



THE UNIVERSITY *of* EDINBURGH

Edinburgh Research Explorer

The genome sequence of a drosophilid fruit fly, *Drosophila funebris* (Fabricius, 1789)[version 1; peer review: awaiting peer review]

Citation for published version:

Obbard, DJ 2023, 'The genome sequence of a drosophilid fruit fly, *Drosophila funebris* (Fabricius, 1789)[version 1; peer review: awaiting peer review]', *Wellcome Open Research*, vol. 8, no. 437. <https://doi.org/10.12688/wellcomeopenres.20035.1>

Digital Object Identifier (DOI):

[10.12688/wellcomeopenres.20035.1](https://doi.org/10.12688/wellcomeopenres.20035.1)

Link:

[Link to publication record in Edinburgh Research Explorer](#)

Document Version:

Publisher's PDF, also known as Version of record

Published In:

Wellcome Open Research

General rights

Copyright for the publications made accessible via the Edinburgh Research Explorer is retained by the author(s) and / or other copyright owners and it is a condition of accessing these publications that users recognise and abide by the legal requirements associated with these rights.

Take down policy


The University of Edinburgh has made every reasonable effort to ensure that Edinburgh Research Explorer content complies with UK legislation. If you believe that the public display of this file breaches copyright please contact openaccess@ed.ac.uk providing details, and we will remove access to the work immediately and investigate your claim.





DATA NOTE

The genome sequence of a drosophilid fruit fly, *Drosophila funebris* (Fabricius, 1789) [version 1; peer review: awaiting peer review]

Darren J. Obbard ¹, Wellcome Sanger Institute Tree of Life programme, Wellcome Sanger Institute Scientific Operations: DNA Pipelines collective, Tree of Life Core Informatics collective, Darwin Tree of Life Consortium

¹Institute of Ecology and Evolution, The University of Edinburgh, Edinburgh, Scotland, UK

V1 First published: 10 Oct 2023, 8:437
<https://doi.org/10.12688/wellcomeopenres.20035.1>
Latest published: 10 Oct 2023, 8:437
<https://doi.org/10.12688/wellcomeopenres.20035.1>

Open Peer Review

Approval Status AWAITING PEER REVIEW

Any reports and responses or comments on the article can be found at the end of the article.

Abstract

We present a genome assembly from an individual male *Drosophila funebris* (drosophilid fruit fly; Arthropoda; Insecta; Diptera; Drosophilidae). The genome sequence is 181.1 megabases in span. Most of the assembly is scaffolded into 7 chromosomal pseudomolecules, including the X and Y sex chromosomes. The mitochondrial genome has also been assembled and is 16.15 kilobases in length.

Keywords

Drosophila funebris, drosophilid fruit fly, genome sequence, chromosomal, Diptera



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

Corresponding author: Darwin Tree of Life Consortium (mark.blaxter@sanger.ac.uk)

Author roles: Obbard DJ: Investigation, Resources, Writing – Original Draft Preparation, Writing – Review & Editing;

Competing interests: No competing interests were disclosed.

Grant information: This work was supported by Wellcome through core funding to the Wellcome Sanger Institute (206194) and the Darwin Tree of Life Discretionary Award (218328). The fly collections were funded by the UK Biotechnology and Biological Sciences Research Council through Grant No. BB/T007516/1 to D.J.O.

The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Copyright: © 2023 Obbard DJ *et al.* This is an open access article distributed under the terms of the [Creative Commons Attribution License](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

How to cite this article: Obbard DJ, Wellcome Sanger Institute Tree of Life programme, Wellcome Sanger Institute Scientific Operations: DNA Pipelines collective *et al.* **The genome sequence of a drosophilid fruit fly, *Drosophila funebris* (Fabricius, 1789) [version 1; peer review: awaiting peer review]** Wellcome Open Research 2023, 8:437 <https://doi.org/10.12688/wellcomeopenres.20035.1>

First published: 10 Oct 2023, 8:437 <https://doi.org/10.12688/wellcomeopenres.20035.1>

Species taxonomy

Eukaryota; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Eremoneura; Cyclorrhapha; Schizophora; Acalyptratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; *Drosophila*; *funnebris* group; *funnebris* subgroup; *Drosophila funnebris* (Fabricius, 1789) (NCBI:txid7221).

Background

Drosophila funnebris (Fabricius, 1789) is a medium to large sized (3.5–4.0 mm) mid-brown drosophilid ‘fruit fly’ (Figure 1A and 1B), and is one of around 30 British and Irish species of *Drosophila* (Chandler, 2023). In life, it is easily distinguished from the other drosophilid species in the region by its mid-brown colour and relatively long yellowish legs. *Drosophila funnebris* (originally placed in *Musca*) was the first drosophilid species to be formally described, and thus provides the type for the genus *Drosophila* and family Drosophilidae. Unfortunately, because it is only distantly related to the laboratory model *D. melanogaster* (which is in the subgenus *Sophophora*), the well-known paraphyly of the genus *Drosophila* cannot be rectified without the undesirable taxonomic instability that would result from renaming *Drosophila melanogaster* to *Sophophora melanogaster* (reviewed in Grimaldi, 2022; O’Grady & Markow, 2009).

