

# ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

|         |                   |
|---------|-------------------|
| TxID    | 1926191           |
| ToLID   | <b>qqLacDent6</b> |
| Species | Lacinius dentiger |
| Class   | Arachnida         |
| Order   | Opiliones         |

| Genome Traits     | Expected             | Observed    |
|-------------------|----------------------|-------------|
| Haploid size (bp) | 573,562,869          | 682,711,259 |
| Haploid Number    | 8 (source: ancestor) | 14          |
| Ploidy            | 2 (source: ancestor) | 2           |
| Sample Sex        | male                 | unknown     |

## EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 6.7.Q57

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

- . Observed Haploid Number is different from Expected
- . Observed sex is different from Sample sex
- . Kmer completeness value is less than 90 for pri
- . Not 90% of assembly in chromosomes for pri

### Curator notes

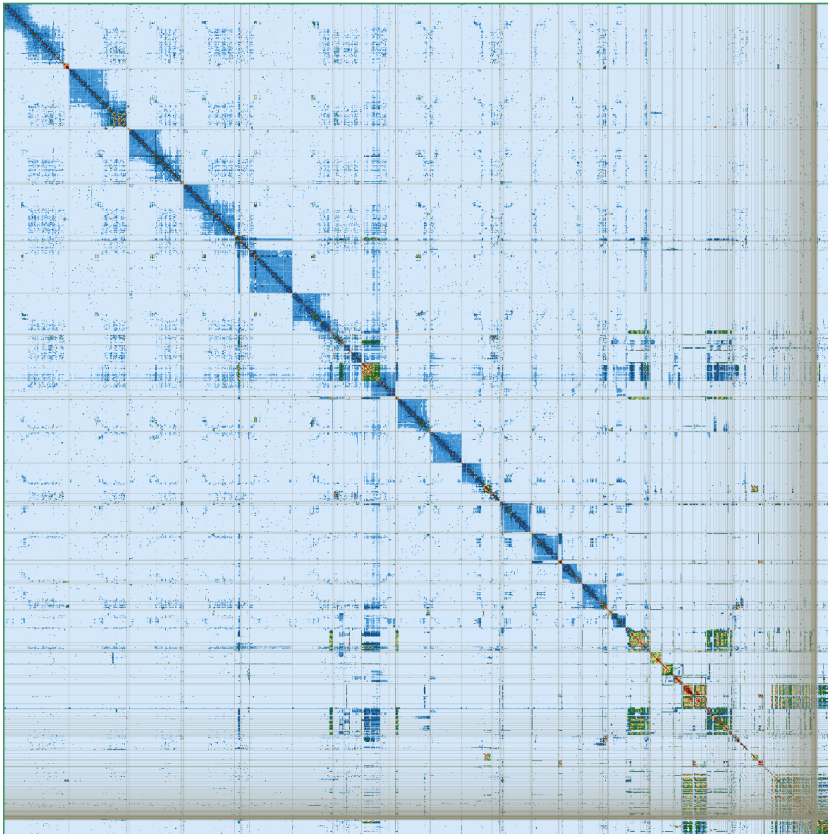
- . Interventions/Gb: None
- . Contamination notes: ""
- . Other observations: "Very difficult to curate with a large number of repetitive regions that could not be placed"

# Quality metrics table

| Metrics      | Pre-curation<br>pri | Curated<br>pri |
|--------------|---------------------|----------------|
| Total bp     | 688,669,353         | 682,711,259    |
| GC %         | 35.93               | 35.92          |
| Gaps/Gbp     | 363.02              | 382.3          |
| Total gap bp | 50,000              | 52,200         |
| Scaffolds    | 527                 | 514            |
| Scaffold N50 | 22,203,647          | 31,462,319     |
| Scaffold L50 | 10                  | 7              |
| Scaffold L90 | 54                  | 43             |
| Contigs      | 777                 | 775            |
| Contig N50   | 5,128,000           | 5,001,931      |
| Contig L50   | 26                  | 26             |
| Contig L90   | 183                 | 182            |
| QV           | 57.2281             | 57.2084        |
| Kmer compl.  | 83.5628             | 83.2873        |
| BUSCO sing.  | 96.9%               | 97.0%          |
| BUSCO dupl.  | 0.9%                | 0.8%           |
| BUSCO frag.  | 0.9%                | 0.9%           |
| BUSCO miss.  | 1.3%                | 1.3%           |

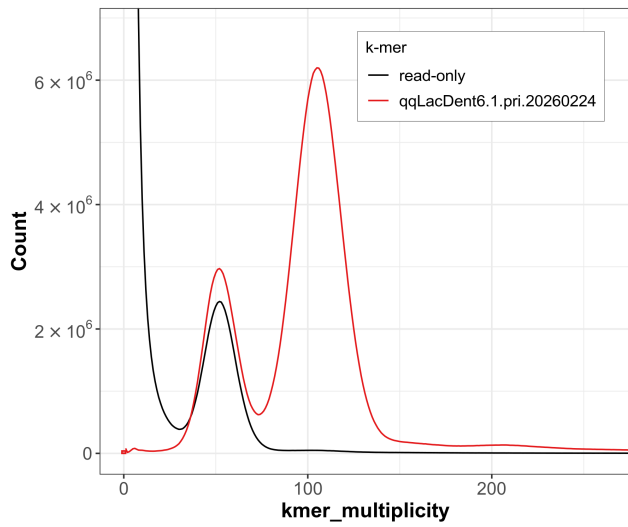
BUSCO: 6.0.0 (euk\_genome\_min, miniprot) / Lineage: arthropoda\_odb12 (genomes:76, BUSCOs:1667)

