



DATA NOTE

The genome sequence of a lauxanid fly, *Meiosimyza decipiens*

(Loew, 1847)

[version 1; peer review: 2 approved, 1 approved with reservations]

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<https://doi.org/10.12688/wellcomeopenres.23785.1>Latest published: 19 May 2025, 10:245
<https://doi.org/10.12688/wellcomeopenres.23785.1>**Abstract**

We present a genome assembly from a male *Meiosimyza decipiens* (fly; Arthropoda; Insecta; Diptera; Lauxaniidae). The genome sequence has a total length of 436.39 megabases. Most of the assembly (99.68%) is scaffolded into 6 chromosomal pseudomolecules, including the X and Y sex chromosomes. The mitochondrial genome has also been assembled and is 16.39 kilobases in length.

Keywords

Meiosimyza decipiens, lauxanid fly genome sequence, chromosomal, Diptera



This article is included in the [Tree of Life gateway](#).

Open Peer Review**Approval Status** ? ✓ ✓

	1	2	3
version 1	?	✓	✓
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Species taxonomy

Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Eremoneura; Cyclorrhapha; Schizophora; Acalyptratae; Lauxanioidea; Lauxaniidae; *Meiosimyza*; *Meiosimyza decipiens* (Loew, 1847) (NCBI:txid1262309)

Background

Meiosimyza decipiens, also known as *Lyciella decipiens* or *Sapromyza decipiens* (Shatalkin, 2000), is a species of true fly in the family Lauxaniidae. The species in this family are often considered difficult to identify, with many of the 14 genera sharing the same general appearance: light brown to yellow, medium-sized flies with few obvious separating marks. In particular, *Lyciella* is a taxon recognised by experienced dipterists by its lack of distinguishing features (Mark Mitchell, pers. comm.).

Meiosimyza decipiens is a common species of British woodlands; the NBN Atlas shows records from Cornwall in the South to Ross and Cromarty in the North (NBN Atlas Partnership, 2025). However, despite its frequency, relatively little is known of its biology, or that of its congeners. Lauxaniid larvae are considered to typically be phytosaprophagous, feeding on decaying leaf litter and maturing quickly (Semelbauer & Kozánek, 2014). This holds for *M. decipiens*, the larvae of which have been found in rotting leaves. Although any further information is scarce, the genome of this species will provide new insights into Lauxaniid biology.

Here we present a chromosome-level genome sequence for *Meiosimyza decipiens*, based on a male specimen from Wytham Woods, Oxfordshire, United Kingdom (Figure 1).

Genome sequence report

Sequencing data

The genome of a specimen of *Meiosimyza decipiens* (Figure 1) was sequenced using Pacific Biosciences single-molecule



Figure 1. Photograph of the *Meiosimyza decipiens* (idLycDeci1) specimen used for genome sequencing.

HiFi long reads, generating 19.70 Gb from 2.10 million reads. GenomeScope analysis of the PacBio HiFi data estimated the haploid genome size at 407.72 Mb, with a heterozygosity of 0.50% and repeat content of 11.59%. These values provide an initial assessment of genome complexity and the challenges anticipated during assembly. Based on this estimated genome size, the sequencing data provided approximately 45.0x coverage of the genome. Chromosome conformation Hi-C sequencing produced 106.39 Gb from 704.56 million reads. Table 1 summarises the specimen and sequencing information.

Assembly statistics

The primary haplotype was assembled, and contigs corresponding to an alternate haplotype were also deposited in INSDC databases. The assembly was improved by manual curation, which corrected 98 misjoins or missing joins and removed two haplotypic duplications. These interventions reduced the scaffold count by 74.74% and increased the scaffold N50 by 1.38%. The final assembly has a total length of 436.39 Mb in 23 scaffolds, with 290 gaps, and a scaffold N50 of 100.65 Mb (Table 2).

The snail plot in Figure 2 provides a summary of the assembly statistics, indicating the distribution of scaffold lengths and other assembly metrics. Figure 3 shows the distribution of scaffolds by GC proportion and coverage. Figure 4 presents a cumulative assembly plot, with separate curves representing different scaffold subsets assigned to various phyla, illustrating the completeness of the assembly.

Most of the assembly sequence (99.69%) was assigned to 6 chromosomal-level scaffolds, representing 4 autosomes and the X and Y sex chromosome. These chromosome-level scaffolds, confirmed by Hi-C data, are named according to size (Figure 5; Table 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 in GenBank.

Assembly quality metrics

The estimated Quality Value (QV) and *k*-mer completeness metrics, along with BUSCO completeness scores, were calculated for each haplotype and the combined assembly. The QV reflects the base-level accuracy of the assembly, while *k*-mer completeness indicates the proportion of expected *k*-mers identified in the assembly. BUSCO scores provide a measure of completeness based on benchmarking universal single-copy orthologues.

The primary haplotype has a QV of 60.8, and the combined primary and alternate assemblies achieve an estimated QV of 61.5. The *k*-mer completeness for the primary haplotype is 91.22%, and for the alternate haplotype it is 89.29%, while the combined primary and alternate assemblies achieve a *k*-mer completeness of 99.64%. BUSCO analysis using the diptera_odb10 reference set ($n = 3,285$) indicated a completeness score of 98.7% (single = 97.9%, duplicated = 0.7%).