Originally from the Palaearctic, *Drosophila funnebris* is a now a global – although not generally common – human commensal (Bächli, 2023; Grimaldi, 2022). Unlike its closest relatives, which are primarily fungus specialists, *D. funnebris* is a facultative fungus breeder that is broadly attracted to decaying plant matter, especially that associated with human activity

(Grimaldi, 2022; Shorrocks & Charlesworth, 1980). In the UK, the adults can be seen in any month of the year but are most often recorded in July to November (GBIF Secretariat, 2023). Specimens have been reared from wild fungi, such as *Boletus edulis* (Chandler, 2021), but using yeasted fruit baits the adults can be collected across a range of habitats and are often found in the largest numbers in association with farms (Figure 1C; Basden, 1954; Shorrocks, 1977). In common with many other human-commensal *Drosophila*, *D. funnebris* can be maintained in laboratory culture. As a consequence, this species appeared as an early genetic model (e.g. Spencer, 1928; Timofeeff-Rissovsy, 1930) and – like *D. melanogaster* – was studied for variation in chromosomal inversions (e.g. Berrie & Sansome, 1948; Dubinin & Tiniakov, 1946). However, it has only intermittently appeared in experimental studies since, usually with a behavioural or ecological focus (Arizmendi *et al.*, 2008; Ewing, 1979; Merrell, 1951).

Here we present a chromosomally complete genome sequence for *Drosophila funnebris*, derived from the DNA of two male offspring from a wild female collected on yeasted banana bait at Drumness Farm, Perthshire, as part of the Darwin Tree of Life Project. This genome sequence will help to resolve relationships among the Drosophilidae and will further build on the value of this family as a model clade for comparative genomics and molecular evolution. This project is a collaborative effort to sequence all named eukaryotic species in the Atlantic Archipelago of Britain and Ireland.

Genome sequence report

The genome was sequenced from one male *Drosophila funnebris* (Figure 1) reared at the University of Edinburgh, Scotland, UK (55.92, –3.17). A total of 133-fold coverage in Pacific Biosciences single-molecule HiFi long reads was generated. Primary assembly contigs were scaffolded with chromosome conformation Hi-C data. Manual assembly curation corrected 19 missing joins or mis-joins, reducing the scaffold number by 1.52%.

The final assembly has a total length of 181.1 Mb in 519 sequence scaffolds with a scaffold N50 of 26.8 Mb (Table 1). A summary of the assembly statistics is shown in Figure 2, while the distribution of assembly scaffolds on GC proportion and coverage is shown in Figure 3. The cumulative assembly plot in Figure 4 shows curves for subsets of scaffolds assigned to different phyla. Most (96.46%) of the assembly sequence was assigned to 7 chromosomal-level scaffolds, representing 5 autosomes and the X and Y sex chromosomes. Chromosome-scale scaffolds confirmed by the Hi-C data are named in order of size (Figure 5; Table 2). The X and Y chromosomes were identified by read coverage. Repetitive scaffolds of the Y chromosome whose location could not be determined were left as unlocalised sequences. While not fully phased, the assembly deposited is of one haplotype. Contigs corresponding to the second haplotype have also been deposited. The mitochondrial genome was also assembled and can be found as a contig within the multifasta file of the genome submission.

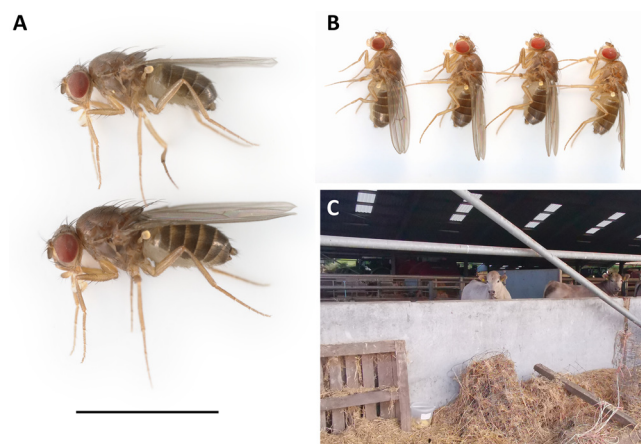


Figure 1. A: Male (above) and female (below) *Drosophila funnebris* presented with a 3 mm scale bar. **B:** The four lab-reared brothers selected for sequencing. Sample SAMEA12110696 (left) was used for Hi-C sequencing, and sample SAMEA12110696 (second left) was used for PacBio sequencing. **C:** The location for the bait from which the mother of the sequenced flies was collected (Drumness, Perthshire, Scotland; 56.320 N, 3.781 W).

