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DATA NOTE

The genome sequence of the Heath Bumblebee, *Bombus jonellus* (Kirby, 1802)

[version 1; peer review: 2 approved]

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Abstract

We present a genome assembly from a female specimen of *Bombus jonellus* (Heath Bumblebee; Arthropoda; Insecta; Hymenoptera; Apidae). The genome sequence has a total length of 357.90 megabases. Most of the assembly (78.06%) is scaffolded into 18 chromosomal pseudomolecules. The mitochondrial genome has also been assembled, with a length of 24.83 kilobases.

Keywords

Bombus jonellus, Heath Bumblebee, genome sequence, chromosomal, Hymenoptera

This article is included in the Tree of Life gateway.

Open Peer Review

Approval Status ✓ ✓

	1	2
version 1 23 May 2025	✓ view	✓ view

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

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Species taxonomy

Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea; Anthophila; Apidae; Apinae; Bombini; *Bombus*; *Pyrobombus*; *Bombus jonellus* (Kirby, 1802) (NCBI: txid85663)

Background

Bombus jonellus, the Heath Bumblebee, lives up to its name by inhabiting mainly heaths in southern England, but across Britain has a wider range of open habitats, often inhabiting moorland and machair in Scotland and various coastal habitats. It is one of the short-faced species with two yellow bands on the thorax and a white 'tail' (tergites four and five), often of similar size to *B. pratorum* but in *B. pratorum* the 'tail' is orange. Note that in the northern Isles of Scotland, the 'tail' is yellow and in males from Orkney and the western Isles, orange, thus easily confused with *B. pratorum*, should that species colonise the northern Isles. The ubiquitous *Bombus hortorum* is superficially similar but usually larger, brighter yellow, shorter-haired and with a longer face. As with many bumblebees, the males of *B. jonellus* have a yellow-haired face while females are black-haired. There are several recent identification keys which include *B. jonellus* (e.g., Benton, 2009; Else & Edwards, 2018; Falk, 2015). Benton (2009) and Else & Edwards (2018) summarise the ecology of *B. jonellus*.

This is typically a bivoltine species but in parts of its range there may only be one generation per year. Nests seem to be established in a variety of locations, on, below and sometimes far above the ground and a wide range of flowers are visited, with Fabaceae reported to be the most important for pollen (Else & Edwards, 2018). Colonies are usually small, from 30 up to 120 workers (Benton, 2009; Else & Edwards, 2018) and queens can be found from March through to September.

Within Britain, Williams (Williams, 1989a) classified *B. jonellus* as a 'widespread' local species, although Benton (2009) suggests that it is less local, more widespread than usually reported. This might not be true of southern England, as this species is disappearing from Dungeness, Kent, which has held on to a rich range of *Bombus* species compared to the increasingly impoverished surrounding areas, probably because of the continued high density of appropriate flowers (Williams, 1989b). Else & Edwards (2018) map a distribution heavily skewed towards northwest/northern Scotland and southeast and southwest England. Throughout central England, *B. jonellus* is virtually absent and is of very scattered distribution in Wales and northern England. GRB was pleased, very early in his entomological career, to find the first *B. jonellus* for Cheshire. The specimen which had its genome sequenced (Figure 1) was collected in Heather-rich moorland in Beinn Eighe NNR, where the species was common.

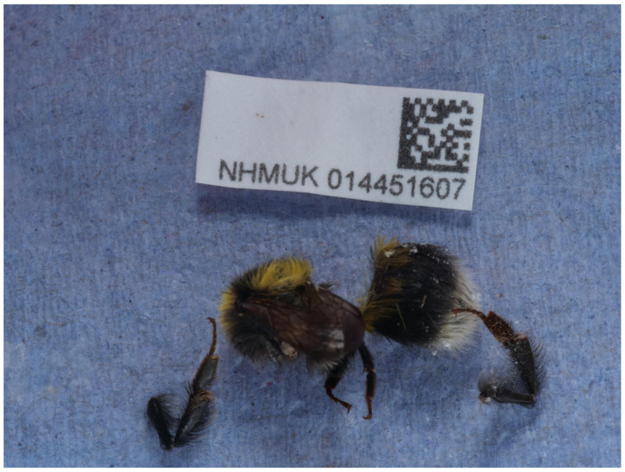

Figure 1. Photograph of the *Bombus jonellus* (iyBomJone1) specimen used for genome sequencing.