Table 1. Specimen and sequencing data for *Meiosimyza decipiens*.

Project information			
Study title	Lyciella decipiens		
Umbrella BioProject	PRJEB68004		
Species	<i>Meiosimyza decipiens</i>		
BioSpecimen	SAMEA112232826		
NCBI taxonomy ID	1262309		
Specimen information			
Technology	ToLID	BioSample accession	Organism part
PacBio long read sequencing	idLycDeci1	SAMEA112233332	Whole organism
Hi-C sequencing	idLycDeci1	SAMEA112233332	Whole organism
Sequencing information			
Platform	Run accession	Read count	Base count (Gb)
Hi-C Illumina NovaSeq 6000	ERR12245602	7.05e+08	106.39
PacBio Sequel IIe	ERR12205275	2.10e+06	19.7

Table 2. Genome assembly data for *Meiosimyza decipiens*.

Genome assembly		
Assembly name	idLycDeci1.1	
Assembly accession	GCA_963680825.1	
Alternate haplotype accession	GCA_963680805.1	
Assembly level for primary assembly	chromosome	
Span (Mb)	436.39	
Number of contigs	313	
Number of scaffolds	23	
Longest scaffold (Mb)	148.74	
Assembly metrics	Measure	Benchmark
Contig N50 length	3.71 Mb	≥ 1 Mb
Scaffold N50 length	100.65 Mb	= chromosome N50
Consensus quality (QV)	Primary: 60.8; alternate: 62.5; combined 61.5	≥ 40
k-mer completeness	Primary: 91.22%; alternate: 89.29%; combined: 99.64%	$\geq 95\%$
BUSCO*	C:98.7%[S:97.9%,D:0.7%] F:0.2%,M:1.1%,n:3,285	$S > 90\%$; $D < 5\%$
Percentage of assembly mapped to chromosomes	99.69%	$\geq 90\%$
Sex chromosomes	X and Y	localised homologous pairs
Organelles	Mitochondrial genome: 16.39 kb	complete single alleles

* BUSCO scores based on the diptera_odb10 BUSCO set using version 5.5.0. C = complete [S = single copy, D = duplicated], F = fragmented, M = missing, n = number of orthologues in comparison.

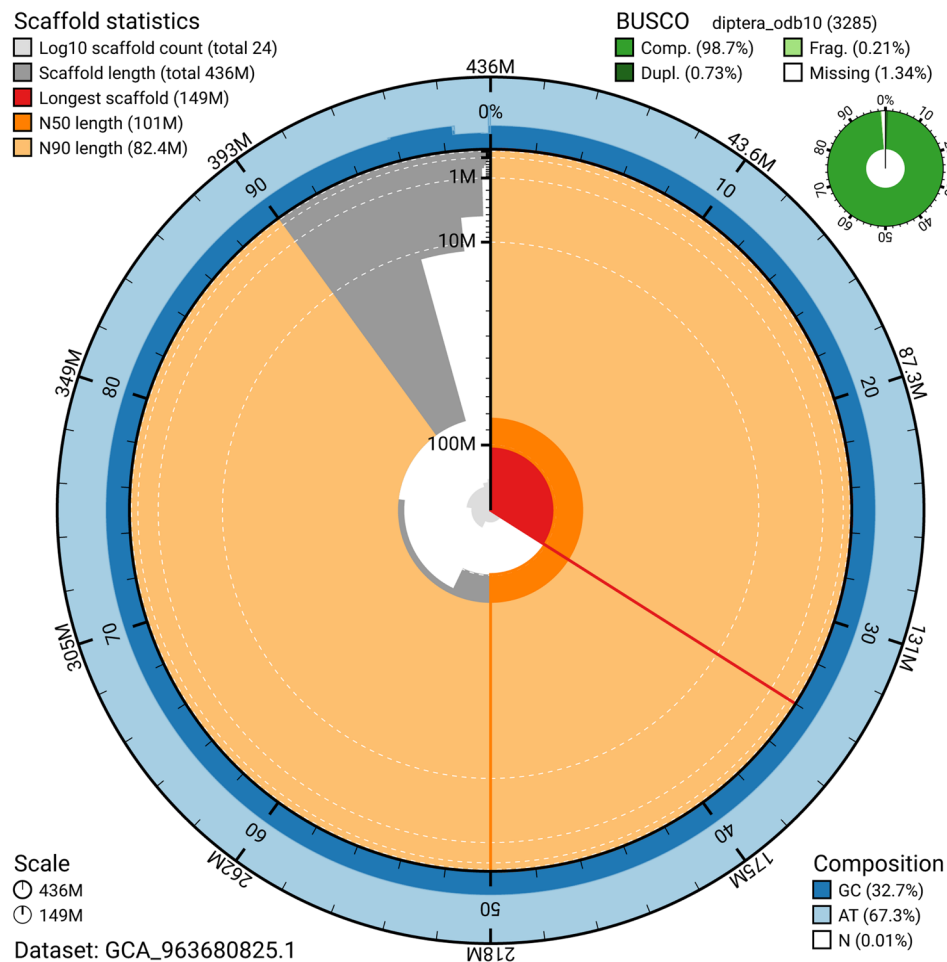


Figure 2. Genome assembly of *Meiosimyza decipiens*, idLycDeci1.1: metrics. The BlobToolKit snail plot provides an overview of assembly metrics and BUSCO gene completeness. The circumference represents the length of the whole genome sequence, and the main plot is divided into 1,000 bins around the circumference. 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 diptera_odb10 set is presented at the top right. An interactive version of this figure is available at https://blobtoolkit.genomehubs.org/view/GCA_963680825.1/snail.