Table 1. Genome data for *Drosophila funebris*, idDroFune2.1.

Project accession data		
Assembly identifier	idDroFune2.1	
Species	<i>Drosophila funebris</i>	
Specimen	idDroFune2	
NCBI taxonomy ID	7221	
BioProject	PRJEB57268	
BioSample ID	SAMEA12110453	
Isolate information	idDroFune2, male: whole organism (DNA sequencing) idDroFune1, male: whole organism (Hi-C scaffolding)	
Assembly metrics*		Benchmark
Consensus quality (QV)	62.9	≥ 50
k-mer completeness	100%	≥ 95%
BUSCO**	C:98.8%[S:98.5%,D:0.2%], F:0.4%,M:0.8%,n:3,285	C ≥ 95%
Percentage of assembly mapped to chromosomes	96.46%	≥ 95%
Sex chromosomes	X and Y chromosomes	localised homologous pairs
Organelles	Mitochondrial genome assembled	complete single alleles
Raw data accessions		
PacificBiosciences SEQUEL II	ERR10462073	
Hi-C Illumina	ERR10466807	
Genome assembly		
Assembly accession	GCA_958295475.1	
Accession of alternate haplotype	GCA_958295065.1	
Span (Mb)	181.1	
Number of contigs	882	
Contig N50 length (Mb)	0.7	
Number of scaffolds	519	
Scaffold N50 length (Mb)	26.8	
Longest scaffold (Mb)	30.03	

* Assembly metric benchmarks are adapted from column VGP-2020 of "Table 1: Proposed standards and metrics for defining genome assembly quality" from (Rhie *et al.*, 2021).

** BUSCO scores based on the diptera_odb10 BUSCO set using v5.3.2. C = complete [S = single copy, D = duplicated], F = fragmented, M = missing, n = number of orthologues in comparison. A full set of BUSCO scores is available at https://blobtoolkit.genomehubs.org/view/Drosophila_funebris/dataset/CATQHR01/busco.

