DATA NOTE

The genome sequence of the Northern Wall Brown, *Lasiommata petropolitana* (Fabricius, 1787) (Lepidoptera: Nymphalidae)

[version 1; peer review: 2 approved]

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Abstract

We present a genome assembly from a female specimen of *Lasiommata petropolitana* (Northern Wall Brown; Arthropoda; Insecta; Lepidoptera; Nymphalidae). The assembly contains two haplotypes with total lengths of 492.84 megabases and 442.93 megabases. Most of haplotype 1 (99.82%) is scaffolded into 30 chromosomal pseudomolecules, including the W and Z sex chromosomes. Haplotype 2 was assembled to scaffold level. The mitochondrial genome has also been assembled, with a length of 15.25 kilobases.

Keywords

Lasiommata petropolitana, Northern Wall Brown, genome sequence, chromosomal, Lepidoptera

Open Peer Review

Approval Status ✓ ✓

	1	2
version 1 28 Aug 2025	✓ view	✓ view

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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; Papilionoidea; Nymphalidae; Satyrinae; Satyrini; Parargina; *Lasiommata*; *Lasiommata petropolitana* (Fabricius, 1787) (NCBI: txid111918)

Background

Lasiommata petropolitana is a butterfly species belonging to the Nymphalidae family. It is characterised by dark brown wings with eye spots and subtle orange patterns (Tolman & Lewington, 2009). Compared to the closely related *L. maera*, *L. petropolitana* has straighter wing margins, a smaller size, and darker, more uniform colouration. The apical eyespot is circular, lacking the accessory eye-dot seen in *L. maera* (Seitz, 1932).

This Euro-Siberian species is found from the Pyrenees and the Alps to Scandinavia, extending into Russia and northeastern China (Spitzer *et al.*, 2017). In northern Europe, it inhabits lowland forests while in central and southern Europe, it is restricted to mountainous regions above 500 metres, favouring rocky, alpine pastures and forest clearings up to 2 200 metres. Its distribution is continuous in the north, becoming fragmented in the southern mountainous regions (Kudrna *et al.*, 2011).

Lasiommata petropolitana is univoltine in mountain regions, with a possible second generation at lower latitudes or in extremely warm years. Adults are on the wing from April to September (Spitzer *et al.*, 2017), varying by altitude and latitude. Larvae primarily feed on grasses such as *Dactylis glomerata*, *Calamagrostis epigejos,* and *Festuca ovina* – in other words, common meadow grass species.

Lasiommata petropolitana represents a distinct evolutionary significant unit (ESU) within the genus *Lasiommata*, showing low haplotype diversification relative to its congeners, which could be due to historical population bottlenecks, restricted gene flow, or a relatively recent divergence from its common ancestor (Platania *et al.*, 2020) The species has undergone regional declines because of habitat loss (Spitzer *et al.*, 2017), with a greater decline in lowlands than in mountainous regions. Despite these local declines, the species is currently classified as Least Concern on the IUCN Red List (Bonifacino *et al.*, 2022).

We present a chromosome-level, haplotype-resolved genome sequence of the Northern Wall Brown, *Lasiommata petropolitana*, sequenced as part of Project Psyche. The sequence data were derived from a female specimen (Figure 1) collected from Brochwald, Meiringen, Switzerland.

Methods

Sample acquisition

The specimen used for genome sequencing was an adult female *Lasiommata petropolitana* (specimen ID SAN28000082, ToLID ilLasPetr1; Figure 1), collected from Brochwald, Meiringen, Switzerland (latitude 46.6743, longitude 8.1334; elevation 1 470 m) on 09/07/2023. The specimen was collected and identified by Irena Klecková (Czech Institute of Entomology).

Figure 1. Voucher photograph of the *Lasiommata petropolitana* (ilLasPetr1) specimen used for genome sequencing.

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 ilLasPetr1 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.

