

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	597850
ToLID	iyAntRoge3
Species	<i>Anthophora rogenhoferi</i>
Class	Insecta
Order	Hymenoptera

Genome Traits	Expected	Observed
Haploid size (bp)	445,419,612	441,476,308
Haploid Number	9 (source: ancestor)	18
Ploidy	1 (source: ancestor)	2
Sample Sex	NA	NA

EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 7.7.Q65

The following metrics were automatically flagged as below EBP recommended standards or different from expected:

- . Observed Haploid Number is different from Expected
- . Observed Ploidy is different from Expected
- . Not 90% of assembly in chromosomes for collapsed

Curator notes

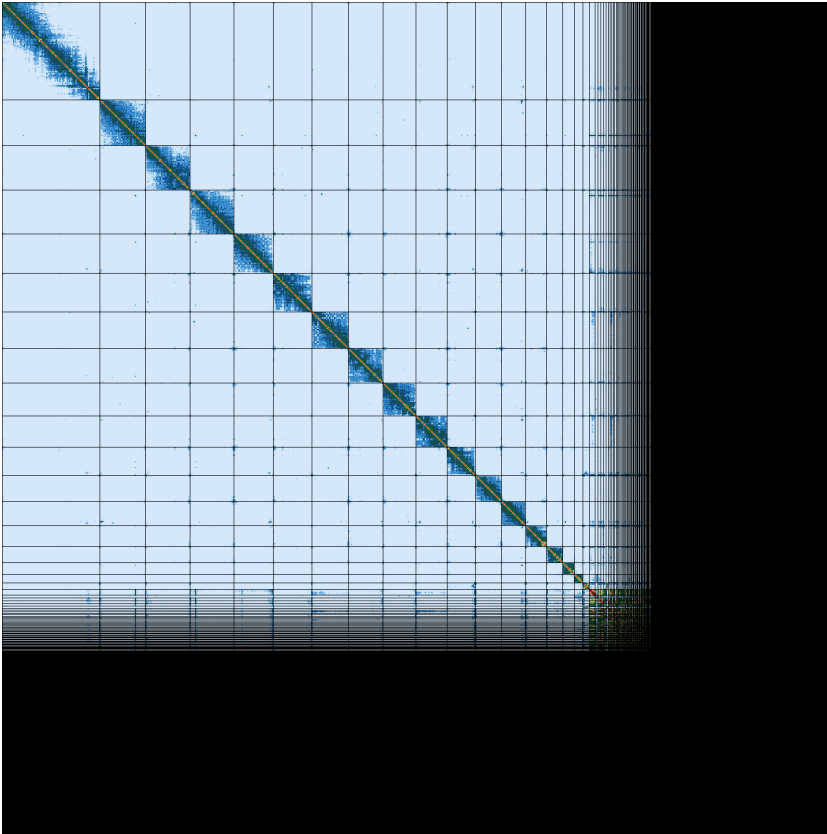
- . Interventions/Gb:
- . Contamination notes: ""
- . Other observations: "The assembly was produced with hifiiasm in Hi-C mode, decontaminated with FCS-GX, and haplotigs purged with purge_dups. Scaffolding was performed with YaHS. Mitochondria was assembled with Oatk."

Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	442,215,395	441,476,308
GC %	40.41	40.42
Gaps/Gbp	36.18	33.98
Total gap bp	3,200	3,000
Scaffolds	1,085	1,086
Scaffold N50	16,560,000	16,560,000
Scaffold L50	9	10
Scaffold L90	350	351
Contigs	1,101	1,101
Contig N50	10,497,625	10,497,625
Contig L50	13	13
Contig L90	366	366
QV	65.2913	65.284
Kmer compl.	91.9202	91.9158
BUSCO sing.	98.7%	99.1%
BUSCO dupl.	0.5%	0.2%
BUSCO frag.	0.1%	0.1%
BUSCO miss.	0.6%	0.6%

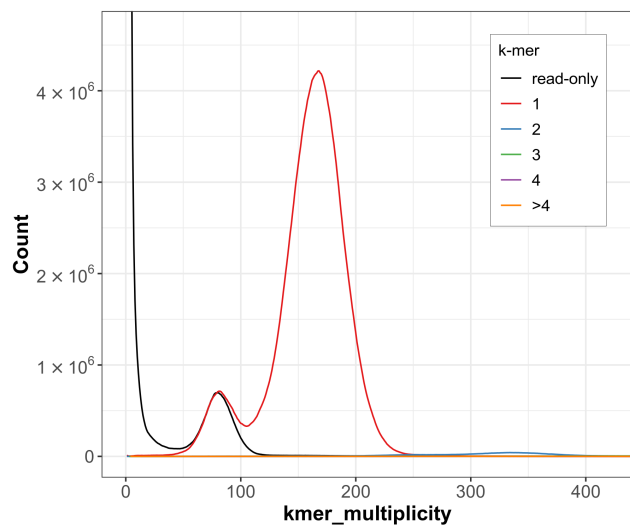
BUSCO: 6.0.0 (euk_genome_min, miniprot) / Lineage: hymenoptera_odb10 (genomes:40, BUSCOs:5991)