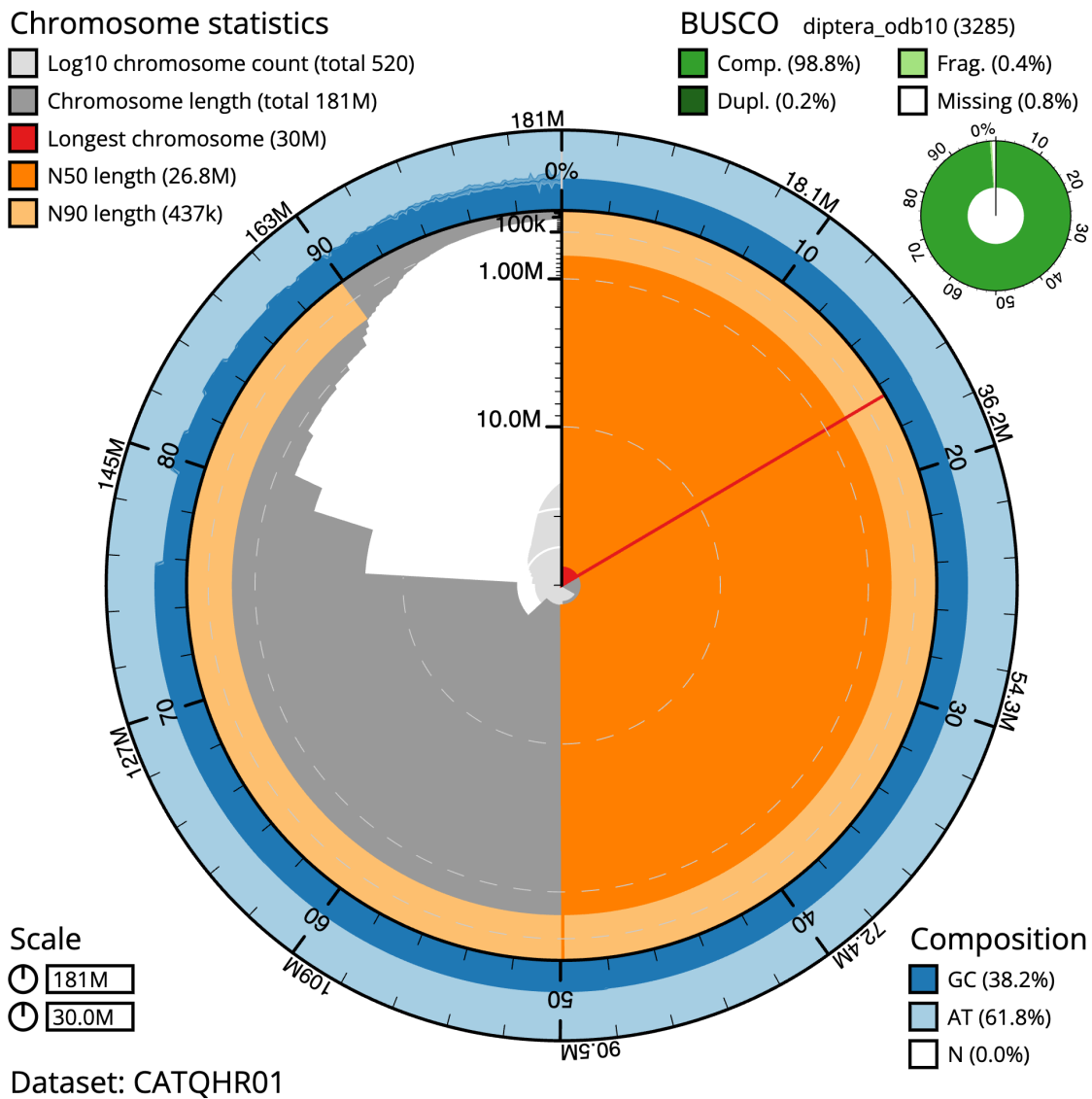


Figure 2. Genome assembly of *Drosophila funebris*, idDroFune2.1: metrics. The BlobToolKit Snailplot shows N50 metrics and BUSCO gene completeness. The main plot is divided into 1,000 size-ordered bins around the circumference with each bin representing 0.1% of the 181,096,236 bp assembly. The distribution of scaffold lengths is shown in dark grey with the plot radius scaled to the longest scaffold present in the assembly (30,028,665 bp, shown in red). Orange and pale-orange arcs show the N50 and N90 scaffold lengths (26,827,462 and 437,266 bp), respectively. The pale grey spiral shows the cumulative scaffold count on a log scale with white scale lines showing successive orders of magnitude. The blue and pale-blue area around the outside of the plot shows the distribution of GC, AT and N percentages in the same bins as the inner plot. A summary of complete, fragmented, duplicated and missing BUSCO genes in the diptera_odb10 set is shown in the top right. An interactive version of this figure is available at https://blobtoolkit.genomehubs.org/view/Drosophila_funebris/dataset/CATQHR01/snail.

The estimated Quality Value (QV) of the final assembly is 62.9 with k -mer completeness of 100%, and the assembly has a BUSCO v5.3.2 completeness of 98.8% (single = 98.5%, duplicated = 0.2%), using the diptera_odb10 reference set ($n = 3,285$).

Metadata for specimens, spectral estimates, sequencing runs, contaminants and pre-curation assembly statistics can be found at <https://links.tol.sanger.ac.uk/species/7221>.

Methods

Sample acquisition and nucleic acid extraction

Drosophila funebris specimens were first-generation male progeny from a wild-collected female. The sequenced flies were reared on *Drosophila* banana malt medium at the University of Edinburgh (latitude 55.92, longitude -3.17), and were harvested on 2021-10-02. The mother was collected from banana/yeast bait at a farm in Perthshire, Scotland (56.32, -3.78) on 2021-08-05, and had been mated prior to collection. The