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 42.49 ng/μL and a yield of 1 997.03 ng, with a fragment size of 15.4 kb. The 260/280 spectrophotometric ratio was 1.95, and the 260/230 ratio was 2.62.

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), following 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 head tissue of the ilLasPetr1 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 and 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

Table 1. Specimen and sequencing data for BioProject PRJEB79190.

Platform	PacBio HiFi	Hi-C
ToLID	ilLasPetr1	ilLasPetr1
Specimen ID	SAN28000082	SAN28000082
BioSample (source individual)	SAMEA115109810	SAMEA115109810
BioSample (tissue)	SAMEA115109848	SAMEA115109849
Tissue	thorax	head
Sequencing platform and model	Revio	Illumina NovaSeq X
Run accessions	ERR13605508	ERR13602171
Read count total	1.25 million	752.17 million
Base count total	14.10 Gb	113.58 Gb

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.

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 41 breaks and 122 joins. The curation process is documented 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

Chromosomal painting was performed using lep_busco_painter using Merian elements, which represent the 32 ancestral linkage groups in Lepidoptera (Wright *et al.*, 2024). Painting was based on gene locations from the lepidoptera_odb10 BUSCO analysis and chromosome lengths from the genome index produced using SAMtools faidx (Danecek *et al.*, 2021). Each complete BUSCO (including both single-copy and duplicated BUSCOs) was assigned to a Merian element using a reference database, and coloured positions were plotted along chromosomes drawn to scale.

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 databases ($k = 31$) 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 implementation of the earlier Snakemake BlobToolKit pipeline (Challis *et al.*, 2020). The pipeline aligns PacBio reads using minimap2 (Li, 2018) and SAMtools (Danecek *et al.*, 2021) to generate coverage tracks. Simultaneously, it queries the GoaT database (Challis *et al.*, 2023) to identify relevant BUSCO lineages and runs BUSCO (Manni *et al.*, 2021). For the three domain-level BUSCO 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 package management via Conda and Bioconda (Grüning *et al.*, 2018), and containerisation through Docker (Merkel, 2014) and Singularity (Kurtzer *et al.*, 2017).

Genome sequence report

Sequence data

The genome of a specimen of *Lasiommata petropolitana* was sequenced using Pacific Biosciences single-molecule HiFi long reads, generating 14.10 Gb (gigabases) from 1.25 million reads, which were used to assemble the genome. GenomeScope2.0 analysis estimated the haploid genome size at 458.03 Mb, with a heterozygosity of 0.95% and repeat content of 23.88%. These estimates guided expectations for the assembly. Based on the estimated genome size, the sequencing data provided approximately 30× coverage. Hi-C sequencing produced 113.58 Gb from 752.17 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 492.84 Mb in 59 scaffolds, with 193 gaps, and a scaffold N50 of 17.55 Mb (Table 2).

Table 2. Genome assembly statistics.

Assembly name	ilLasPetr1.hap1.1	ilLasPetr1.hap2.1
Assembly accession	GCA_964261845.1	GCA_964261895.1
Assembly level	chromosome	scaffold
Span (Mb)	492.84	442.93
Number of chromosomes	30	N/A
Number of contigs	252	178
Contig N50	4.28 Mb	5.14 Mb
Number of scaffolds	59	41
Scaffold N50	17.55 Mb	17.32 Mb
Longest scaffold length (Mb)	27.04	N/A
Sex chromosomes	W and Z	N/A
Organelles	Mitochondrial genome: 15.25 kb	N/A

Most of the assembly sequence (99.82%) was assigned to 30 chromosomal-level scaffolds, representing 28 autosomes and the W and Z sex chromosomes. The exact order and orientation of the contigs on chromosome W (11.8–21.2 Mbp) are unknown. The sex chromosomes were identified by Hi-C signal and read coverage. The chromosome-level scaffolds, confirmed by Hi-C data, are named according to size (Figure 2; Table 3). Chromosome painting with Merian elements illustrates the distribution