Table 2 provides assembly metric benchmarks adapted from Rhie *et al.* (2021) and the Earth BioGenome Project Report on Assembly Standards September 2024. The assembly achieves the EBP reference standard of 6.C.61.

Methods

Sample acquisition and DNA barcoding

An adult male *Meiosimyza decipiens* (specimen ID Ox002649, ToLID idLycDeci1) was collected from Wytham Woods, Oxfordshire, United Kingdom (latitude 51.77, longitude -1.34) on 2022-08-10, using a sweep net. The specimen was collected by James McCulloch and Liam Crowley (University of Oxford), identified by James McCulloch and then preserved on dry ice.

The initial identification was verified by an additional DNA barcoding process according to the framework developed by Twyford *et al.* (2024). A small sample was dissected from the specimen and stored in ethanol, while the remaining parts were shipped on dry ice to the Wellcome Sanger Institute (WSI) (Pereira *et al.*, 2022). The tissue was lysed, the COI marker region was amplified by PCR, and amplicons were sequenced and compared to the BOLD database, confirming the species identification (Crowley *et al.*, 2023). Following whole genome sequence generation, the relevant DNA barcode region was also used alongside the initial barcoding data for sample tracking at the WSI (Twyford *et al.*, 2024). The standard operating procedures for Darwin Tree of Life barcoding have been deposited on protocols.io (Beasley *et al.*, 2023).