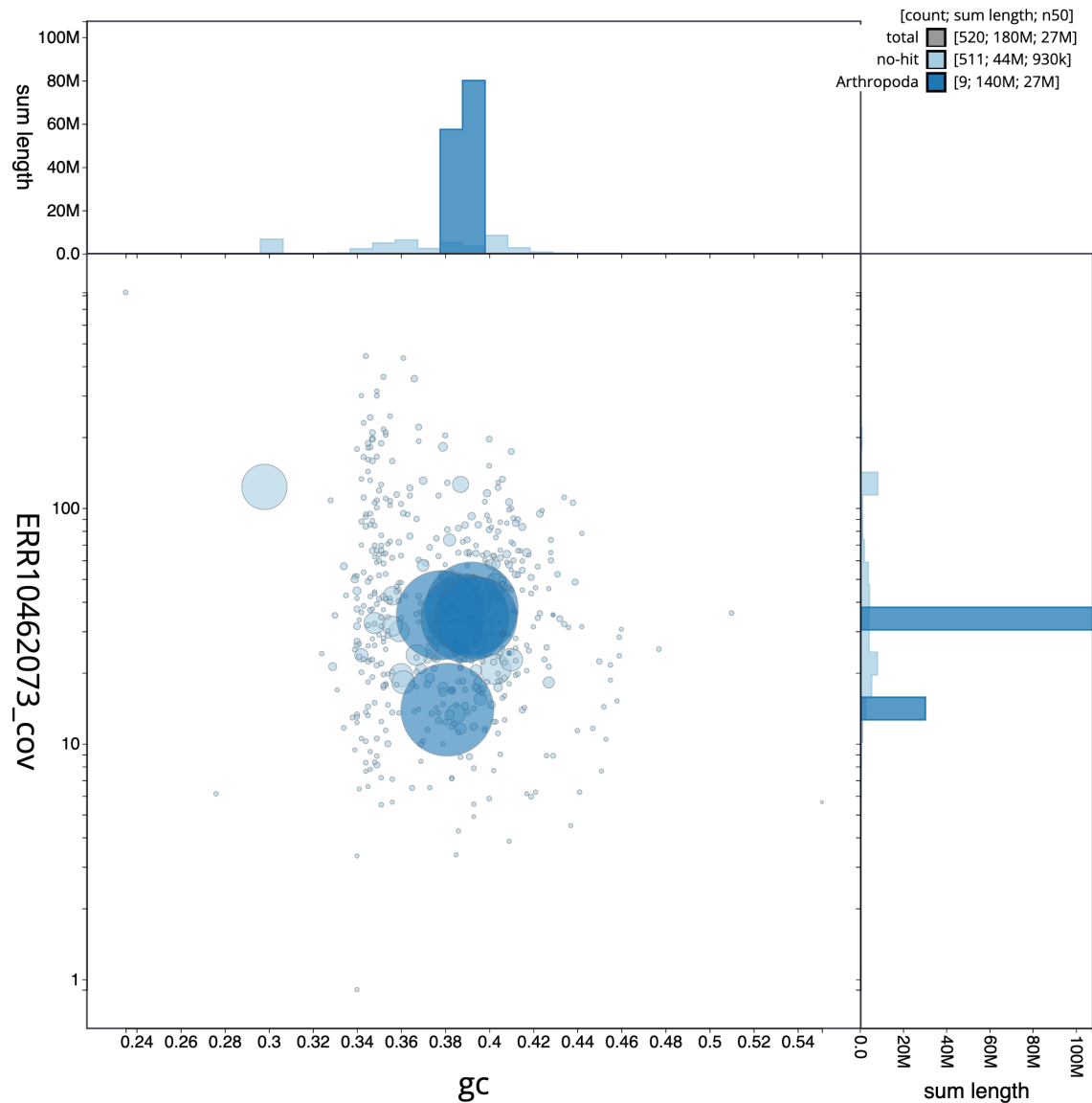


Figure 3. Genome assembly of *Drosophila funebris*, idDroFune2.1: BlobToolKit GC-coverage plot. Scaffolds are coloured by phylum. Circles are sized in proportion to scaffold length. Histograms show the distribution of scaffold length sum along each axis. An interactive version of this figure is available at https://blobtoolkit.genomehubs.org/view/Drosophila_funebris/dataset/CATQHR01/blob.

flies were collected and identified by Darren Obbard (University of Edinburgh), and species identification was confirmed by examination of the progeny. Each living anaesthetised fly was placed directly into the collection tube and frozen from live at -80°C . The sample with specimen ID SAN00001902 (ToLID idDroFune2) was used for DNA sequencing and the sample with specimen ID SAN00001901 (ToLID idDroFune1) was used for Hi-C scaffolding.

DNA was extracted at the Tree of Life laboratory, Wellcome Sanger Institute (WSI). The idDroFune2 sample was weighed and dissected on dry ice. Tissue from the whole organism was disrupted using a Nippi Powermasher fitted with a BioMasher

pestle. High molecular weight (HMW) DNA was extracted using the Qiagen MagAttract HMW DNA extraction kit. HMW DNA was sheared into an average fragment size of 12–20 kb in a Megaruptor 3 system with speed setting 30. Sheared DNA was purified by solid-phase reversible immobilisation using AMPure PB beads with a 1.8X ratio of beads to sample to remove the shorter fragments and concentrate the DNA sample. The concentration of the sheared and purified DNA was assessed using a Nanodrop spectrophotometer and Qubit Fluorometer and Qubit dsDNA High Sensitivity Assay kit. Fragment size distribution was evaluated by running the sample on the FemtoPulse system.