Genome sequence report

Sequencing data

The genome of a specimen of *Bombus jonellus* (Figure 1) was sequenced using Pacific Biosciences single-molecule HiFi long reads, generating 27.20 Gb from 2.58 million reads, which were used to assemble the genome. GenomeScope analysis estimated the haploid genome size at 401.80 Mb, with a heterozygosity of 0.38% and repeat content of 42.03%. These estimates guided expectations for the assembly. Based on the estimated genome size, the sequencing data provided approximately 65 coverage. Hi-C sequencing produced 139.13 Gb from 921.40 million reads, and was used to scaffold the assembly. Table 1 summarises the specimen and sequencing details.

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 30 misjoins or missing joins. These interventions decreased the scaffold count by 3.46% and increased the scaffold N50 by 4.58%. The final assembly has a total length of 357.90 Mb in 250 scaffolds, with 118 gaps, and a scaffold N50 of 14.15 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 (78.06%) was assigned to 18 chromosomal-level scaffolds. These chromosome-level scaffolds,

Table 1. **Specimen and sequencing data for *Bombus jonellus*.**

Project information			
Study title	Bombus jonellus		
Umbrella BioProject	PRJEB64937		
Species	*Bombus jonellus*		
BioSpecimen	SAMEA14448317		
NCBI taxonomy ID	85663		
Specimen information			
Technology	**ToLID**	**BioSample accession**	**Organism part**
PacBio long read sequencing	iyBomJone1	SAMEA14448516	thorax
Hi-C sequencing	iyBomJone1	SAMEA14448517	head
Sequencing information			
Platform	**Run accession**	**Read count**	**Base count (Gb)**
Hi-C Illumina NovaSeq 6000	ERR11837502	9.21e+08	139.13
PacBio Sequel IIe	ERR11843415	2.58e+06	27.2

Table 2. **Genome assembly data for *Bombus jonellus*.**

Genome assembly		
Assembly name	iyBomJone1.1	
Assembly accession	GCA_964197665.1	
Alternate haplotype accession	*GCA_964197655.1*	
Assembly level for primary assembly	chromosome	
Span (Mb)	357.90	
Number of contigs	368	
Number of scaffolds	250	
Longest scaffold (Mb)	22.69	
Assembly metric	**Measure**	***Benchmark***
Contig N50 length	2.76 Mb	*≥ 1 Mb*
Scaffold N50 length	14.15 Mb	*= chromosome N50*
Consensus quality (QV)	Primary: 62.7; alternate: 63.9; combined: 63.5	*≥ 40*
k-mer completeness	Primary: 88.02%; alternate: 87.17%; combined: 97.56%	*≥ 95%*
BUSCO*	C:97.6%[S:97.3%,D:0.3%], F:0.4%,M:2.1%,n:5,991	*S > 90%; D < 5%*
Percentage of assembly assigned to chromosomes	78.06%	*≥ 90%*
Sex chromosomes	None	*localised homologous pairs*
Organelles	Mitochondrial genome: 24.83 kb	*complete single alleles*

* BUSCO scores based on the hymenoptera_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.