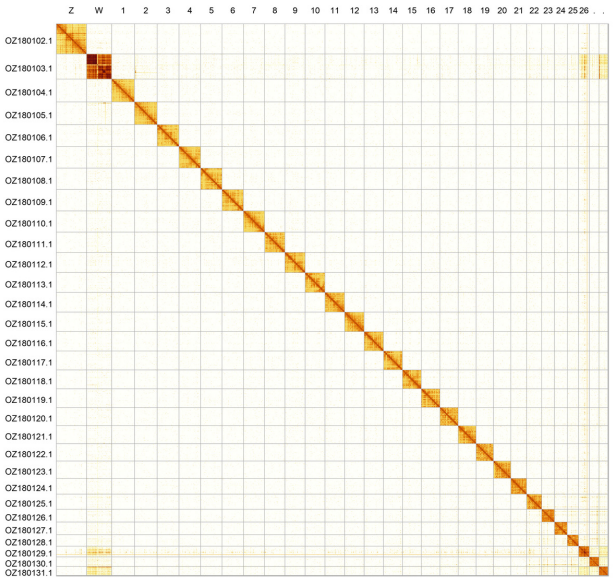

Figure 2. Hi-C contact map of the *Lasiommata petropolitana* genome assembly. Assembled chromosomes are shown in order of size and labelled along the axes. The plot was generated using PretextSnapshot.

Table 3. Chromosomal pseudomolecules in the haplotype 1 genome assembly of *Lasiommata petropolitana* ilLasPetr1.

INSDC accession	Molecule	Length (Mb)	GC%	Assigned Merian elements
OZ180104.1	1	20.35	37	M1
OZ180105.1	2	20.27	36.50	M2
OZ180106.1	3	19.42	36.50	M8
OZ180107.1	4	19.35	37	M17;M20
OZ180108.1	5	19.06	36.50	M9
OZ180109.1	6	19.06	37	M3
OZ180110.1	7	19	37	M19;M26
OZ180111.1	8	18.03	36.50	M5
OZ180112.1	9	18.03	37	M12
OZ180113.1	10	17.63	36.50	M18
OZ180114.1	11	17.55	37	M7
OZ180115.1	12	17.43	37	M14;M29
OZ180116.1	13	17.31	37	M16
OZ180117.1	14	16.84	37	M4
OZ180118.1	15	16.78	37	M6
OZ180119.1	16	16.62	37	M21
OZ180120.1	17	16.29	37	M22
OZ180121.1	18	16.02	37	M15
OZ180122.1	19	15.46	37.50	M11
OZ180123.1	20	15.44	37	M10
OZ180124.1	21	14.06	37.50	M13
OZ180125.1	22	13.50	38	M23
OZ180126.1	23	11.42	38	M24
OZ180127.1	24	11.32	38	M28
OZ180128.1	25	10.18	38	M27
OZ180129.1	26	9.61	40	M30
OZ180130.1	27	8.57	39	M25
OZ180131.1	28	7.87	40	M31
OZ180103.1	W	22.45	39	N/A
OZ180102.1	Z	27.04	36.50	MZ

of orthologues along chromosomes and highlights patterns of chromosomal evolution relative to Lepidopteran ancestral linkage groups (Figure 3).

The mitochondrial genome was also assembled. 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 64.3, and for haplotype 2, 64.2. When the two haplotypes are combined, the assembly achieves an estimated QV of 64.3. The *k*-mer completeness is 81.50% for haplotype 1, 76.71% for haplotype 2, and 99.31% for the combined haplotypes (Figure 4). BUSCO analysis using the lepidoptera_odb10 reference set (n = 5 286) (Kriventseva *et al.*, 2019) identified 98.4% of the expected gene set (single = 97.8%, duplicated = 0.6%) for haplotype 1. The snail plot in Figure 5 summarises the scaffold length distribution and other assembly statistics for haplotype 1. The blob plot in Figure 6 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) the Earth BioGenome Project Report on Assembly Standards September 2024. The EBP metric, calculated for the haplotype 1, is **6.C.Q64**, meeting the recommended reference standard.

