-tol/curationpretext
Seqtk	1.3	https://github.com/lh3/seqtk
Singularity	3.9.0	https://github.com/sylabs/singularity
TreeVal	1.4.0	https://github.com/sanger-tol/treeval
YaHS	1.2a.2	https://github.com/c-zhou/yahs

References

Allio R, Schomaker-Bastos A, Romiguier J, *et al.*: **MitoFinder: efficient automated large-scale extraction of mitogenomic data in target enrichment phylogenomics.** *Mol Ecol Resour.* 2020; **20**(4): 892–905.
PubMed Abstract | Publisher Full Text | Free Full Text

Altschul SF, Gish W, Miller W, *et al.*: **Basic Local Alignment Search Tool.** *J Mol Biol.* 1990; **215**(3): 403–410.
PubMed Abstract | Publisher Full Text

Bateman A, Martin MJ, Orchard S, *et al.*: **UniProt: the Universal Protein Knowledgebase in 2023.** *Nucleic Acids Res.* 2023; **51**(D1): D523–D531.
PubMed Abstract | Publisher Full Text | Free Full Text

Boyes D, Eljounaidi K, University of Oxford and Wytham Woods Genome Acquisition Lab: **The genome sequence of the Beautiful Golden Y, *Autographa pulchrina* (Haworth, 1809) [version 1; peer review: 2 approved].** *Wellcome Open Res.* 2023; **8**: 375.
PubMed Abstract | Publisher Full Text | Free Full Text

Buchfink B, Reuter K, Drost HG: **Sensitive protein alignments at Tree-of-Life scale using DIAMOND.** *Nat Methods.* 2021; **18**(4): 366–368.
PubMed Abstract | Publisher Full Text | Free Full Text

Challis R, Richards E, Rajan J, *et al.*: **BlobToolKit – interactive quality assessment of genome assemblies.** *G3 (Bethesda).* 2020; **10**(4): 1361–1374.
PubMed Abstract | Publisher Full Text | Free Full Text

Cheng H, Concepcion GT, Feng X, *et al.*: **Haplotype-resolved *de novo* assembly using phased assembly graphs with hifiasm.** *Nat Methods.* 2021; **18**(2): 170–175.
PubMed Abstract | Publisher Full Text | Free Full Text

Cheng H, Jarvis ED, Fedrigo O, *et al.*: **Haplotype-resolved assembly of diploid**

genomes without parental data. *Nat Biotechnol.* 2022; **40**(9): 1332–1335.
PubMed Abstract | Publisher Full Text | Free Full Text

Danecek P, Bonfield JK, Liddle J, *et al.*: **Twelve years of SAMtools and BCFtools.** *GigaScience.* 2021; **10**(2): giab008.
PubMed Abstract | Publisher Full Text | Free Full Text

Di Tommaso P, Chatzou M, Floden EW, *et al.*: **Nextflow enables reproducible computational workflows.** *Nat Biotechnol.* 2017; **35**(4): 316–319.
PubMed Abstract | Publisher Full Text

Ewels P, Magnusson M, Lundin S, *et al.*: **MultiQC: summarize analysis results for multiple tools and samples in a single report.** *Bioinformatics.* 2016; **32**(19): 3047–3048.
PubMed Abstract | Publisher Full Text | Free Full Text

Ewels PA, Peltzer A, Fillinger S, *et al.*: **The nf-core framework for community-curated bioinformatics pipelines.** *Nat Biotechnol.* 2020; **38**(3): 276–278.
PubMed Abstract | Publisher Full Text

Formenti G, Abueg L, Brajuka A, *et al.*: **Gfastats: conversion, evaluation and manipulation of genome sequences using assembly graphs.** *Bioinformatics.* 2022; **38**(17): 4214–4216.
PubMed Abstract | Publisher Full Text | Free Full Text

Goater B, Ronkay L, Fibiger M: **Catocalinae & Plusiinae**. Sorø: Entomological Press, 2003; **10**.
Reference Source