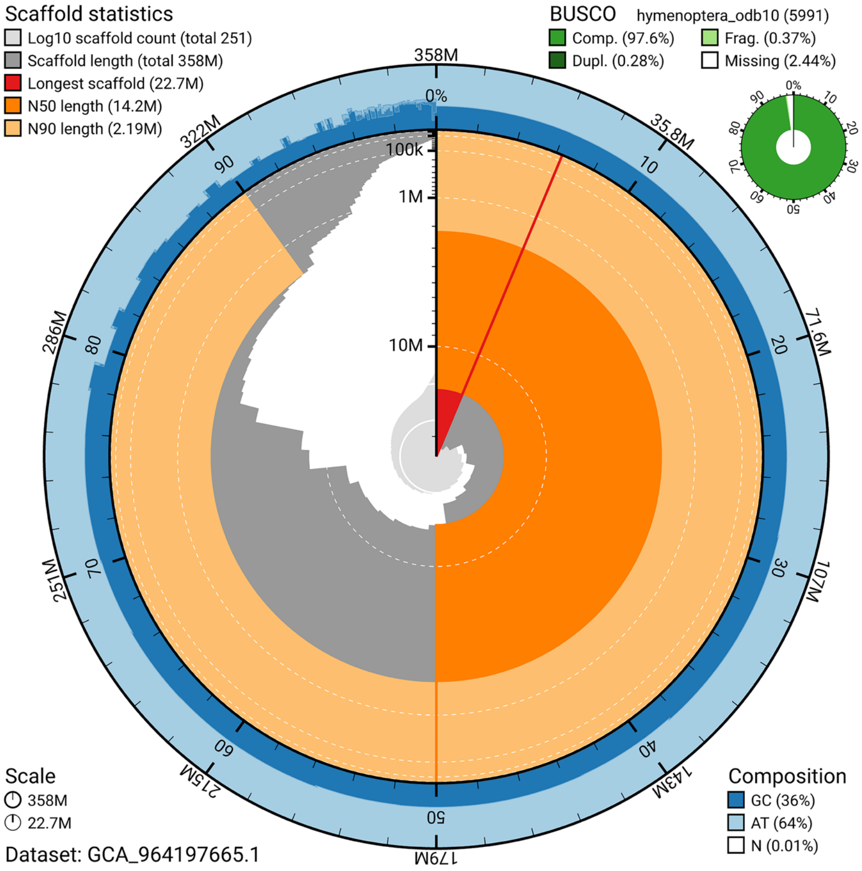

Figure 2. Genome assembly of *Bombus jonellus*, iyBomJone1.1: metrics. The BlobToolKit snail plot provides an overview of assembly metrics and BUSCO gene completeness. The circumference represents the length of the whole genome sequence, and the main plot is divided into 1,000 bins around the circumference. 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 set is presented at the top right. An interactive version of this figure is available at https://blobtoolkit.genomehubs.org/view/GCA_964197665.1/dataset/GCA_964197665.1/snail.

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.

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 combined primary and alternate assemblies achieve an estimated QV of 63.5. The *k*-mer recovery for the primary haplotype is 88.02%, and for the alternate haplotype 87.17%; the combined primary and alternate assemblies have a *k*-mer recovery of 97.56%. BUSCO v.5.5.0 analysis using the hymenoptera_odb10 reference set (n = 5,991) identified 97.6% of the expected gene set (single = 97.3%, duplicated = 0.3%).

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 **6.7.Q62**.

Methods

Sample acquisition and DNA barcoding

The specimen used for genome sequencing was an adult female *Bombus jonellus* (specimen ID NHMUK014451607, ToLID iyBomJone1), collected from Beinn Eighe National Nature Reserve National Nature Reserve, Scotland, United Kingdom, Scotland, United Kingdom (latitude 57.63,

