

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

| | |
|---------|-----------------------|
| TxID | 3054493 |
| ToLID | ibLobCanal |
| 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

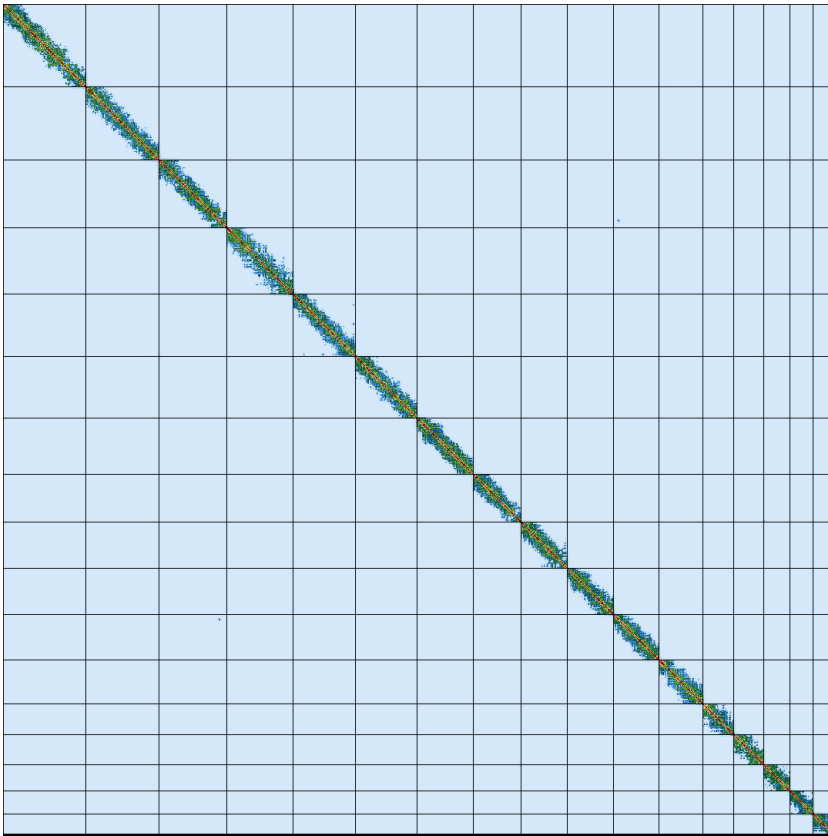
- . Interventions/Gb: 11
- . Contamination notes: "78 scaffolds detected as contaminants with BTK were removed from the curated assembly."
- . Other observations: "Curation made 0 cuts in contigs, 3 breaks at gaps and 13 joins. Sex chromosome unknown. Mitogenome was assenbled into a single circular contig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

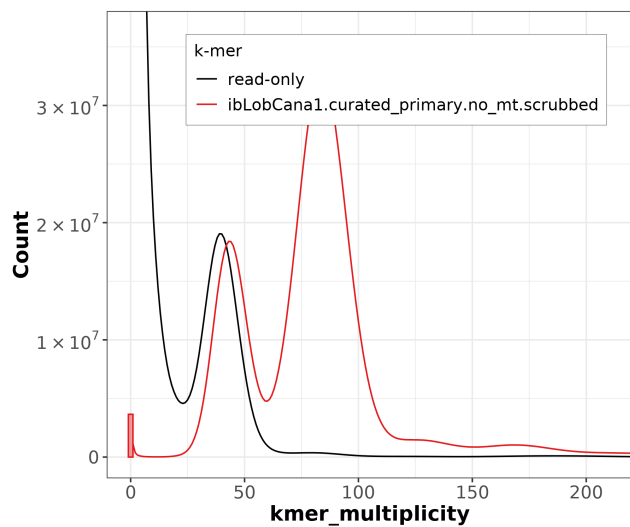
BUSCO: 5.4.0 (euk_genome_met, metaeuk) / Lineage: insecta_odb10 (genomes:75, BUSCOs:1367)

HiC contact map of curated assembly

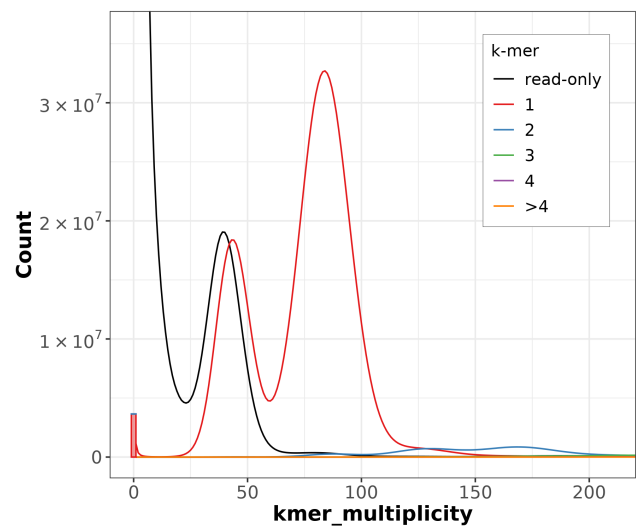


collapsed [\[LINK\]](#)