Howard C, Denton A, Jackson B, *et al.*: **On the path to reference genomes for all biodiversity: lessons learned and laboratory protocols created in the Sanger Tree of Life core laboratory over the first 2000 species.** *bioRxiv.* 2025.
Publisher Full Text

Howe K, Chow W, Collins J, *et al.*: **Significantly improving the quality of genome assemblies through curation.** *GigaScience.* 2021; **10**(1): giaa153.
PubMed Abstract | Publisher Full Text | Free Full Text

Kerpedjiev P, Abdennur N, Lekschas F, *et al.*: **HiGlass: web-based visual exploration and analysis of genome interaction maps.** *Genome Biol.* 2018; **19**(1): 125.
PubMed Abstract | Publisher Full Text | Free Full Text

Kriventseva EV, Kuznetsov D, Tegenfeldt F, *et al.*: **OrthoDB v10: sampling the diversity of animal, plant, fungal, protist, bacterial and viral genomes for evolutionary and functional annotations of orthologs.** *Nucleic Acids Res.* 2019; **47**(D1): D807–D811.
PubMed Abstract | Publisher Full Text | Free Full Text

Kurtzer GM, Sochat V, Bauer MW: **Singularity: scientific containers for mobility of compute.** *PLoS One.* 2017; **12**(5): e0177459.
PubMed Abstract | Publisher Full Text | Free Full Text

Li H: **Minimap2: pairwise alignment for nucleotide sequences.** *Bioinformatics.* 2018; **34**(18): 3094–3100.
PubMed Abstract | Publisher Full Text | Free Full Text

Macek J, Dvořák J, Traxler L, *et al.*: **Motýli a Housenky Střední Evropy II. Noční Motýli – můrovití**. Praha: Academia, 2009.
Reference Source

Manni M, Berkeley MR, Seppey M, *et al.*: **BUSCO update: novel and streamlined workflows along with broader and deeper phylogenetic coverage for scoring of eukaryotic, prokaryotic, and viral genomes.** *Mol Biol Evol.* 2021; **38**(10): 4647–4654.
PubMed Abstract | Publisher Full Text | Free Full Text

Merkel D: **Docker: lightweight Linux containers for consistent development and deployment.** *Linux J.* 2014; **2014**(239): 2.
Reference Source

Nowacki J: **The Noctuids (Lepidoptera, Noctuidae) of Central Europe**. Bratislava: František Slamka, 1998.
Reference Source

Ranallo-Benavidez TR, Jaron KS, Schatz MC: **GenomeScope 2.0 and Smudgeplot for reference-free profiling of polyploid genomes.** *Nat Commun.* 2020; **11**(1): 1432.
PubMed Abstract | Publisher Full Text | Free Full Text

Rao SSP, Huntley MH, Durand NC, *et al.*: **A 3D map of the human genome at kilobase resolution reveals principles of chromatin looping.** *Cell.* 2014; **159**(7): 1665–1680.
PubMed Abstract | Publisher Full Text | Free Full Text

Rhie A, McCarthy SA, Fedrigo O, *et al.*: **Towards complete and error-free genome assemblies of all vertebrate species.** *Nature.* 2021; **592**(7856): 737–746.
PubMed Abstract | Publisher Full Text | Free Full Text

Rhie A, Walenz BP, Koren S, *et al.*: **Merqury: reference-free quality, completeness, and phasing assessment for genome assemblies.** *Genome Biol.* 2020; **21**(1): 245.
PubMed Abstract | Publisher Full Text | Free Full Text

Schoch CL, Ciufo S, Domrachev M, *et al.*: **NCBI Taxonomy: a comprehensive update on curation, resources and tools.** *Database (Oxford).* 2020; **2020**: baaa062.
PubMed Abstract | Publisher Full Text | Free Full Text