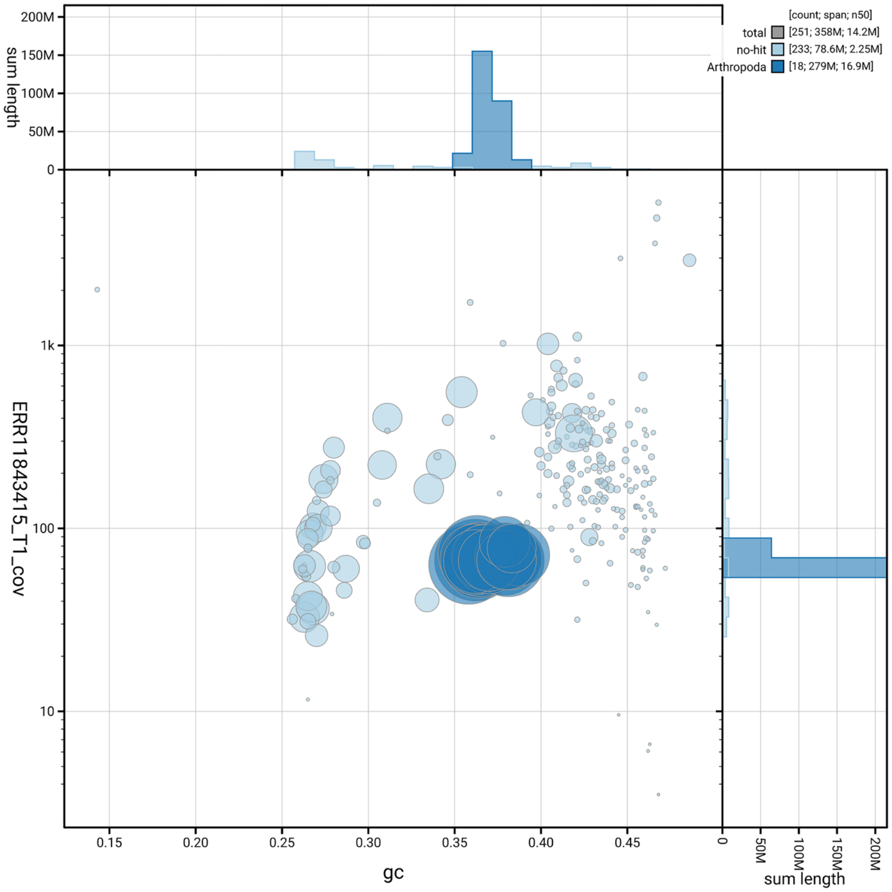

Figure 3. Genome assembly of *Bombus jonellus*, iyBomJone1.1: BlobToolKit GC-coverage plot. Blob plot showing sequence coverage (vertical axis) and GC content (horizontal axis). The circles represent scaffolds, with the size proportional to scaffold length and the colour representing phylum membership. 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_964197665.1/dataset/GCA_964197665.1/blob.

longitude –5.35) on 2021-09-10, using an aerial net. The specimen was collected by Gavin Broad, David Lees, Inez Januszczak and Chris Fletcher (Natural History Museum), identified by Gavin Broad (Natural History Museum) and preserved by dry freezing (–80 °C).

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).

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 iyBomJone1 sample was prepared for DNA extraction by weighing and dissecting it on dry ice (Jay *et al.*, 2023). Tissue from the thorax was homogenised using a PowerMasher II tissue disruptor (Denton *et al.*, 2023a).