HiC contact map of curated assembly



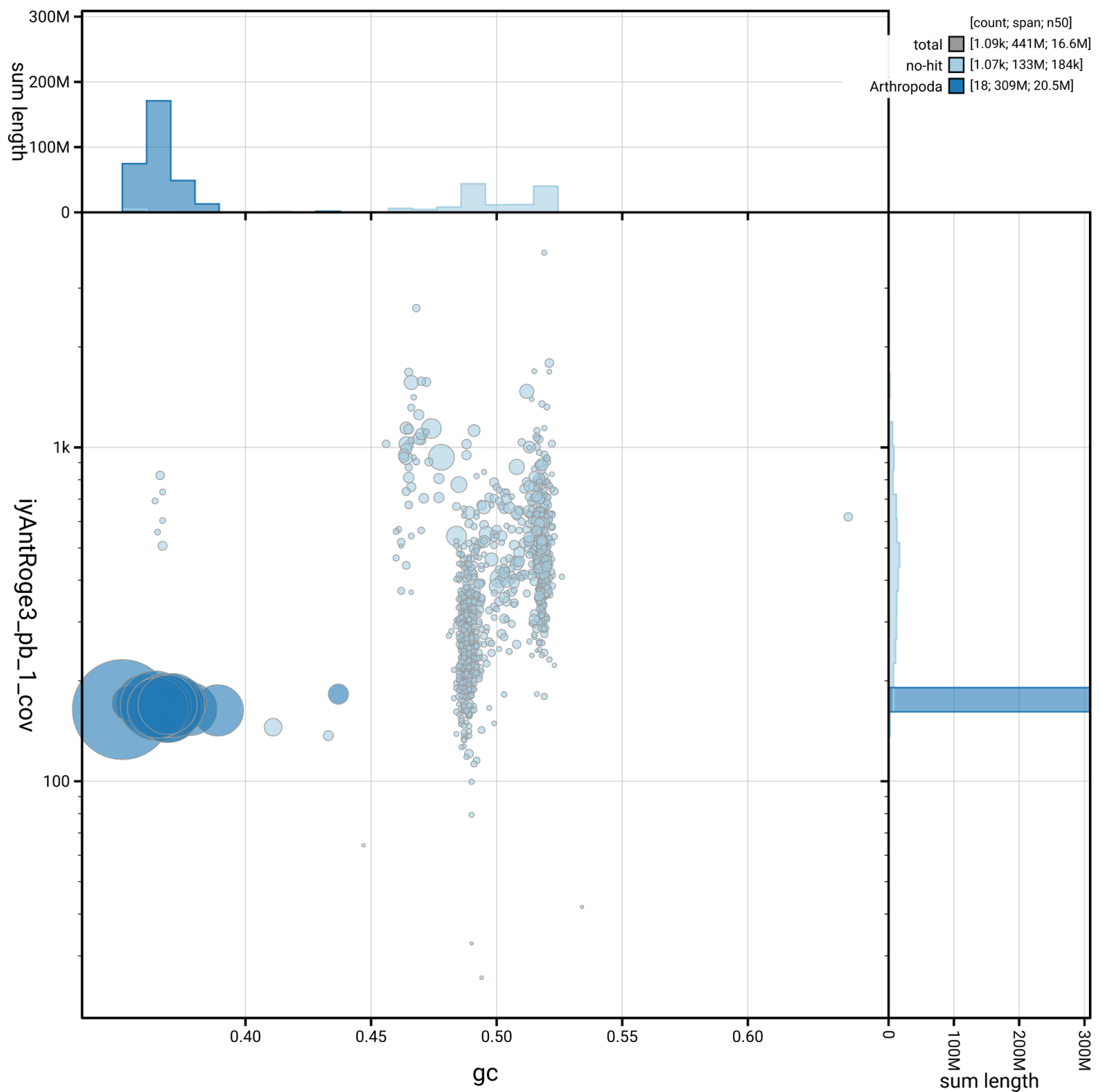
collapsed [\[LINK\]](#)

K-mer spectra of curated assembly



Distribution of k-mer counts per copy numbers found in asm

Post-curation contamination screening



collapsed. Bubble plot circles are scaled by sequence length, positioned by coverage and GC proportion, and coloured by taxonomy. Histograms show total assembly length distribution on each axis.

Data profile

Data	PacBio HiFi	Arima HiC v2
Coverage	50x	27x

Assembly pipeline

- **hifiasm-hic**
 - |_ *ver*: 0.25.0-r726
 - |_ *key param*: --h1
 - |_ *key param*: --h2
- **purge_dups**
 - |_ *ver*: 1.2.5
 - |_ *key param*: NA
- **YaHS**
 - |_ *ver*: 1.2a.2
 - |_ *key param*: NA
- **NBIS/Earth-Biogenome-Project-pilot**
 - |_ *ver*: 99c8937
 - |_ *key param*: NA
- **sanger-tol/blobtoolkit**
 - |_ *ver*: 0.8.0
 - |_ *key param*: NA
- **Oatk**
 - |_ *ver*: 1.0
 - |_ *key param*: -m hymenoptera.fam

Curation pipeline

- **sanger-tol/curationpretext**
 - |_ *ver*: 1.4.2
 - |_ *key param*: NA
- **sanger-tol/agp-tpf-utils**
 - |_ *ver*: 1.2.3
 - |_ *key param*: NA

Submitter: Guilherme B. Dias

Affiliation: SciLifeLab

Date and time: 2025-10-03 10:16:12 CEST