

ERGA Assembly Report

v24.09.10

Tags: ERGA-BGE

| | |
|---------|----------------------|
| TxID | 554486 |
| ToLID | ilCoeOedi1 |
| Species | Coenonympha oedippus |
| Class | Insecta |
| Order | Lepidoptera |

| Genome Traits | Expected | Observed |
|-------------------|----------------------|-------------|
| Haploid size (bp) | 400,913,152 | 397,580,023 |
| Haploid Number | 29 (source: direct) | 29 |
| Ploidy | 2 (source: ancestor) | 2 |
| Sample Sex | ZW | ZW |

EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 6.7.Q56

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

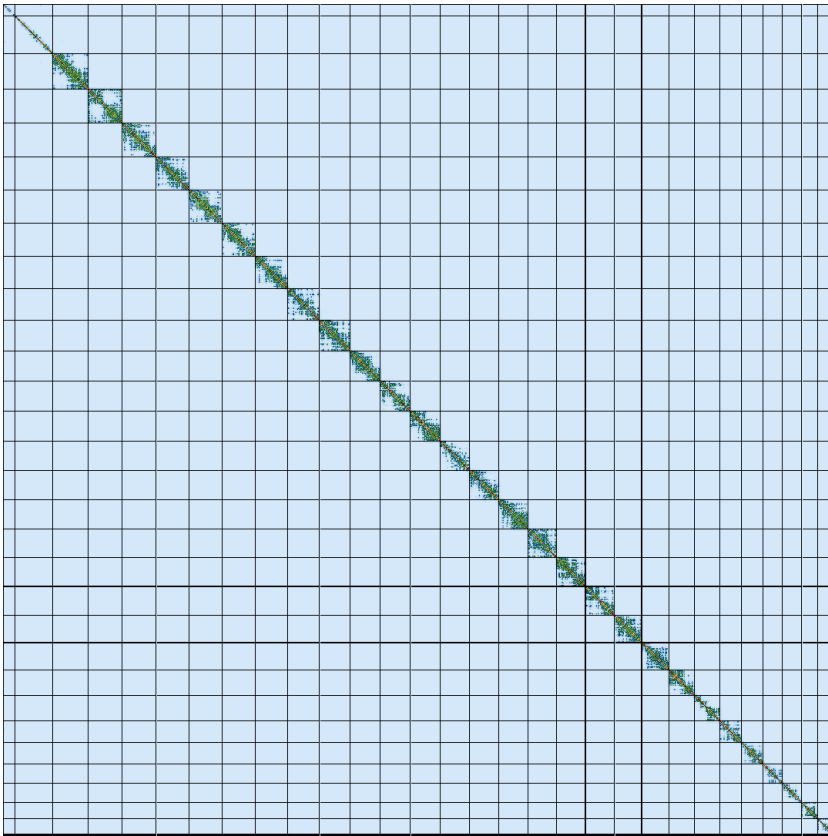
- . Interventions/Gb: 100
- . Contamination notes: "1 scaffold matching Wolbachia was removed from the Flye assembly"
- . Other observations: "We curated the Flye assembly with exception of the W scaffold that was better reconstructed by Nextdenovo. We replaced the Flye W scaffold for the nextdenovo W scaffold. In addition, 83 small scaffolds with remaining W fragments or just too short were removed from the curated Flye assembly"

Quality metrics table

| Metrics | Pre-curation collapsed | Curated collapsed |
|--------------|---------------------------|----------------------|
| Total bp | 398,249,265 | 397,580,023 |
| GC % | 37.32 | 37.32 |
| Gaps/Gbp | 778.41 | 812.42 |
| Total gap bp | 61,900 | 64,500 |
| Scaffolds | 165 | 62 |
| Scaffold N50 | 14,195,870 | 14,242,255 |
| Scaffold L50 | 13 | 13 |
| Scaffold L90 | 26 | 26 |
| Contigs | 475 | 385 |
| Contig N50 | 2,683,349 | 2,773,664 |
| Contig L50 | 46 | 45 |
| Contig L90 | 156 | 153 |
| QV | 55.0646 | 56.0202 |
| Kmer compl. | 71.2387 | 70.8353 |
| BUSCO sing. | 97.5% | 97.7% |
| BUSCO dupl. | 1.3% | 1.2% |
| BUSCO frag. | 0.2% | 0.2% |
| BUSCO miss. | 1.0% | 0.9% |