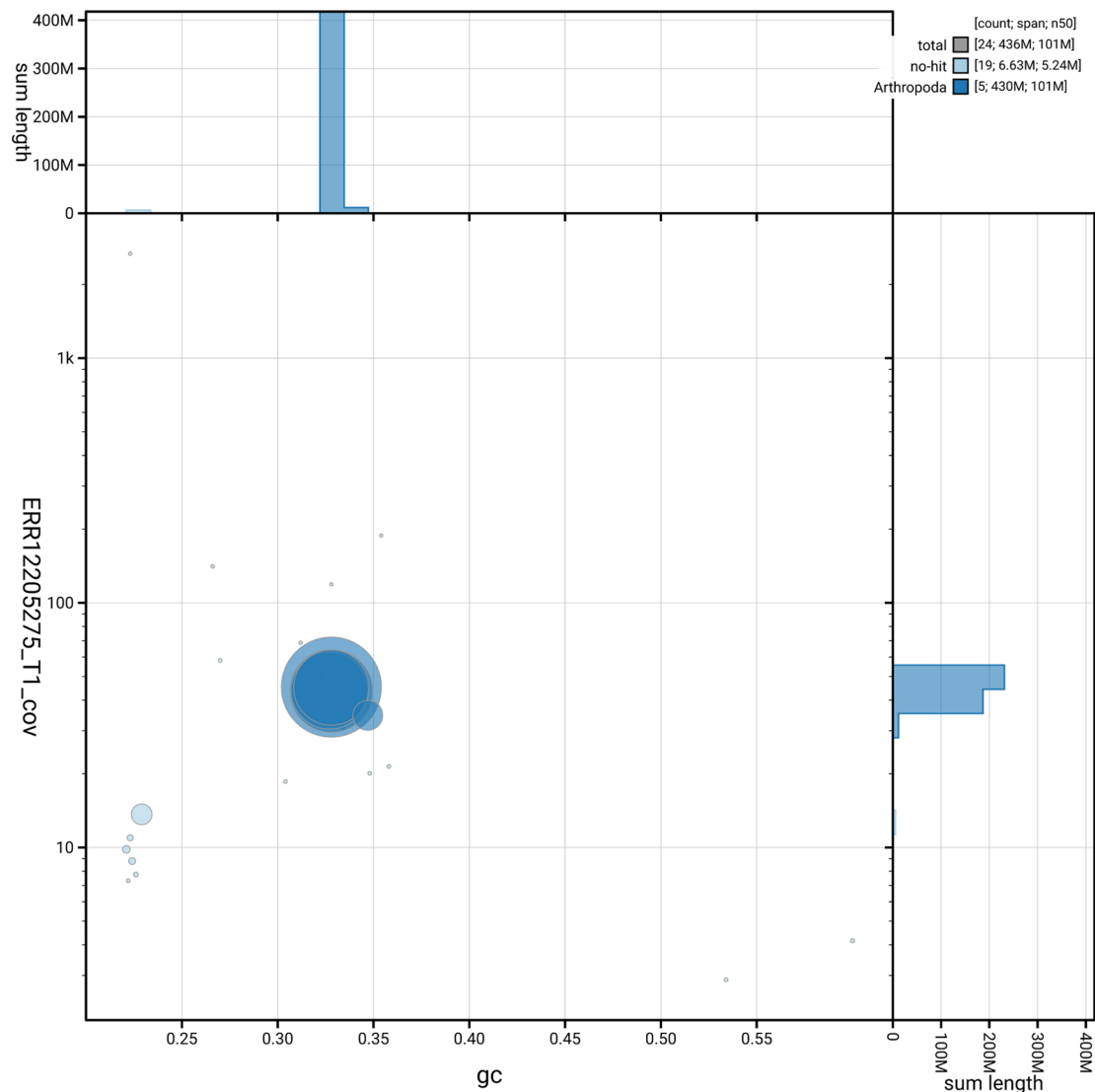


Figure 3. Genome assembly of *Meiosimyza decipiens*, idLycDeci1.1: BlobToolKit GC-coverage plot. Blob plot showing sequence coverage (vertical axis) and GC content (horizontal axis). The circles represent scaffolds, with the size proportional to scaffold length and the colour representing phylum membership. 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 at https://blobtoolkit.genomehubs.org/view/GCA_963680825.1/blob.

Metadata collection for samples adhered to the Darwin Tree of Life project standards described by Lawniczak *et al.* (2022).

Nucleic acid extraction

The workflow for high molecular weight (HMW) DNA extraction at the Wellcome Sanger Institute (WSI) Tree of Life Core Laboratory includes a sequence of procedures: sample preparation and homogenisation, DNA extraction, fragmentation and purification. Detailed protocols are available on protocols.io (Denton *et al.*, 2023b). The idLycDeci1 sample was prepared for DNA extraction by weighing and dissecting it on dry ice

(Jay *et al.*, 2023). Tissue from the whole organism was homogenised using a PowerMasher II tissue disruptor (Denton *et al.*, 2023a). HMW DNA was extracted using the Automated MagAttract v2 protocol (Oatley *et al.*, 2023a). For ultra-low input (ULI) PacBio sequencing, DNA was fragmented using the Covaris g-TUBE method (Oatley *et al.*, 2023c). Sheared DNA was purified by solid-phase reversible immobilisation, using AMPure PB beads to eliminate shorter fragments and concentrate the DNA (Oatley *et al.*, 2023b). The concentration of the sheared and purified DNA was assessed using a Nanodrop spectrophotometer and Qubit Fluorometer using the

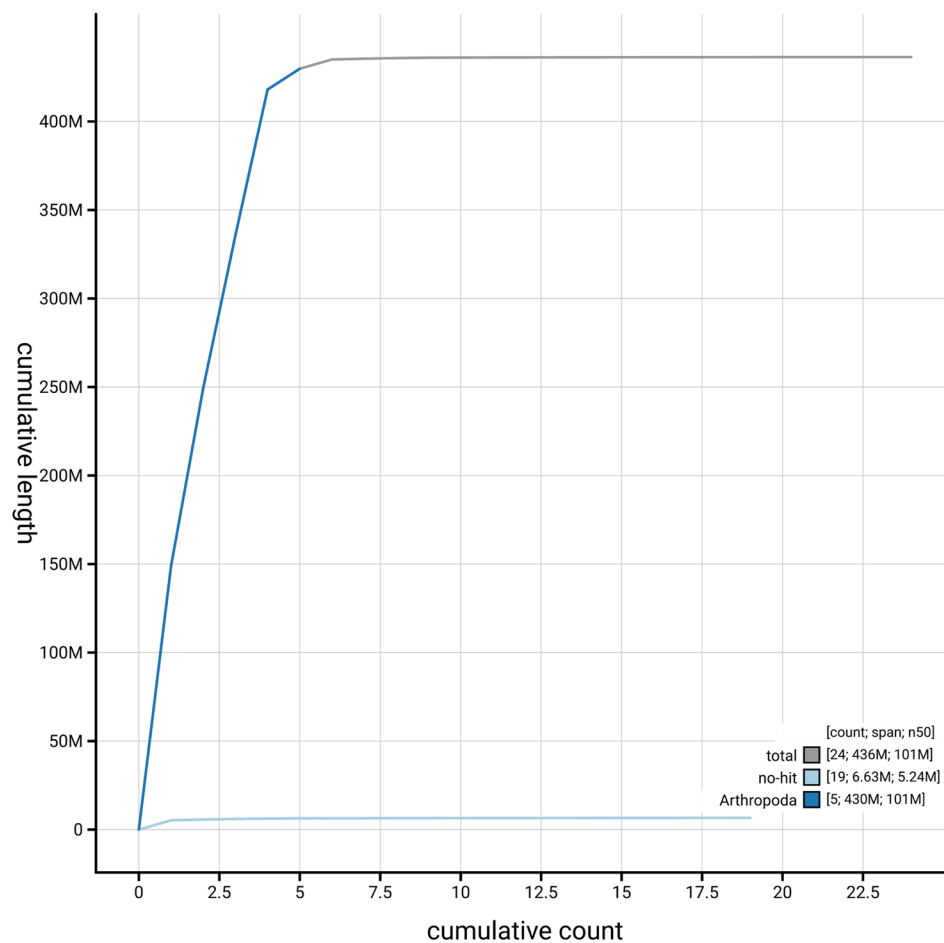


Figure 4. Genome assembly of *Meiosimyza decipiens*, idLycDeci1.1: BlobToolKit cumulative sequence plot. The grey line shows cumulative length for all scaffolds. Coloured lines show cumulative lengths of scaffolds assigned to each phylum using the buscogenes taxrule. An interactive version of this figure is available at https://blobtoolkit.genomehubs.org/view/GCA_963680825.1/cumulative.