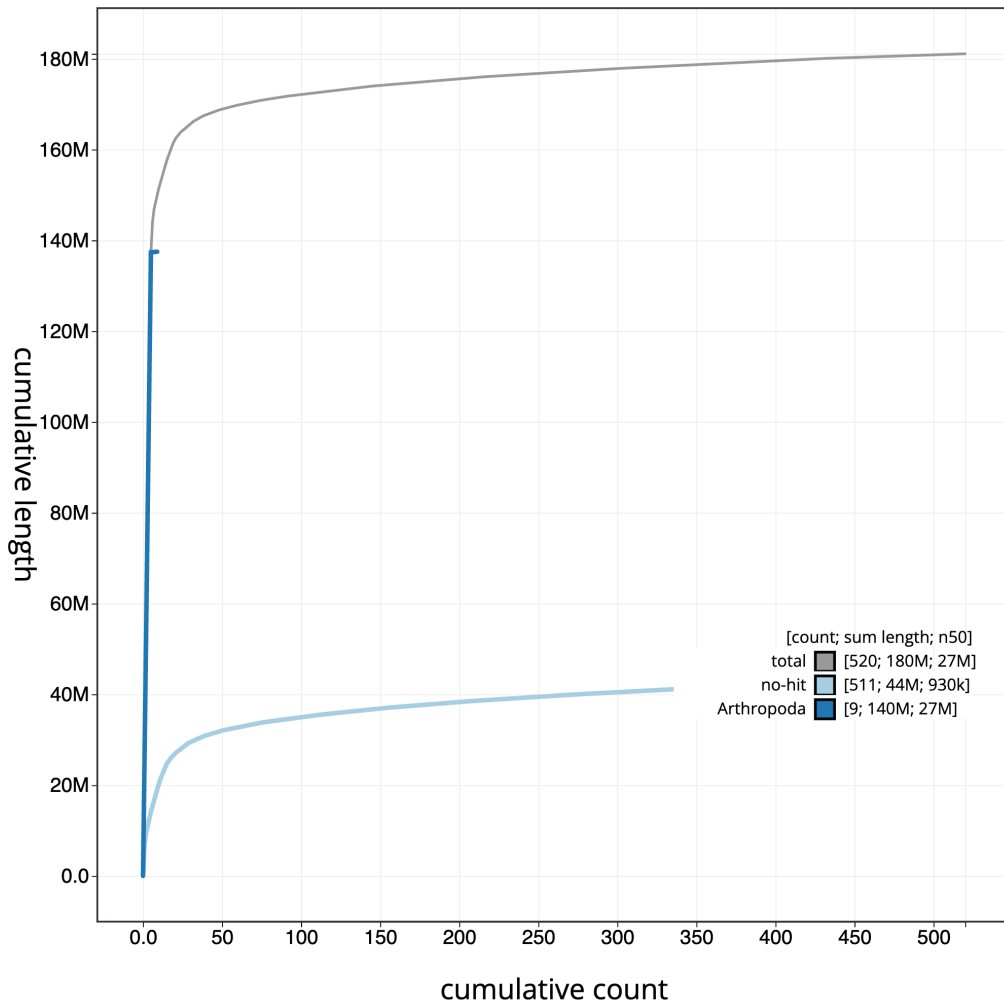


Figure 4. Genome assembly of *Drosophila funebris*, idDroFune2.1: BlobToolKit cumulative sequence plot. The grey line shows cumulative length for all scaffolds. Coloured lines show cumulative lengths of scaffolds assigned to each phylum using the buscogenes taxrule. An interactive version of this figure is available at https://blobtoolkit.genomehubs.org/view/Drosophila_funebris/dataset/CATQHR01/cumulative.

Sequencing

Pacific Biosciences HiFi circular consensus DNA sequencing libraries were constructed according to the manufacturers' instructions. DNA sequencing was performed by the Scientific Operations core at the WSI on a Pacific Biosciences SEQUEL II (HiFi) instruments. Hi-C data were generated from tissue of idDroFune1 using the Arima2 kit and sequenced on the Illumina NovaSeq 6000 instrument.

Genome assembly, curation and evaluation

Assembly was carried out with HiCanu (Nurk *et al.*, 2020) and haplotypic duplication was identified and removed with `purge_dups` (Guan *et al.*, 2020). The assembly was then scaffolded with Hi-C data (Rao *et al.*, 2014) using YaHS (Zhou *et al.*, 2023). The assembly was checked for

contamination and corrected as described previously (Howe *et al.*, 2021). Manual curation was performed using HiGlass (Kerpedjiev *et al.*, 2018) and Pretext (Harry, 2022). The mitochondrial genome was assembled using MitoHiFi (Uliano-Silva *et al.*, 2023), which runs MitoFinder (Allio *et al.*, 2020) or MITOS (Bernt *et al.*, 2013) and uses these annotations to select the final mitochondrial contig and to ensure the general quality of the sequence.

A Hi-C map for the final assembly was produced using `bwa-mem2` (Vasimuddin *et al.*, 2019) in the Cooler file format (Abdennur & Mirny, 2020). To assess the assembly metrics, the *k*-mer completeness and QV consensus quality values were calculated in Merqury (Rhie *et al.*, 2020). This work was done using Nextflow (Di Tommaso *et al.*, 2017)