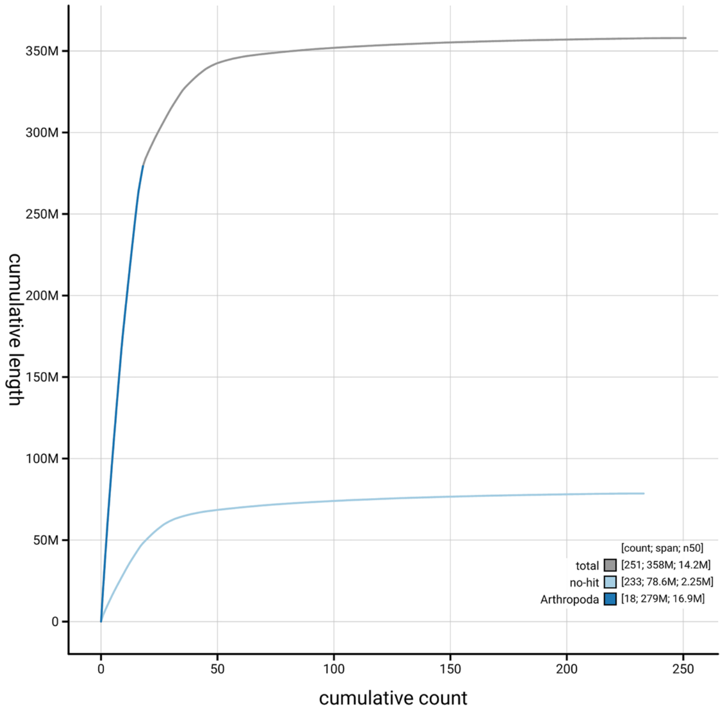

Figure 4. Genome assembly of *Bombus jonellus*, iyBomJone1.1: BlobToolKit cumulative sequence plot. The grey line shows cumulative length for all scaffolds. Coloured lines show cumulative lengths of scaffolds assigned to each phylum using the buscogenes taxrule. An interactive version of this figure is available at https://blobtoolkit.genomehubs.org/view/GCA_964197665.1/dataset/GCA_964197665.1/cumulative.

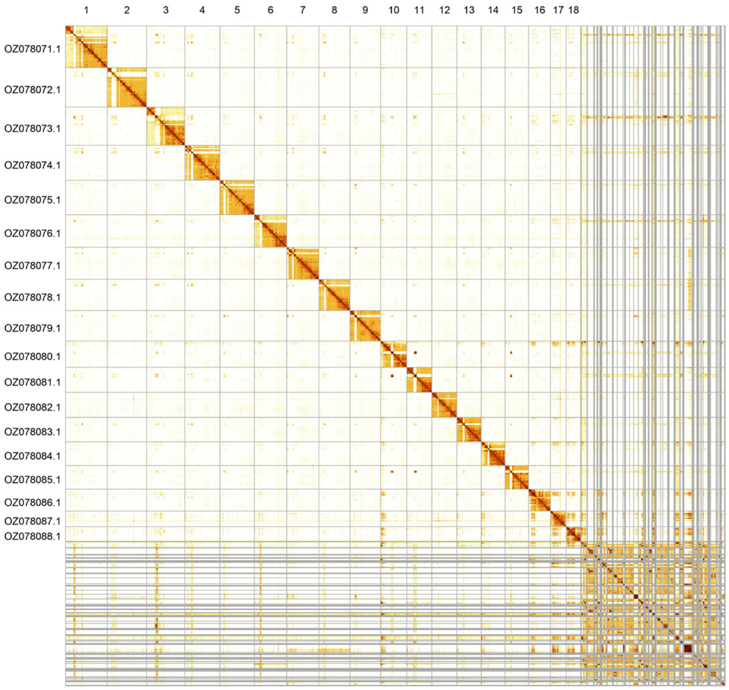

Figure 5. Genome assembly of *Bombus jonellus*: Hi-C contact map of the iyBomJone1.1 assembly, visualised using PretextSnapshot. Chromosomes are shown in order of size from left to right and top to bottom. An interactive version of this figure may be viewed at https://genome-note-higlass.tol.sanger.ac.uk/l/?d=PUlRBbxQR3COirbclnKaPA.

Table 3. Chromosomal pseudomolecules in the genome assembly of *Bombus jonellus*, iyBomJone1.