Qubit dsDNA High Sensitivity Assay kit. Fragment size distribution was evaluated by running the sample on the FemtoPulse system.

Hi-C sample preparation

Tissue from the whole organism of the idLycDeci1 sample was processed for Hi-C sequencing at the WSI Scientific Operations core, using the Arima-HiC v2 kit. In brief, 20–50 mg of frozen tissue (stored at -80°C) was fixed, and the DNA crosslinked using a TC buffer. After crosslinking, the tissue was homogenised using the Diagnocine Power Masher-II and BioMasher-II tubes and pestles. Following the Arima-HiC v2 kit manufacturer's instructions, crosslinked DNA was digested using a restriction enzyme master mix. The 5'-overhangs were filled in and labelled with biotinylated nucleotides and proximally ligated. An overnight incubation was carried out for enzymes to digest remaining proteins and for crosslinks to reverse. A clean up was performed with SPRIselect beads prior to library preparation. Additionally, the biotinylation percentage was estimated

using the Qubit Fluorometer v4.0 (Thermo Fisher Scientific) and Qubit HS Assay Kit and Arima-HiC v2 QC beads.

Library preparation and sequencing

Library preparation and sequencing were performed at the WSI Scientific Operations core.

PacBio HiFi

The sample requires Covaris g-TUBE shearing to approximately 10 kb prior to library preparation. Ultra-low input libraries were prepared using PacBio SMRTbell® Express Template Prep Kit 2.0 and PacBio SMRTbell® gDNA Sample Amplification Kit. To begin, samples were normalised to 20 ng of DNA. Initial removal of single-strand overhangs, DNA damage repair, and end repair/A-tailing were performed per manufacturer's instructions. From the SMRTbell® gDNA Sample Amplification Kit, amplification adapters were then ligated. A 0.85X pre-PCR clean-up was performed with Promega ProNex beads and the sample was then divided into two for

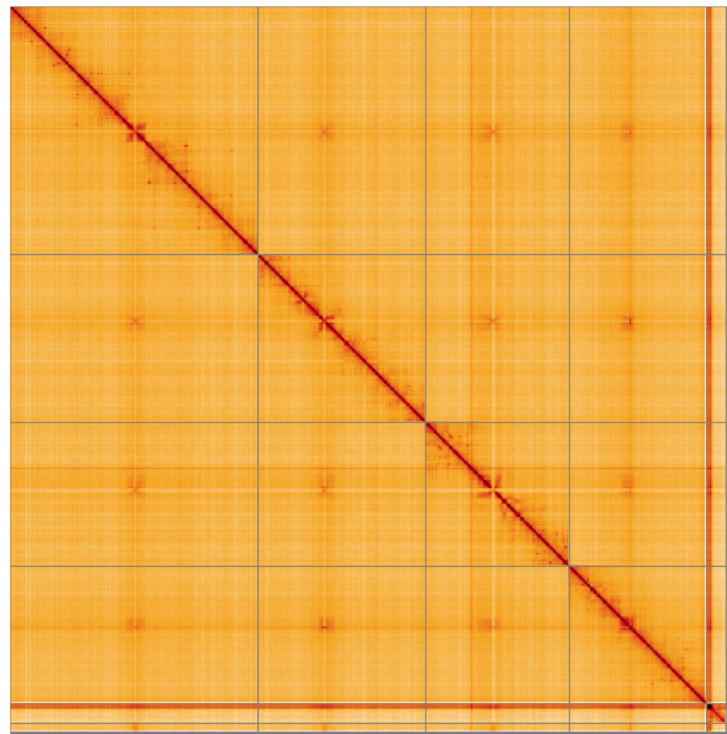


Figure 5. Genome assembly of *Meiosimyza decipiens*: Hi-C contact map of the idLycDeci1.1 assembly, visualised using HiGlass. Chromosomes are shown in order of size from left to right and top to bottom. An interactive version of this figure may be viewed at https://genome-note-higlass.tol.sanger.ac.uk/l/?d=Z31HCpX7S_yUc1ZIS-xV0Q.

Table 3. Chromosomal pseudomolecules in the genome assembly of *Meiosimyza decipiens*, idLycDeci1.

INSDC accession	Name	Length (Mb)	GC%
OY804258.1	1	148.74	33
OY804259.1	2	100.65	33
OY804260.1	3	86.24	32.5
OY804261.1	4	82.4	33
OY804262.1	X	11.75	34.5
OY804263.1	Y	5.24	23
OY804264.1	MT	0.02	22.5

a dual PCR. PCR reactions A and B each followed the PCR programs as described in the manufacturer's protocol. A 0.85X post-PCR clean-up was performed with ProNex beads for PCR reactions A and B and DNA concentration was quantified using the Qubit Fluorometer v4.0 (Thermo Fisher Scientific) and Qubit HS Assay Kit and fragment size analysis was carried out using the Agilent Femto Pulse Automated Pulsed Field CE Instrument (Agilent Technologies) and gDNA 55kb BAC analysis kit. PCR reactions A and B were then pooled, ensuring

the total mass was ≥ 500 ng in 47.4 μ l. The pooled sample then repeated the process for DNA damage repair, end repair/A-tailing and additional hairpin adapter ligation. A 1X clean-up was performed with ProNex beads and DNA concentration was quantified using the Qubit and fragment size analysis was carried out using the Agilent Femto Pulse Automated Pulsed Field CE Instrument (Agilent Technologies). Size selection was performed using Sage Sciences' PippinHT system with target fragment size determined by analysis from the Femto Pulse, usually a value between 4000 and 9000 bp. Size selected libraries were then cleaned-up using 1.0X ProNex beads and normalised to 2 nM before proceeding to sequencing.