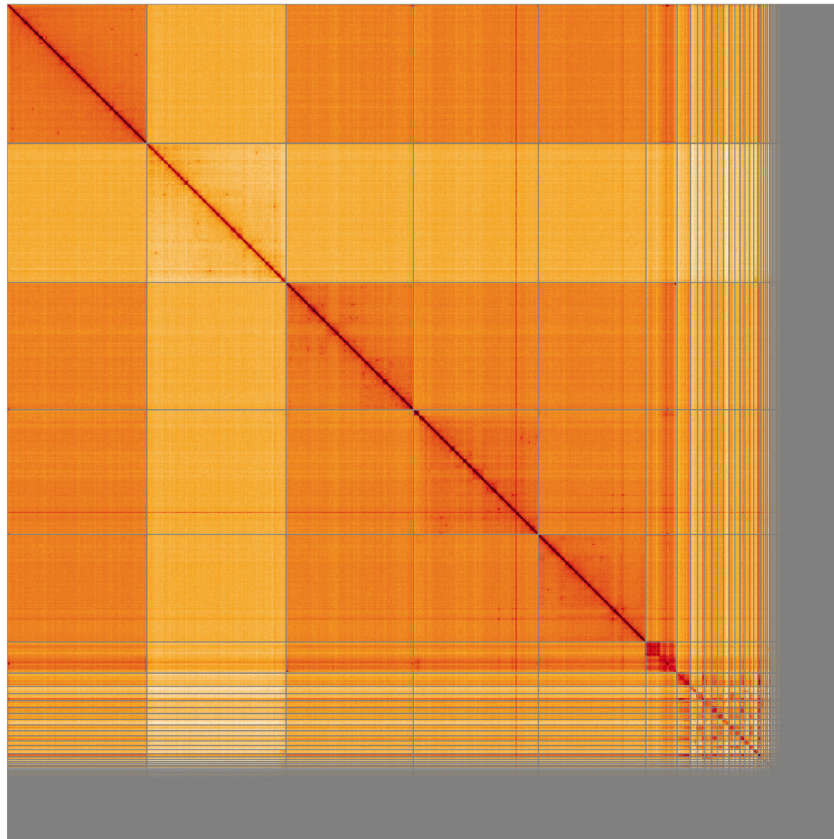


Figure 5. Genome assembly of *Drosophila funebris*, idDroFune2.1: Hi-C contact map of the idDroFune2.1 assembly, visualised using HiGlass. Chromosomes are shown in order of size from left to right and top to bottom. An interactive version of this figure may be viewed at <https://genome-note-higlass.tol.sanger.ac.uk/!/?d=dBGzsWLuRGOh668piP9ZIQ>.

Table 2. Chromosomal pseudomolecules in the genome assembly of *Drosophila funebris*, idDroFune2.

INSDC accession	Chromosome	Length (Mb)	GC%
OY282423.1	1	30.03	39.0
OY282425.1	2	27.41	38.0
OY282426.1	3	26.83	39.0
OY282427.1	4	23.16	39.5
OY282428.1	5	6.71	30.0
OY282424.1	X	29.94	38.0
OY282422.1	Y	2.85	40.5
OY282429.1	MT	0.02	23.5

DSL2 pipelines “sanger-tol/readmapping” (Surana *et al.*, 2023a) and “sanger-tol/genomenote” (Surana *et al.*, 2023b). The genome was analysed within the BlobToolKit

environment (Challis *et al.*, 2020) and BUSCO scores (Manni *et al.*, 2021; Simão *et al.*, 2015) were calculated.

Table 3 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

Table 3. Software tools: versions and sources.

Software tool	Version	Source
BlobToolKit	4.1.7	https://github.com/blobtoolkit/blobtoolkit
BUSCO	5.3.2	https://gitlab.com/ezlab/busco
Hicanu	2.2	https://github.com/marbl/canu
HiGlass	1.11.6	https://github.com/higlass/higlass
Mercury	MercuryFK	https://github.com/thegenemyers/MERQURY.FK
MitoHiFi	2	https://github.com/marcelauliano/MitoHiFi
PretextView	0.2	https://github.com/wtsi-hpag/PretextView
purge_dups	1.2.3	https://github.com/dfguan/purge_dups
sanger-tol/genomenote	v1.0	https://github.com/sanger-tol/genomenote
sanger-tol/readmapping	1.1.0	https://github.com/sanger-tol/readmapping/tree/1.1.0
yahs-1.2a.2	yahs-1.2a.2	https://github.com/c-zhou/yahs

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 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: *Drosophila funebris*. Accession number PRJEB57268; <https://identifiers.org/ena.embl/PRJEB57268>. (Wellcome Sanger Institute, 2023) The genome sequence is released openly for reuse. The *Drosophila funebris* 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](#).

Author information

Members of the Wellcome Sanger Institute Tree of Life programme are listed here: <https://doi.org/10.5281/zenodo.4783585>.

Members of Wellcome Sanger Institute Scientific Operations: DNA Pipelines collective are listed here: <https://doi.org/10.5281/zenodo.4790455>.

Members of the Tree of Life Core Informatics collective are listed here: <https://doi.org/10.5281/zenodo.5013541>.

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

Acknowledgements

We thank Mr Sandy Bayne for permission to collect specimens.

