

# ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	3054493
ToLID	<b>ibLobCanal</b>
Species	Loboptera canariensis
Class	Insecta
Order	Blattodea

Genome Traits	Expected	Observed
Haploid size (bp)	1,975,410,362	2,217,202,221
Haploid Number	17 (source: ancestor)	17
Ploidy	2 (source: ancestor)	2
Sample Sex	XX	XX

## EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 6.8.Q40

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

- . Kmer completeness value is less than 90 for collapsed

### Curator notes

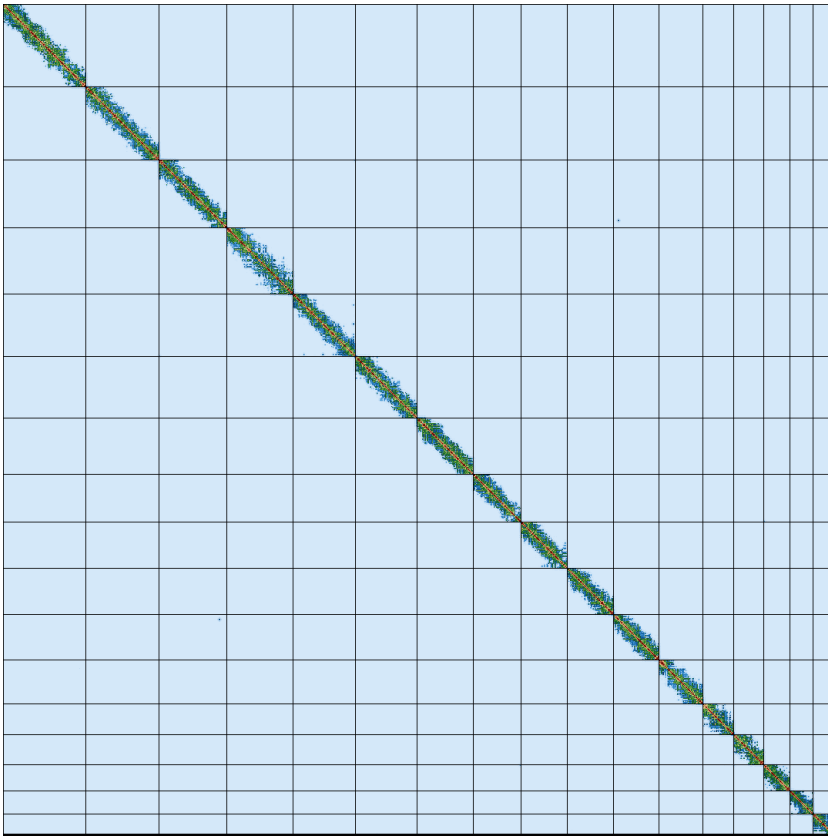
- . Interventions/Gb: 11
- . Contamination notes: "78 scaffolds detected as contaminants with BTK were removed from the curated assembly."
- . Other observations: "Curation made 0 cuts in contigs, 3 breaks at gaps and 13 joins. Sex chromosome unknown. Mitogenome was assenbled into a single circular contig of 16,194 bp of high sequence accuracy."

# Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	2,257,139,729	2,217,202,221
GC %	34.91	34.73
Gaps/Gbp	217.09	225.51
Total gap bp	98,000	100,000
Scaffolds	129	41
Scaffold N50	151,223,706	151,223,706
Scaffold L50	7	7
Scaffold L90	15	14
Contigs	619	541
Contig N50	8,565,483	8,641,591
Contig L50	81	79
Contig L90	291	277
QV	40.8518	40.8397
Kmer compl.	79.6128	77.859
BUSCO sing.	97.3%	97.4%
BUSCO dupl.	1.8%	1.7%
BUSCO frag.	0.6%	0.7%
BUSCO miss.	0.3%	0.2%