Samples were sequenced using the Sequel IIe system (Pacific Biosciences, California, USA). The concentration of the library loaded onto the Sequel IIe was in the range 40–135 pM. The SMRT link software, a PacBio web-based end-to-end workflow manager, was used to set-up and monitor the run, as well as perform primary and secondary analysis of the data upon completion.

Hi-C

For Hi-C library preparation, DNA was fragmented using the Covaris E220 sonicator (Covaris) and size selected using SPRISelect beads to 400 to 600 bp. The DNA was then enriched using the Arima-HiC v2 kit Enrichment beads. Using the NEBNext Ultra II DNA Library Prep Kit (New England

Biolabs) for end repair, a-tailing, and adapter ligation. This uses a custom protocol which resembles the standard NEBNext Ultra II DNA Library Prep protocol but where library preparation occurs while DNA is bound to the Enrichment beads. For library amplification, 10 to 16 PCR cycles were required, determined by the sample biotinylation percentage. The Hi-C sequencing was performed using paired-end sequencing with a read length of 150 bp on an Illumina NovaSeq 6000 instrument.

Genome assembly, curation and evaluation

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 first assembled using Hifiasm (Cheng *et al.*, 2021) with the --primary option. Haplotypic duplications were identified and removed using purge_dups (Guan *et al.*, 2020). The Hi-C reads were mapped to the primary contigs using bwa-mem2 (Vasimuddin *et al.*, 2019). The contigs were further scaffolded using the provided Hi-C data (Rao *et al.*, 2014) 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 MERQUERY.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 (article in preparation). Flat files and maps used in curation were generated in TreeVal (Pointon *et al.*, 2023). Manual curation was primarily conducted using PretextView (Harry, 2022), with additional insights provided by JBrowse2 (Diesh *et al.*, 2023) and HiGlass (Kerpedjiev *et al.*, 2018). Scaffolds were visually inspected and corrected as described by Howe *et al.* (2021). Any identified contamination, missed joins, and mis-joins were corrected, and duplicate sequences were tagged and removed. The sex chromosomes were assigned based on read coverage analysis. The curation process is documented at <https://gitlab.com/wtsi-grit/rapid-curation> (article in preparation).

Assembly quality assessment

The Merquery.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 the primary and alternate haplotypes using the k -mer databases ($k = 31$) that were computed prior to genome assembly. The analysis outputs included assembly QV scores and completeness statistics.

A Hi-C contact map was produced for the final version of the assembly. The Hi-C reads were aligned using bwa-mem2 (Vasimuddin *et al.*, 2019) and the alignment files were combined using SAMtools (Danecek *et al.*, 2021). The Hi-C alignments were converted into a contact map using BEDTools (Quinlan & Hall, 2010) and the Cooler tool suite (Abdennur & Mirny, 2020). The contact map is visualised in HiGlass (Kerpedjiev *et al.*, 2018).

The blobtoolkit pipeline is a Nextflow port of the previous Snakemake Blobtoolkit pipeline (Challis *et al.*, 2020). It aligns the PacBio reads in SAMtools and minimap2 (Li, 2018) and generates coverage tracks for regions of fixed size. In parallel, it queries the GoaT database (Challis *et al.*, 2023) to identify all matching BUSCO lineages to run BUSCO (Manni *et al.*, 2021). For the three domain-level BUSCO lineages, the pipeline aligns the BUSCO genes to the UniProt Reference Proteomes database (Bateman *et al.*, 2023) with DIAMOND blastp (Buchfink *et al.*, 2021). The genome is also divided into chunks according to the density of the BUSCO genes from the closest taxonomic lineage, and each chunk is aligned to the UniProt Reference Proteomes database using DIAMOND blastx. Genome sequences without a hit are chunked using seqtk and aligned to the NT database with blastn (Altschul *et al.*, 1990). The blobtools suite combines all these 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), relying on the Conda package manager, the Bioconda initiative (Grünig *et al.*, 2018), the Biocontainers infrastructure (da Veiga Leprevost *et al.*, 2017), as well as the Docker (Merkel, 2014) and Singularity (Kurtzer *et al.*, 2017) containerisation solutions.

Table 4 contains a list of relevant software tool versions and sources.

Wellcome Sanger Institute – Legal and Governance

The materials that have contributed to this genome note have been supplied by a Darwin Tree of Life Partner. The submission of materials by a Darwin Tree of Life Partner is subject to the ‘**Darwin Tree of Life Project Sampling Code of Practice**’, which can be found in full on the Darwin Tree of Life website [here](#). By agreeing with and signing up to the Sampling Code of Practice, the Darwin Tree of Life Partner agrees they will meet the legal and ethical requirements and standards set out within this document in respect of all samples acquired for, and supplied to, the Darwin Tree of Life Project.