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 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

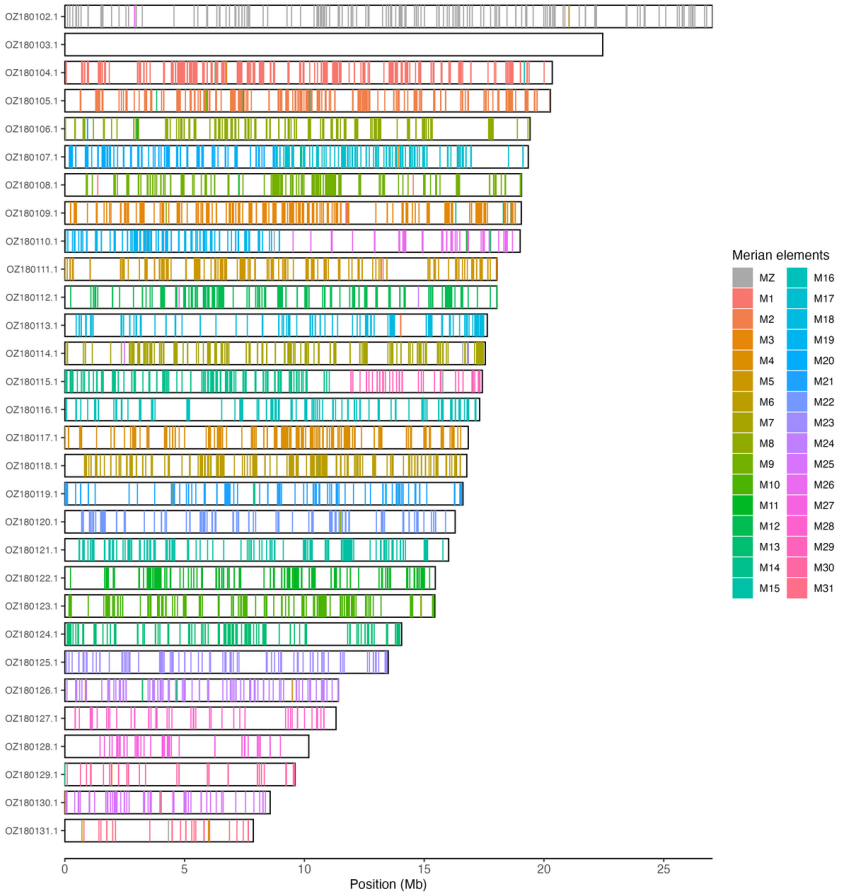

Figure 3. Merian elements painted across chromosomes in the ilLasPetr1.hap1.1 assembly of *Lasiommata petropolitana*. Chromosomes are drawn to scale, with the positions of orthologues shown as coloured bars. Each orthologue is coloured by the Merian element that it belongs to. All orthologues which could be assigned to Merian elements are shown.