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](#)

Arizmendi C, Zuleta V, Ruiz-Dubreuil G, et al.: **Genetics analysis of larval**

foraging behavior in *Drosophila funebris*. *Behav Genet.* 2008; **38**(5): 525–530.
[PubMed Abstract](#) | [Publisher Full Text](#)

Bächli G: **TaxoDros: The Database on Taxonomy of Drosophilidae.** 2023; [Accessed 29 May 2023].
[Reference Source](#)

Basden EB: **The distribution and biology of Drosophilidae (Diptera) in Scotland, including a new species of *Drosophila*.** *Transactions of the Royal Society of Edinburgh.* 1954; **62**(3): 603–654.
[Publisher Full Text](#)

Bernt M, Donath A, Jühling F, *et al.*: **MITOS: Improved *de novo* metazoan mitochondrial genome annotation.** *Mol Phylogenet Evol.* 2013; **69**(2): 313–319.
[PubMed Abstract](#) | [Publisher Full Text](#)

Berrie GK, Sansome FW: **Wild population studies; *Drosophila funebris* near Manchester.** *J Genet.* 1948; **49**(2): 151–152.
[PubMed Abstract](#) | [Publisher 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](#)

Chandler P: **Checklist of Diptera of the British Isles.** 2023.
[Reference Source](#)

Chandler PJ: **Diptera of Windsor Forest and Great Park.** *Dipterists Digest.* 2021; **28**.
[Reference Source](#)

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](#)

Dubinin NP, Tiniakov GG: **Inversion gradients and natural selection in ecological races of *Drosophila funebris*.** *Genetics.* 1946; **31**(6): 537–45.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)

Ewing AW: **Complex courtship songs in the *Drosophila funebris* species group: Escape from an evolutionary bottleneck.** *Anim Behav.* 1979; **27**: 343–349.
[Publisher Full Text](#)

GBIF Secretariat: ***Drosophila funebris* Occurrence Download.** GBIF.org, 2023.
[Publisher Full Text](#)

Grimaldi DA: **The *Drosophila funebris* Species Group in North America (Diptera: Drosophilidae).** *Am Mus Novit* 2022; 1–25.
[Publisher 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; [Accessed 19 October 2022].
[Reference Source](#)

Howe K, Chow W, Collins J, *et al.*: **Significantly improving the quality of genome assemblies through curation.** *GigaScience.* Oxford University Press, 2021; **10**(1): g1aa153.
[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](#)

Manni M, Berkeley MR, Seppye 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](#)

Merrell DJ: **Interspecific competition between *Drosophila funebris* and *Drosophila melanogaster*.** *Am Nat.* 1951; **85**: 159–169.
[Publisher Full Text](#)

Nurk S, Walenz BP, Rhie A, *et al.*: **HiCanu: Accurate assembly of segmental duplications, satellites, and allelic variants from high-fidelity long reads.** *Genome Res.* 2020; **30**(9): 1291–1305.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)

O'Grady PM, Markow TA: **Phylogenetic taxonomy in *Drosophila*.** Problems and prospects. *Fly (Austin).* 2009; **3**(1): 10–14.
[PubMed Abstract](#) | [Publisher 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.*: **Merquy: Reference-free quality, completeness, and phasing assessment for genome assemblies.** *Genome Biol.* 2020; **21**(1): 245.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)

Shorrocks B: **An ecological classification of European *Drosophila* species.** *Oecologia.* 1977; **26**(4): 335–345.
[PubMed Abstract](#) | [Publisher Full Text](#)

Shorrocks B, Charlesworth P: **The distribution and abundance of the British fungal-breeding *Drosophila*.** *Ecol Entomol.* 1980; **5**(1): 61–78.
[Publisher Full Text](#)

Simão FA, Waterhouse RM, Ioannidis P, *et al.*: **BUSCO: assessing genome assembly and annotation completeness with single-copy orthologs.** *Bioinformatics.* 2015; **31**(19): 3210–3212.
[PubMed Abstract](#) | [Publisher Full Text](#)

Spencer WP: **New mutations in *Drosophila funebris* Fabriciusi.** *J Exp Zool.* 1928; **51**: 177–197.
[Publisher Full Text](#)

Surana P, Muffato M, Qi G: **sanger-tol/readmapping: sanger-tol/readmapping v1.1.0 - Hebridean Black (1.1.0).** *Zenodo.* 2023a; [Accessed 21 July 2023].
[Publisher Full Text](#)

Surana P, Muffato M, Sadasivan Baby C: **sanger-tol/genomenote (v1.0.dev).** *Zenodo.* 2023b; [Accessed 21 July 2023].
[Publisher Full Text](#)

Timofeeff-Rissovsy HA: **Induced gene-variations in *Drosophila funebris*.** *J Hered.* 1930; **21**: 167–171.
[Publisher 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](#)

Wellcome Sanger Institute: **The genome sequence of a drosophilid fruit fly, *Drosophila funebris* (Fabricius, 1789).** European Nucleotide Archive. [dataset], accession number PRJEB57268, 2023.

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](#)