Further, 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

Table 4. Software tools: versions and sources.

Software tool	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	427104ea91c78c3b8b8b49f1a7d6bbeaa869ba1c	https://github.com/thegenemyers/FASTK
Gfastats	1.3.6	https://github.com/vgl-hub/gfastats
Goat CLI	0.2.5	https://github.com/genomehubs/goat-cli
Hifiasm	0.19.5-r587	https://github.com/chhylp123/hifiasm
HiGlass	44086069ee7d4d3f6f3f0012569789ec138f42b84a a44357826c0b6753eb28de	https://github.com/higlass/higlass
MercuryFK	d00d98157618f4e8d1a9190026b19b471055b22e	https://github.com/thegenemyers/MERURY.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
NCBI Datasets	15.12.0	https://github.com/ncbi/datasets
Nextflow	23.04.1	https://github.com/nextflow-io/nextflow
PretextView	0.2.5	https://github.com/sanger-tol/PretextView
purge_dups	1.2.5	https://github.com/dfguan/purge_dups
samtools	1.19.2	https://github.com/samtools/samtools
sanger-tol/ascc	-	https://github.com/sanger-tol/ascc
sanger-tol/blobtoolkit	0.5.1	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

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 further undertaken according to a Research Collaboration Agreement or Material Transfer Agreement entered into by the Darwin Tree of Life Partner,

Genome Research Limited (operating as the Wellcome Sanger Institute), and in some circumstances other Darwin Tree of Life collaborators.

Data availability

European Nucleotide Archive: *Lyciella decipiens*. Accession number PRJEB68004; <https://identifiers.org/ena.embl/PRJEB68004>. The genome sequence is released openly for

reuse. The *Meiosimyza decipiens* genome sequencing initiative is part of the Darwin Tree of Life (DTOL) project. 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 the [Ensembl](#) pipeline at the European Bioinformatics Institute. Raw data and assembly accession identifiers are reported in [Table 1](#) and [Table 2](#).

Author information

Members of the University of Oxford and Wytham Woods Genome Acquisition Lab are listed here: <https://doi.org/10.5281/zenodo.12157525>.

Members of the Darwin Tree of Life Barcoding collective are listed here: <https://doi.org/10.5281/zenodo.12158331>.

Members of the Wellcome Sanger Institute Tree of Life Management, Samples and Laboratory team are listed here: <https://doi.org/10.5281/zenodo.12162482>.

Members of Wellcome Sanger Institute Scientific Operations: Sequencing Operations are listed here: <https://doi.org/10.5281/zenodo.12165051>.

Members of the Wellcome Sanger Institute Tree of Life Core Informatics team are listed here: <https://doi.org/10.5281/zenodo.12160324>.

Members of the Tree of Life Core Informatics collective are listed here: <https://doi.org/10.5281/zenodo.12205391>.

Members of the Darwin Tree of Life Consortium are listed here: <https://doi.org/10.5281/zenodo.4783558>.

References

- Abdennur N, Mirny LA: **Cooler: scalable storage for Hi-C data and other genomically labeled arrays.** *Bioinformatics.* 2020; **36**(1): 311–316. [PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
- 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](#)
- Beasley J, Uhl R, Forrest LL, et al.: **DNA barcoding SOPs for the Darwin Tree of Life project.** *protocols.io.* 2023; [Accessed 25 June 2024]. [Publisher 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, Kumar S, Sotero-Caio C, et al.: **Genomes on a Tree (GoaT): a versatile, scalable search engine for genomic and sequencing project metadata across the eukaryotic Tree of Life [version 1; peer review: 2 approved].** *Wellcome Open Res.* 2023; **8**: 24. [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](#)
- Crowley L, Allen H, Barnes I, et al.: **A sampling strategy for genome sequencing the British terrestrial arthropod fauna [version 1; peer review: 2 approved].** *Wellcome Open Res.* 2023; **8**: 123. [PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
- da Veiga Leprevost F, Grünig BA, Alves Aflitos S, et al.: **BioContainers: an open-source and community-driven framework for software standardization.** *Bioinformatics.* 2017; **33**(16): 2580–2582. [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](#)
- Denton A, Oatley G, Cornwell C, et al.: **Sanger Tree of Life sample homogenisation: PowerMash.** *protocols.io.* 2023a. [Publisher Full Text](#)
- Denton A, Yatsenko H, Jay J, et al.: **Sanger Tree of Life wet laboratory protocol collection V.1.** *protocols.io.* 2023b. [Publisher Full Text](#)
- Diesh C, Stevens GJ, Xie P, et al.: **JBrowse 2: a modular genome browser with views of synteny and structural variation.** *Genome Biol.* 2023; **24**(1): 74. [PubMed Abstract](#) | [Publisher Full Text](#) | [Free 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](#)
- Grünig B, Dale R, Sjödin A, et al.: **Bioconda: sustainable and comprehensive software distribution for the life sciences.** *Nat Methods.* 2018; **15**(7): 475–476. [PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
- Guan D, McCarthy SA, Wood J, et al.: **Identifying and removing haplotypic duplication in primary genome assemblies.** *Bioinformatics.* 2020; **36**(9): 2896–2898. [PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
- Harry E: **PretextView (Paired REad TEXTure Viewer): a desktop application for viewing pretext contact maps.** 2022. [Reference Source](#)
- Howe K, Chow W, Collins J, et al.: **Significantly improving the quality of genome assemblies through curation.** *GigaScience.* 2021; **10**(1): g1aa153. [PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
- Jay J, Yatsenko H, Narváez-Gómez JP, et al.: **Sanger Tree of Life sample preparation: triage and dissection.** *protocols.io.* 2023. [Publisher 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](#)
- 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](#)
- Lawnczak MKN, Davey RP, Rajan J, et al.: **Specimen and sample metadata standards for biodiversity genomics: a proposal from the Darwin Tree of Life project [version 1; peer review: 2 approved with reservations].** *Wellcome Open Res.* 2022; **7**: 187. [Publisher Full Text](#)