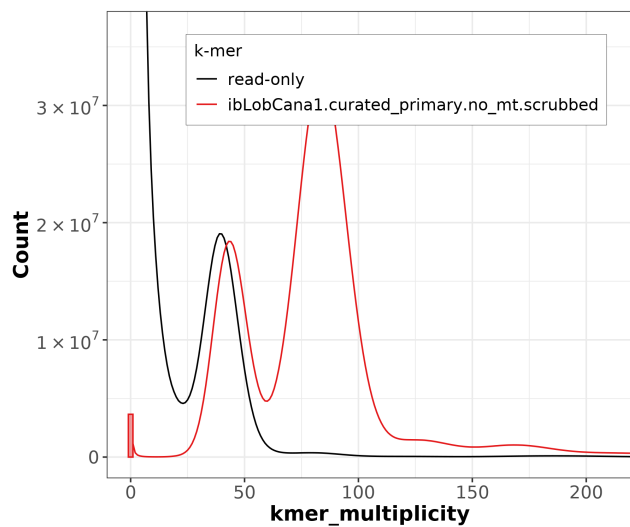
BUSCO: 5.4.0 (euk\_genome\_met, metaeuk) / Lineage: insecta\_odb10 (genomes:75, BUSCOs:1367)

# HiC contact map of curated assembly

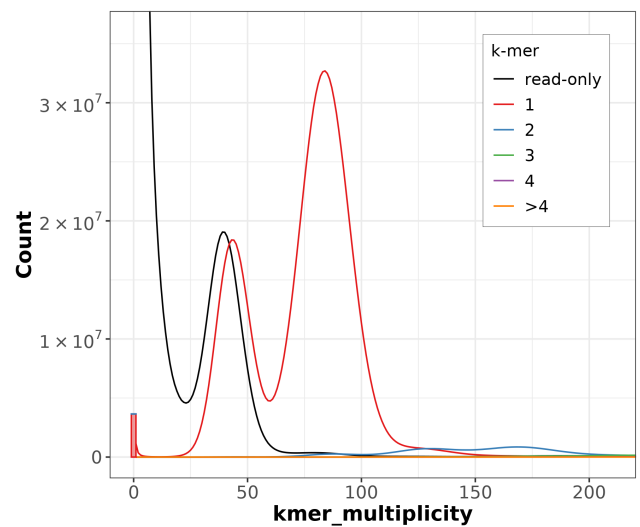


collapsed [\[LINK\]](#)