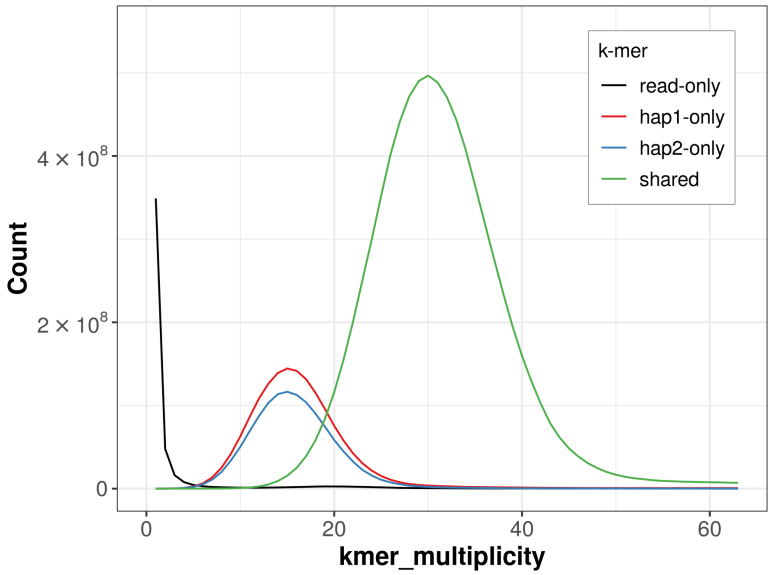

Figure 4. Evaluation of *k*-mer completeness using MerquryFK. This plot illustrates the recovery of *k*-mers from the original read data in the final assemblies. The horizontal axis represents *k*-mer multiplicity, and the vertical axis shows the number of *k*-mers. The black curve represents *k*-mers 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.

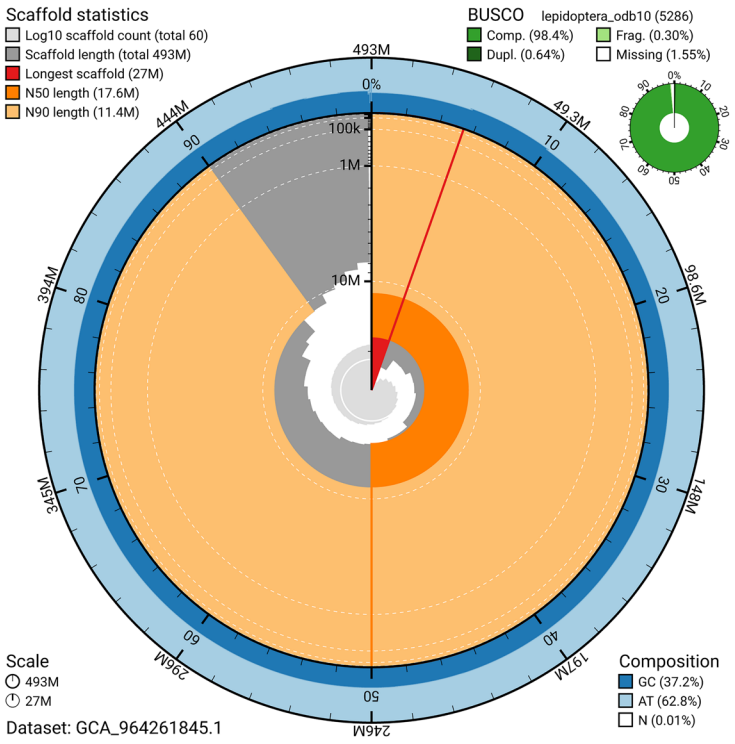

Figure 5. Assembly metrics for ilLasPetr1.hap1.1. The BlobToolKit snail plot provides an overview of assembly metrics and BUSCO gene completeness. The circumference represents the length of the whole genome sequence, and the main plot is divided into 1,000 bins around the circumference. The outermost 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.