- Li H: **Minimap2: pairwise alignment for nucleotide sequences.** *Bioinformatics.* 2018; **34**(18): 3094–3100.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
- Manni M, Berkeley MR, Seppely 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. [Accessed 2 April 2024].
[Reference Source](#)
- NBN Atlas Partnership: **Meiosimyza decipiens map on the NBN Atlas.** 2025.
[Reference Source](#)
- Oatley G, Denton A, Howard C: **Sanger Tree of Life HMW DNA extraction: automated MagAttract v.2.** *protocols.io.* 2023a.
[Publisher Full Text](#)
- Oatley G, Sampaio F, Howard C: **Sanger Tree of Life fragmented DNA clean up: automated SPRI.** *protocols.io.* 2023b.
[Publisher Full Text](#)
- Oatley G, Sampaio F, Kitchin L, *et al.*: **Sanger Tree of Life HMW DNA fragmentation: covaris g-TUBE for ULI PacBio.** *protocols.io.* 2023c; [Accessed 13 June 2024].
[Publisher Full Text](#)
- Pereira L, Sivell O, Sivess L, *et al.*: **DTOL Taxon-specific Standard Operating Procedure for the terrestrial and freshwater arthropods working group.** 2022.
[Publisher Full Text](#)
- Pointon DL, Eagles W, Sims Y, *et al.*: **sanger-tol/treeval v1.0.0 – Ancient Atlantis.** 2023.
[Publisher Full Text](#)
- Quinlan AR, Hall IM: **BEDTools: a flexible suite of utilities for comparing genomic features.** *Bioinformatics.* 2010; **26**(6): 841–842.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
- 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](#)
- Semelbauer M, Kozánek M: **Immature stages of Meiosimyza Hendel 1925 and related genera (Diptera, Lauxaniidae).** *Org Divers Evol.* 2014; **14**: 89–103.
[Publisher Full Text](#)
- Shatalkin AI: **Keys to the Palearctic flies of the family Lauxaniidae (Diptera).** 2000; **5**.
[Reference Source](#)
- Twyford AD, Beasley J, Barnes I, *et al.*: **A DNA barcoding framework for taxonomic verification in the Darwin Tree of Life project [version 1; peer review: 2 approved].** *Wellcome Open Res.* 2024; **9**: 339.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
- Uliano-Silva M, Ferreira JGRN, Krashennikova 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](#)
- 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 14 July 2025

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This is the first report of the high quality genome sequence of the lauxanid fly *Meiosimyza decipiens*. The genome assembly reported here is of size 436.9 Mb and the mitochondrial genome is of size 16.39 kb. The sequencing was carried out using high end technology to arrive at a high quality genome sequence. The data are available for download from the links provided in the article.

The link in captions of figures 2,3 &4 land on the same page. The authors can correct the link at this stage.

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: Bioinformatics; Genomics

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 12 June 2025

<https://doi.org/10.21956/wellcomeopenres.26234.r124226>

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**Komal Kumar Bollepogu Raja** 

Baylor College of Medicine, Houston, Texas, USA

The article by McCulloch and Crowley et al. presents the genome sequence of *Meiosimzya decipens* with a total length of 436.389 Megabases. The introduction is brief as not much is known about the biology of this species. The assembly metrics are impressive and meet the current standards in genome sequencing. For instance, the combined k-mer completeness is 99.64% and the BUSCO percentage is 99.64. The methodology is good and allows for reproducibility. All standard bioinformatics tools have been used by the authors. Overall, the data is well presented, high-quality and is a good genomic resource for further research.

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:** Bioinformatics, genomics, single cell genomics and Neurobiology

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 June 2025

<https://doi.org/10.21956/wellcomeopenres.26234.r124218>

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**Christophe Klopp** 

INRAE, Castanet-Tolosan, France

The authors present the first genome assembly of *Meiosimyza decipiens*. The data types and processing steps are standard.

It is not clear from the material and methods if the Hi-C was used during the assembly to split haplotypes. This should be added.

The authors did not scaffold the second haplotype which has close to the same length as the primary one. In a pangenome perspective this would have been appreciated by downstream users.

It would have been interesting to have the comment of the authors on the low N50 (3.7Mb) origin for such a small genome assembled with 45x of HiFi.

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?

Partly

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

Yes

Competing Interests: No competing interests were disclosed.**Reviewer Expertise:** Genome assembly and annotation

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, however I have significant reservations, as outlined above.