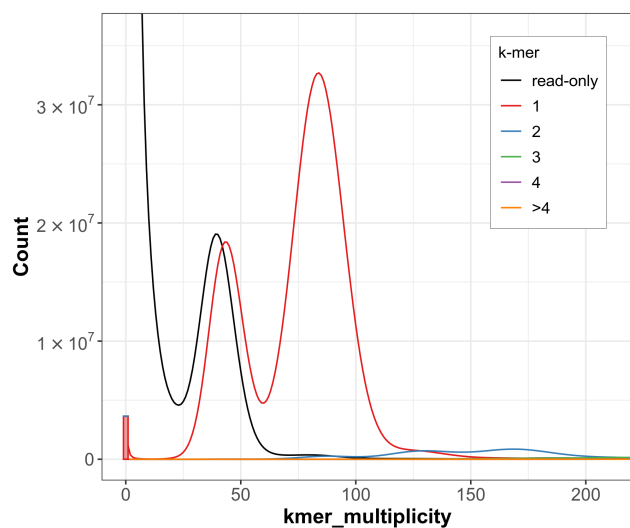
# K-mer spectra of curated assembly



Distribution of k-mer counts coloured by their presence in reads/assemblies

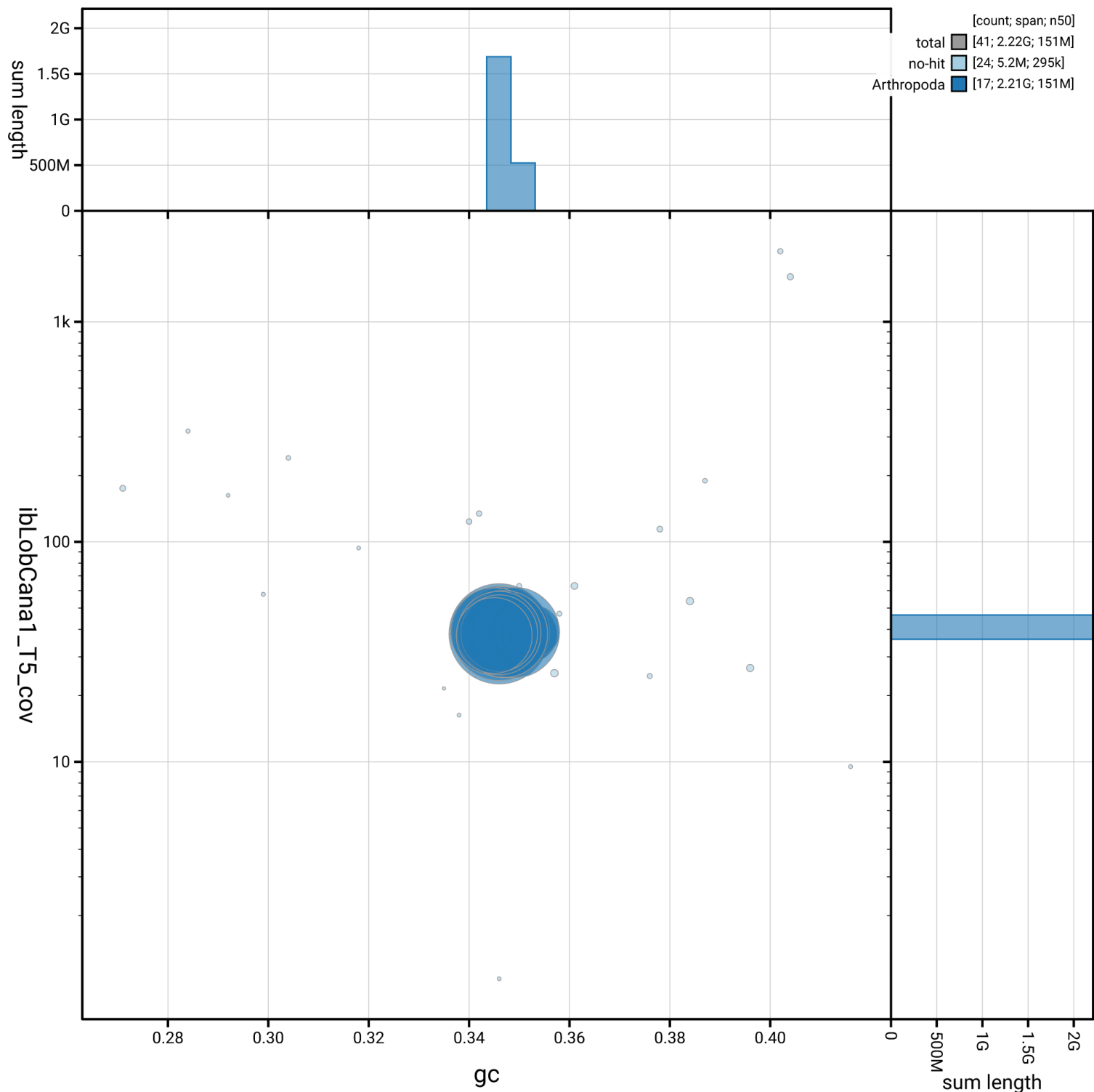


Distribution of k-mer counts per copy numbers found in asm



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	ONT	Illumina	OmniC
Coverage	57	65	42

## Assembly pipeline

- **CLAWS pipeline**
  - |\_ ver: 2.2.0
  - |\_ key param: NA
- **Trim\_galore**
  - |\_ ver: 0.6.7
  - |\_ key param: NA
- **Filtlong**
  - |\_ ver: 0.2.1
  - |\_ key param: NA
- **flye**
  - |\_ ver: 2.9.1
  - |\_ key param: NA
- **nextdenovo**
  - |\_ ver: 2.5.0
  - |\_ key param: NA
- **hypo**
  - |\_ ver: 1.0.3
  - |\_ key param: NA
- **purge\_dups**
  - |\_ ver: 1.2.6
  - |\_ key param: NA
- **YaHS**
  - |\_ ver: 1.2a
  - |\_ key param: NA
- **FOAM pipeline**
  - |\_ ver: 0.5
  - |\_ key param: NA
- **mitos**
  - |\_ ver: 2.1.3
  - |\_ key param: NA

## Curation pipeline

- **PretextView**
  - |\_ ver: 0.2.5
  - |\_ key param: NA
- **Blobtoolkit nexflow pipeline**
  - |\_ ver: 0.6.0
  - |\_ key param: NA
- **GRIT\_Rapid**
  - |\_ ver: 2.0
  - |\_ key param: NA

Affiliation: CNAG Barcelona

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