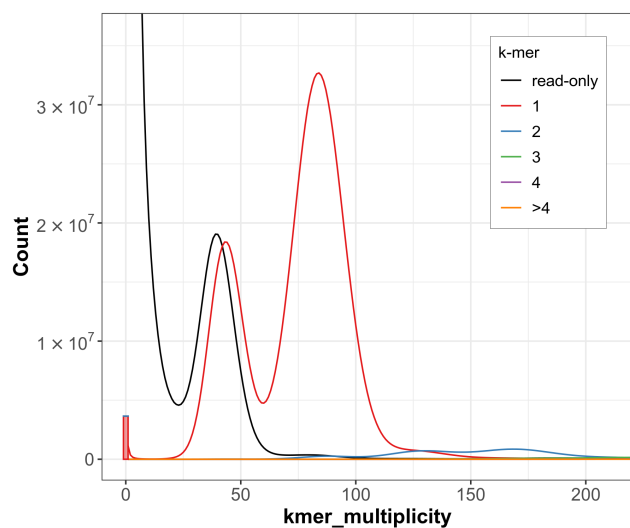
K-mer spectra of curated assembly



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

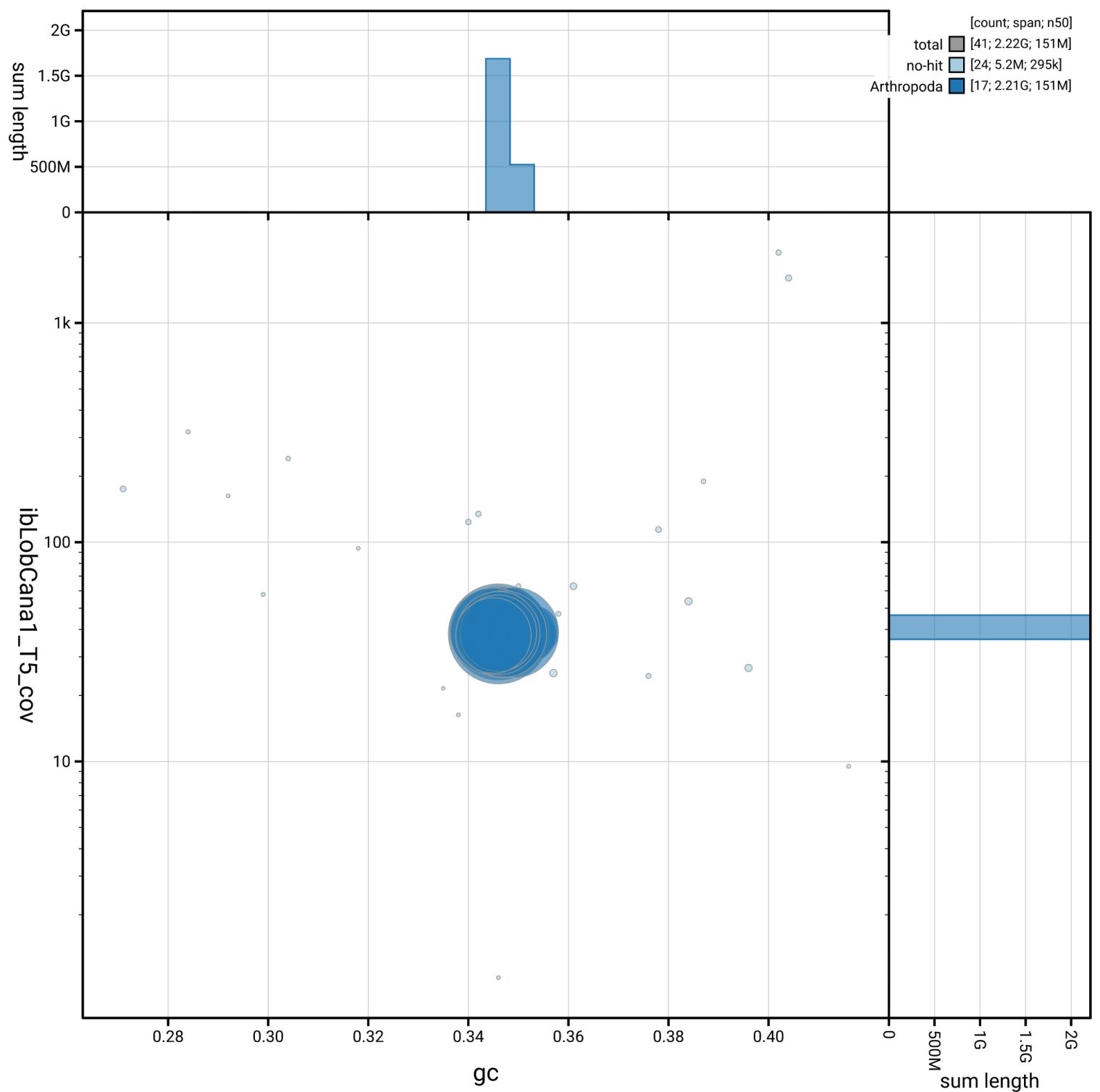


Distribution of k-mer counts per copy numbers found in asm



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

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Date and time: 2024-12-12 10:02:34 CET