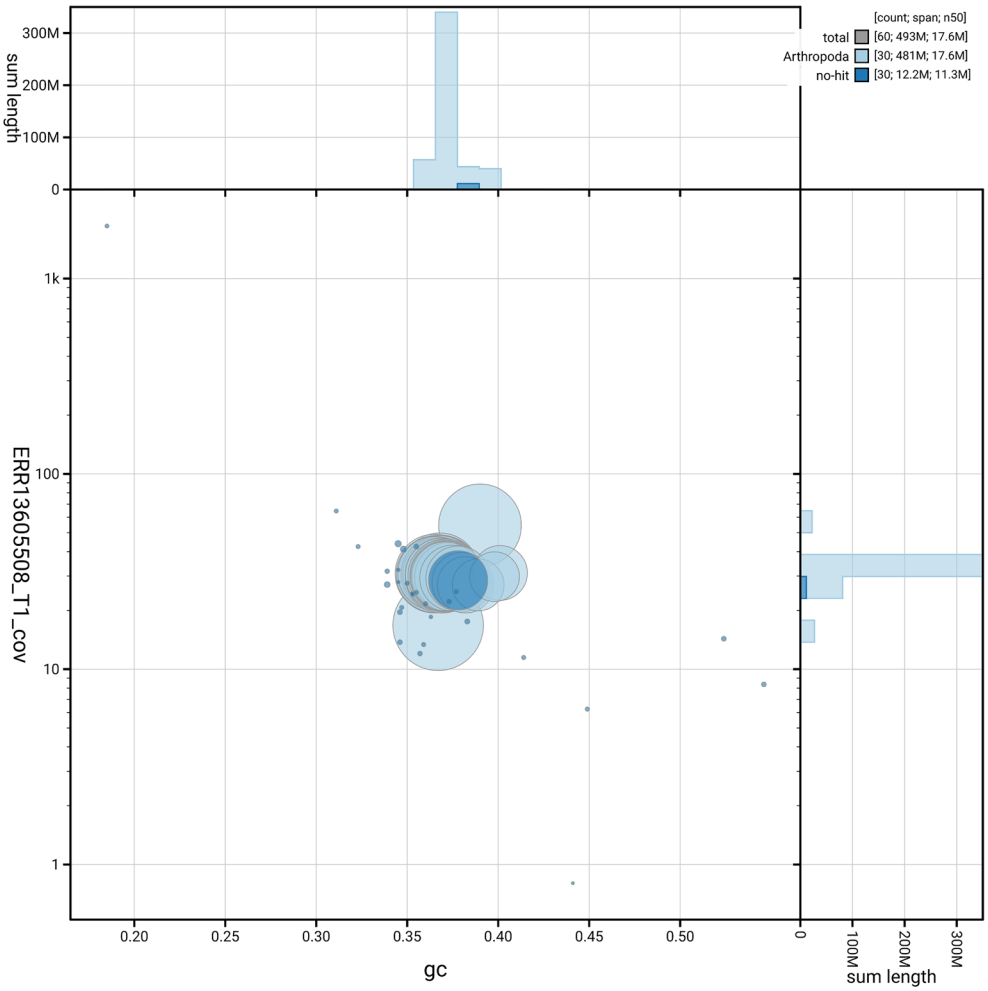

Figure 6. BlobToolKit GC-coverage plot for ilLasPetr1.hap1.1. Blob plot showing sequence coverage (vertical axis) and GC content (horizontal axis). The circles represent scaffolds, with the size proportional to scaffold length and the colour representing phylum membership. The histograms along the axes 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 *Lasiommata petropolitana* assembly.

Measure	Value	Benchmark
EBP summary (haplotype 1)	6.7.Q64	6.C.Q40
Contig N50 length	4.28 Mb	≥ 1 Mb
Scaffold N50 length	17.55 Mb	= chromosome N50
Consensus quality (QV)	Haplotype 1: 64.3; haplotype 2: 64.2; combined: 64.3	≥ 40
k-mer completeness	Haplotype 1: 81.50%; Haplotype 2: 76.71%; combined: 99.31%	≥ 95%
BUSCO	C:98.4%[S:97.8%,D:0.6%],F:0.3%,M:1.2%,n:5286	S > 90%; D < 5%
Percentage of assembly assigned to chromosomes	0%	≥ 90%

- 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: Lasiommata petropolitana (northern wall brown). Accession number PRJEB79190. The genome sequence is released openly for reuse. The *Lasiommata petropolitana* 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. The genome will be annotated using available RNA-Seq data and presented through Ensembl at the European Bioinformatics Institute. 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

- Wellcome Sanger Institute Tree of Life Management, Samples and Laboratory team
- Wellcome Sanger Institute Scientific Operations – Sequencing Operations
- Wellcome Sanger Institute Tree of Life Core Informatics team
- Tree of Life Core Informatics collective
- 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+/
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
GoaT CLI	0.2.5	https://github.com/genomehubs/goat-cli
Hifiasm	0.19.8-r603	https://github.com/chhylp123/hifiasm
HiGlass	1.13.4	https://github.com/higlass/higlass
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	N/A	https://github.com/sanger-tol/PretextSnapshot
PretextView	0.2.5	https://github.com/sanger-tol/PretextView