# HiC contact map of curated assembly

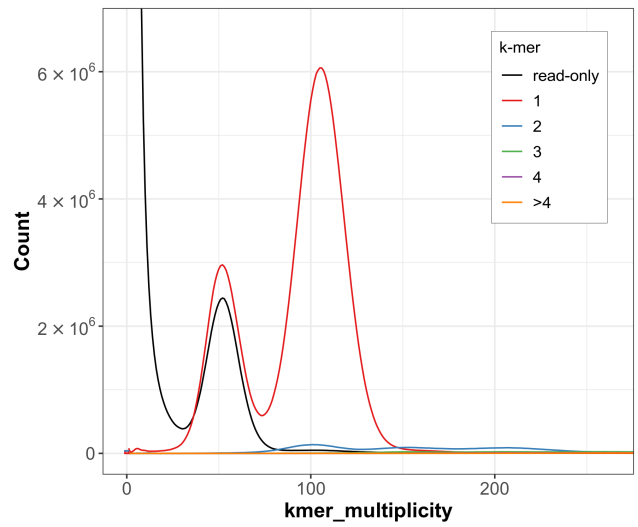


pri [\[LINK\]](#)

# K-mer spectra of curated assembly

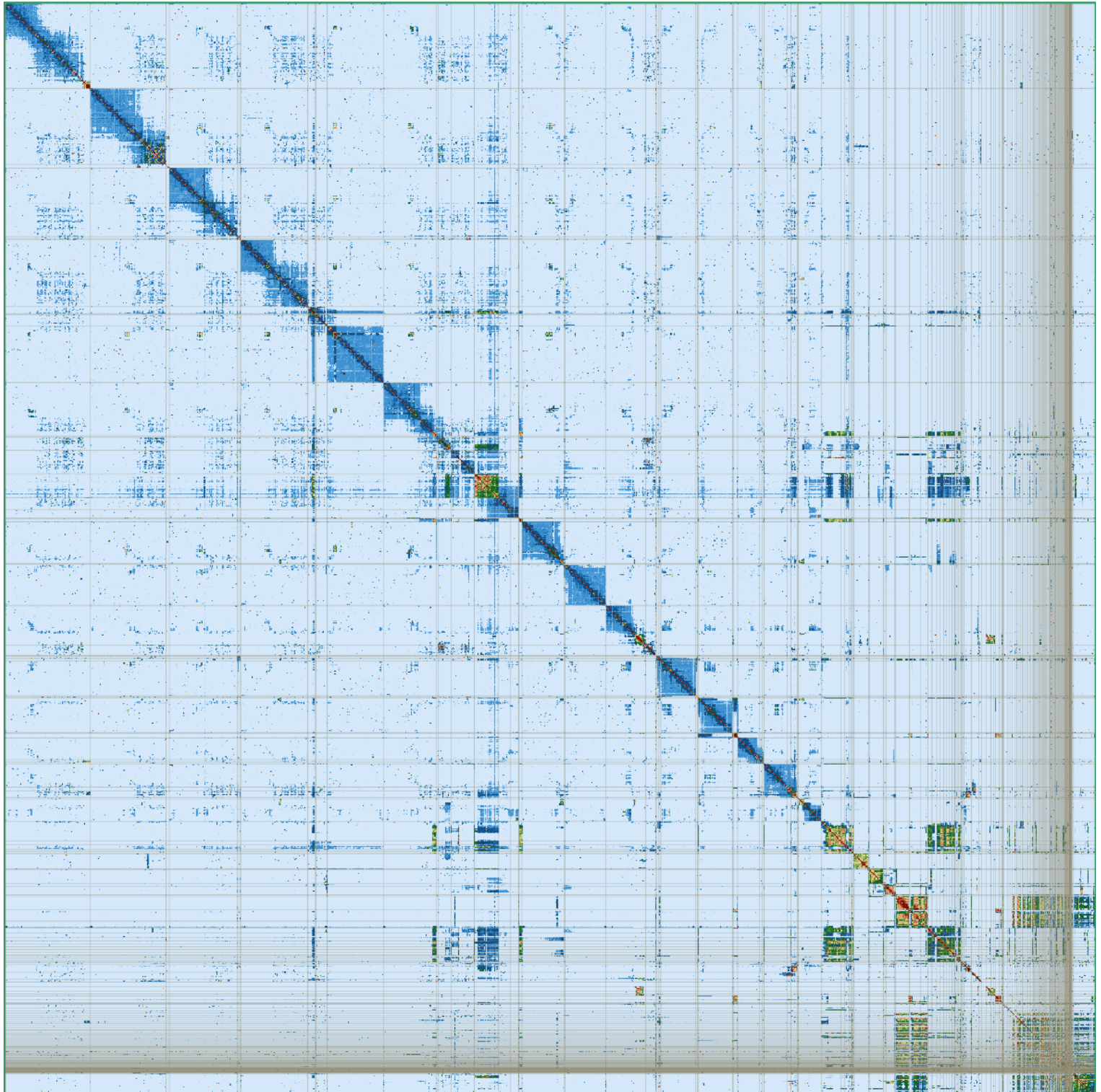


Distribution of k-mer counts coloured by their presence in reads/assemblies



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

# Post-curation contamination screening



**pri.** 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 | HiC |
|----------|-----|-----|
| Coverage | NA  | NA  |

# Assembly pipeline

- **hifiasm**
  - |\_ *ver*: 0.25.0
  - |\_ *key param*: NA
- **purge-dups**
  - |\_ *ver*: 1.2.6
  - |\_ *key param*: NA
- **yahs**
  - |\_ *ver*: 1.1a
  - |\_ *key param*: NA
- **fcs-gx**
  - |\_ *ver*: 0.5.0
  - |\_ *key param*: NA

# Curation pipeline

- **PretextView**
  - |\_ *ver*: 1.0.0
  - |\_ *key param*: NA

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