INSDC accession	Name	Length (Mb)	GC%
OZ078071.1	1	22.69	36
OZ078072.1	2	21.47	36
OZ078073.1	3	20.71	36.5
OZ078074.1	4	18.96	36.5
OZ078075.1	5	18.68	36.5
OZ078076.1	6	17.54	38
OZ078077.1	7	17.45	38
OZ078078.1	8	16.88	36
OZ078079.1	9	16.57	37
OZ078080.1	10	14.15	36.5
OZ078081.1	11	13.64	36
OZ078082.1	12	13.53	38
OZ078083.1	13	13.19	38
OZ078084.1	14	12.93	38.5
OZ078085.1	15	12.79	37
OZ078086.1	16	11.87	38
OZ078087.1	17	8.49	38
OZ078088.1	18	7.82	38.5
OZ078089.1	MT	0.02	14.5

HMW DNA was extracted in the WSI Scientific Operations core using the Automated MagAttract v2 protocol (Oatley *et al.*, 2023). The DNA was sheared into an average fragment size of 12–20 kb in a Megaruptor 3 system (Bates *et al.*, 2023). Sheared DNA was purified by solid-phase reversible immobilisation, using AMPure PB beads to eliminate shorter fragments and concentrate the DNA (Strickland *et al.*, 2023). 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.

Hi-C sample preparation and crosslinking

Hi-C data were generated from the head of the iyBomJone1 sample using the Arima-HiC v2 kit (Arima Genomics) with 20–50 mg of frozen tissue (stored at –80 °C). As per manufacturer's instructions, tissue was fixed, and the DNA crosslinked using a TC buffer with 22% formaldehyde concentration, and a final formaldehyde concentration of 2%. The tissue was then homogenised using the Diagnocine Power Masher-II. The crosslinked DNA was digested using a restriction enzyme master mix, then biotinylated and ligated. A clean up was performed with SPRIselect beads prior to library preparation. DNA concentration was quantified using the Qubit Fluorometer v4.0 (Thermo Fisher Scientific) and Qubit HS Assay Kit, and sample biotinylation percentage was estimated using the Arima-HiC v2 QC beads.

Library preparation and sequencing

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

PacBio HiFi

Samples need to have an average fragment size exceeding 8 kb and a total mass over 400 ng to proceed to the low-input SMRTbell Prep Kit 3.0 protocol (Pacific Biosciences), depending on genome size and sequencing depth required. Libraries were prepared using the SMRTbell Prep Kit 3.0 as per the manufacturer's instructions. The kit includes the reagents required for end repair/A-tailing, adapter ligation, post-ligation SMRTbell bead cleanup, and nuclease treatment. Size-selection and clean-up were carried out using diluted AMPure PB beads (Pacific Biosciences). DNA concentration was quantified using the Qubit Fluorometer v4.0 (ThermoFisher Scientific) with Qubit 1X dsDNA HS assay kit and the final library fragment size analysis was carried out using the Agilent Femto Pulse Automated Pulsed Field CE Instrument (Agilent Technologies) and the gDNA 55kb BAC analysis kit.

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, the biotinylated DNA constructs were fragmented using a Covaris E220 sonicator and size-selected to 400–600 bp using SPRISelect beads. DNA was then enriched using Arima-HiC v2 Enrichment beads. The NEBNext Ultra II DNA Library Prep Kit (New England Biolabs) was used for end repair, A-tailing, and adapter ligation, following a modified protocol in which library preparation is carried out while the DNA remains bound to the enrichment beads. PCR amplification was performed using KAPA HiFi HotStart mix and custom dual-indexed adapters (Integrated DNA Technologies) in a 96-well plate format. Depending on sample concentration and biotinylation percentage determined at the crosslinking stage, samples were amplified for 10–16 PCR cycles. Post-PCR clean-up was carried out using SPRISelect beads. The libraries were quantified using the Accuclear Ultra High Sensitivity dsDNA Standards Assay kit (Biotium) and normalised to 10 ng/μL before sequencing. Hi-C sequencing was performed on the Illumina NovaSeq 6000 instrument using 150 bp paired-end reads.