Software	Version	Source
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
Seqtk	1.3	https://github.com/lh3/seqtk
Singularity	3.9.0	https://github.com/sylabs/singularity
TreeVal	1.2.0	https://github.com/sanger-tol/treeval
YaHS	1.2a.2	https://github.com/c-zhou/yahs

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Open Peer Review

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Version 1

Reviewer Report 29 December 2025

https://doi.org/10.21956/wellcomeopenres.27251.r139455

✔ **Paula Escuer Pifarré**
University of Neuchâtel, Neuchâtel, Spain

Here the authors present the genome assembly of a female individual of the Lepidoptera specie *Lasiommata petropolitana*. Haplotype 1 have a total size of 492 Mb aprox assembled in 30 chromosomal scaffolds including the W and Z sex chromosomes, as well as the mitochondrial genome, haplotype 2 is assembled at scaffold level. The paper is nicely written and methods are clear, following the standard assembly and annotation pipeline used for all the genomes from Psyche Project.

Some minor comments:
- in the introduction, at the sentence "*Lasiommata petropolitana* represents a distinct evolutionary significant unit (ESU) within the genus *Lasiommata*, showing low haplotype diversification relative to its congeners, which could be due to historical population bottlenecks, restricted gene flow, or a relatively recent divergence from its common ancestor (Platania *et al.*, 2020) The species " there is a full stop missing before "The species".

- I would recommend ending the introduction justifying what this genome could bring or be interesting for. (e. g. phylogenetics, genetic studies to develope conservation plans etc.)

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: Genomics, Bioinformatics, Conservation

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 23 December 2025

https://doi.org/10.21956/wellcomeopenres.27251.r139451

Emily C Giles
Cawthron Institute (Ringgold ID: 5732), Nelson, Nelson, New Zealand

The authors present a haplotype resolved genome assembly for the Northern Wall Brown, a butterfly. The rationale for generating this assembly is not well detailed beyond stating that it is evolutionarily different from other members of the genus. The non-butterfly researcher is left wondering why the genus as a whole is interesting and why resources should be used to generate assemblies for multiple species of this genus.

A large proportion of the assembly (99%) falls into 30 pseudo chromosomes. The mitochondrial genome is also assembled. The authors used the same specimen for the PacBio HiFi library and the HiC library. They generated 1.2 million reads from the PacBio library and 752 million reads for the HiC library. The HiFi reads were assembled using Hifiasm in the Hi-C phasing mode. Scaffolding was done by mapping the HiC reads to the primary assembly and using YaHS to handle misassembles. The mitogenome was assembled using MitoHiFi. The assembly was decontaminated with the ASCC pipeline. This pipeline is nicely explained on the Sanger page that is linked, however it is noted that the pipeline is in a raw state of development. The pipeline developers indicate that the tool has been used on 500+ datasets, but one wonders what is the taxonomic breadth that this pipeline can handle? Prokaryotes, eukaryotes, microalgae to lions? Furthermore, is this pipeline applicable to genome assemblies of varying quality or only for PacBio HiFi primary assemblies? It would be nice to have this pipeline peer reviewed, but the description on the webpage is a great resource for the community.

The resulting genome assembly appears to be of high quality and contiguity. Heterozygosity does not appear to be overly low, despite the hypothesis that the species has experienced genetic bottlenecks. The coverage is not overly high (30X), but scaffold N50 is large and the contact map indicates that the assembly was well scaffolded. The sex chromosomes are large compared to the autosomes; this is interesting for researchers that don't work with butterflies. Complete BUSCOs are extremely high and duplicated BUSCOs are very low. Overall, this looks like a great assembly.

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

Partly

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, population genomics, marine genomics, speciation

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.