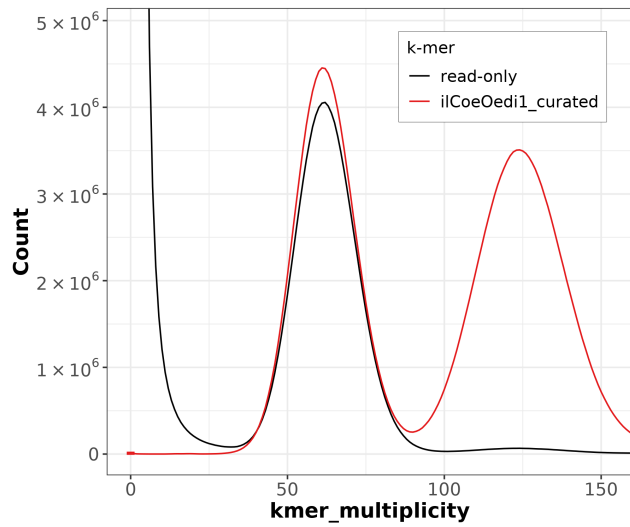
BUSCO 5.4.0 Lineage: insecta_odb10 (genomes:75, BUSCOs:1367)

HiC contact map of curated assembly

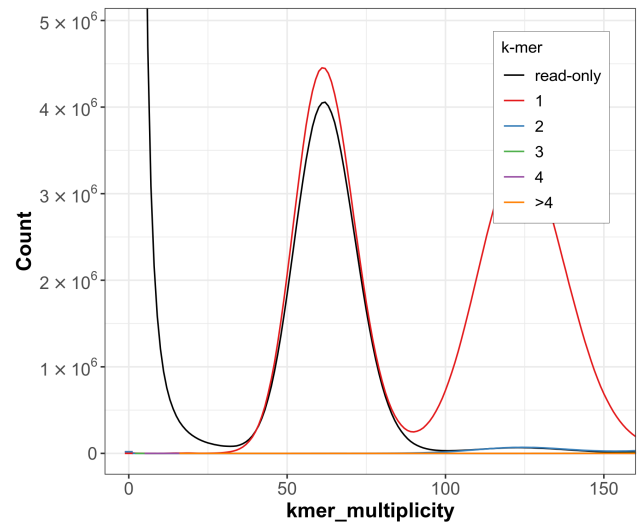


collapsed [\[LINK\]](#)