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 (Rao *et al.*, 2014) were mapped to the primary contigs using bwa-mem2 (Vasimuddin *et al.*, 2019), and the contigs were scaffolded using 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. Flat files and maps used in curation were generated via the TreeVal pipeline (Pointon *et al.*, 2023). Manual curation was conducted primarily in PretextView (Harry, 2022) and HiGlass (Kerpedjiev *et al.*, 2018), with additional insights provided by JBrowse2 (Diesh *et al.*, 2023). Scaffolds were visually inspected and corrected as described by Howe *et al.* (2021). Any identified contamination, missed joins, and mis-joins were amended, and duplicate sequences were tagged and removed. 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

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 the primary and alternate 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 in the blobtoolkit pipeline, a Nextflow (Di Tommaso *et al.*, 2017) port of the previous Snakemake Blobtoolkit pipeline (Challis *et al.*, 2020). It aligns the PacBio reads in SAMtools (Danecek *et al.*, 2021) 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 (Grüning *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.

Table 4. Software tools: versions and sources.

Software tool	Version	Source
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
DIAMOND	2.1.8	https://github.com/bbuchfink/diamond
fasta_windows	0.2.4	https://github.com/tolkit/fasta_windows
FastK	666652151335353eef2fcd58880bcef5bc2928e1	https://github.com/thegenemyers/FASTK
GenomeScope2.0	2.0.1	https://github.com/tbenavi1/genomescope2.0

Software tool	Version	Source
Gfastats	1.3.6	https://github.com/vgl-hub/gfastats
GoaT CLI	0.2.5	https://github.com/genomehubs/goat-cli
Hifiasm	0.16.1	https://github.com/chhylp123/hifiasm
HiGlass	44086069ee7d4d3f6f3f0012569789ec138f42b84aa44357826c0b6753eb28de	https://github.com/higlass/higlass
MerquryFK	d00d98157618f4e8d1a9190026b19b471055b22e	https://github.com/thegenemyers/MERQURY.FK
Minimap2	2.24-r1122	https://github.com/lh3/minimap2
MitoHiFi	None	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
PretextView	0.2.5	https://github.com/sanger-tol/PretextView
purge_dups	1.2.3	https://github.com/dfguan/purge_dups
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	1.1a.2	https://github.com/c-zhou/yahs

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 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: Bombus jonellus. Accession number PRJEB64937; https://identifiers.org/ena.embl/PRJEB64937. The genome sequence is released openly for reuse. The *Bombus jonellus* genome sequencing initiative is part of the Darwin Tree of Life Project (PRJEB40665) and the Sanger Institute Tree of Life Programme (PRJEB43745). 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 Natural History Museum Genome Acquisition Lab are listed here: https://doi.org/10.5281/zenodo.12159242.

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.

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Open Peer Review

Current Peer Review Status: ✓ ✓

Version 1

Reviewer Report 13 June 2025

https://doi.org/10.21956/wellcomeopenres.26753.r124962

✓ **Erich D Jarvis**
Rockefeller University, Millbrook, USA

This is a good genomic data note. It is well written, explained well, with good figures. The genome assembly is good. Not sure why the authors did not use the Hi-C phasing mode to get two relatively complete haplotypes. In future assemblies, it would be good to do so. No changes though are necessary for the current Data Note

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 and Neuroscience

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 30 May 2025

https://doi.org/10.21956/wellcomeopenres.26753.r124303

✓ **Jason Charamis**

Foundation for Research and Technology - Hellas, Irákleion, Greece

This data note presents a high-quality genome assembly of the Heath Bumblebee (Bombus jonellus), contributing valuable genomic resources to the Darwin Tree of Life project. The technical work is solid and the manuscript is generally well-written.

The assembly achieves good quality metrics with 357.90 Mb total length and 78.06% scaffolded into 18 chromosomes, while it also has a high BUSCO completeness score (97.6%) with low duplication rate.

I have only two comments to make:

1. The introduction would benefit from brief discussion of why the B. jonellus genome is scientifically important beyond its contribution to the Darwin Tree of Life project.

2. The manuscript does not discuss broader implications of this genomic resource in ecological studies.

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: Arthropod Comparative 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.