Uliano-Silva M, Ferreira JGRN, Krasheninnikova K, *et al.*: **MitoHiFi: a python pipeline for mitochondrial genome assembly from PacBio high fidelity reads.** *BMC Bioinformatics.* 2023; **24**(1): 288.
PubMed Abstract | Publisher Full Text | Free Full Text

Vasimuddin M, Misra S, Li H, *et al.*: **Efficient architecture-aware acceleration of BWA-MEM for multicore systems.** In: *2019 IEEE International Parallel and Distributed Processing Symposium (IPDPS).* IEEE, 2019; 314–324.
Publisher Full Text

Wright CJ, Stevens L, Mackintosh A, *et al.*: **Comparative genomics reveals the dynamics of chromosome evolution in Lepidoptera.** *Nat Ecol Evol.* 2024; **8**(4): 777–790.
PubMed Abstract | Publisher Full Text | Free Full Text

Zhou C, McCarthy SA, Durbin R: **YaHS: Yet another Hi-C Scaffolding tool.** *Bioinformatics.* 2023; **39**(1): btac808.
PubMed Abstract | Publisher Full Text | Free Full Text

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Version 1

Reviewer Report 16 February 2026

https://doi.org/10.21956/wellcomeopenres.28385.r146432

✔ **Xue Qing**
Nanjing Agricultural University, Nanjing, China

This data presents the first complete genome sequence of the Gold Spangle moth, Autographa bractea, as part of the Project Psyche initiative. The genome was assembled from a single male specimen using PacBio HiFi sequencing and Hi-C scaffolding.

This genome note is exemplary in both technical rigor and clarity. It provides a valuable genomic resource for Lepidoptera research and contributes to the broader goals of the Tree of Life. The detailed protocols, use of state-of-the-art tools, and open data practices make it a model for future genome reports. Overall, this manuscript can be indexed with minor revision. below are my comments:

1. the abstract could briefly mention the evolutionary or conservation significance of this genome to broaden its impact.
2. Figure legends could be more self-explanatory, allowing readers to understand them independently. Some specialized terms (e.g., "Merian elements") could include a short explanation for non-specialists.
3. adding a brief discussion on how this genome compares to related species would enhance its value for comparative genomics.

Is the rationale for creating the dataset(s) clearly described?
Yes

Are the protocols appropriate and is the work technically sound?
Yes

Are sufficient details of methods and materials provided to allow replication by others?
Yes

Are the datasets clearly presented in a useable and accessible format?

Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: comparative genomics of invertbrates

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Reviewer Report 05 February 2026

https://doi.org/10.21956/wellcomeopenres.28385.r146428

Gen Morinaga
University of Calgary, Calgary, Alberta, Canada

In the genome note titled “The genome sequence of the Gold Spangle, *Autographa bractea* (Denis & Schiffermuller), 1775 (Lepidoptera: Noctuidae)”, Cornet et al., sequence the genome of an individual Gold Spangle moth (*A. bractea*) using the PacBio HiFi sequencing platform. Furthermore, they combine these sequences with Hi-C sequencing of the same individual to produce haplotype representation assemblies, both of which exhibit high gene content completeness, with the primary haplotype also exhibiting a high degree of contiguity after scaffolding and manual curation. Lastly, they identify the sex chromosome and assemble and annotate the mitochondrial genome. They “painted” (i.e., positionally identified) Merian elements on each chromosome and presented it in a very nice figure.
I believe the work presented is done to a high standard using state-of-the-art bioinformatic tools. I especially appreciated the detailed methods. The writing is generally very clear, and though I prefer using an “active voice” (e.g., “The genome was assembled…” vs. “We assembled the genome…”), the use of the “passive voice” in this work is not a hinderance to the reader.

Is the rationale for creating the dataset(s) clearly described?
Yes

Are the protocols appropriate and is the work technically sound?
Yes

Are sufficient details of methods and materials provided to allow replication by others?
Yes

Are the datasets clearly presented in a useable and accessible format?
Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Evolutionary biology; Genomics; Comparative Genomics; Bioinformatics

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.