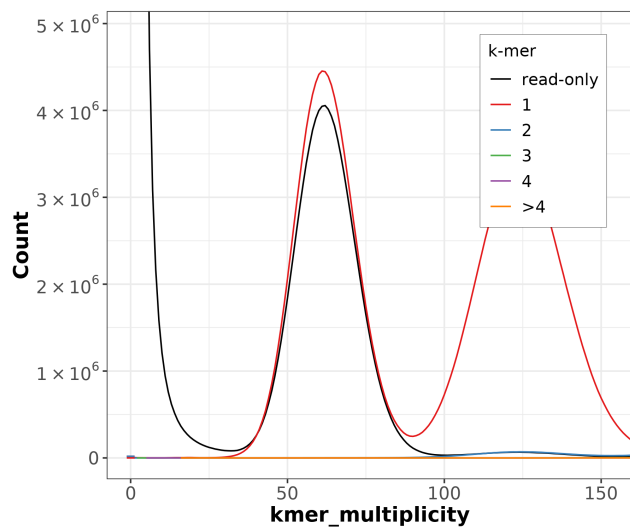
K-mer spectra of curated assembly



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

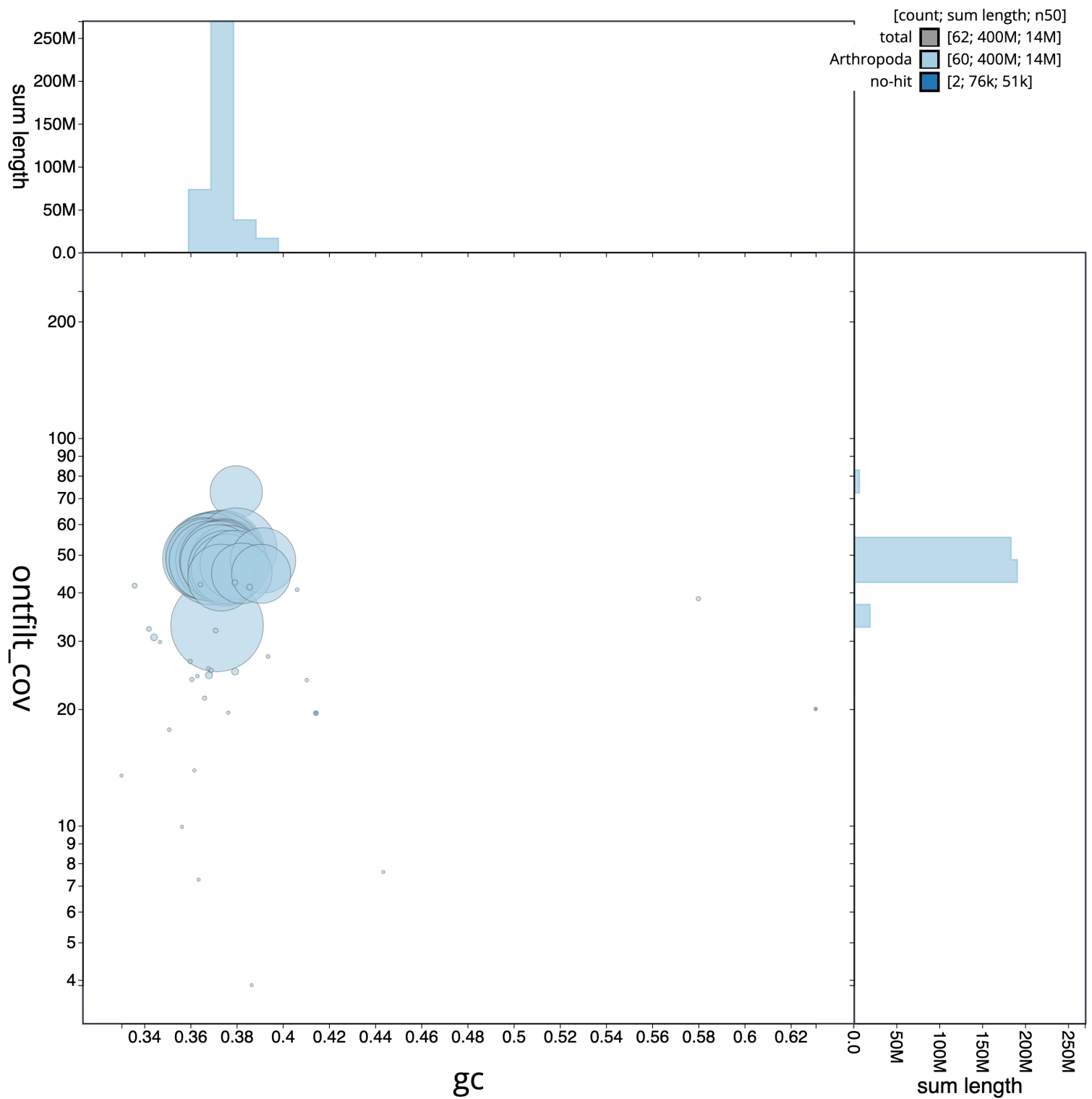


Distribution of k-mer counts per copy numbers found in asm



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 | 226x | 75x | 183x |

Assembly pipeline

```
- Trim_galore
  | _ ver: 0.6.7
  | _ key param: --gzip
  | _ key param: =q 20
  | _ key param: --paired
  | _ key param: retain_unpaired
  | _ key param: --max_n
  | _ key param: =0
- Filtlong
  | _ ver: 0.2.1
  | _ key param: --minlen
  | _ key param: =1000
  | _ key param: --min_mean_q
  | _ key param: =80
  | _ key param: --target_bases
  | _ key param: =27000000000
- 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
```

Curation pipeline

```
- PretextView
  | _ ver: 0.2.5
  | _ key param: NA
- GRIT_Rapid
  | _ ver: 2.0
  | _ key param: NA
```

Submitter: Fernando Cruz
Affiliation: CNAG Barcelona

Date and time: 2024-10-21 18:24:29 CEST