

# ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	441337
ToLID	<b>iqDolAran1</b>
Species	Dolichopoda araneiformis
Class	Insecta
Order	Orthoptera

Genome Traits	Expected	Observed
Haploid size (bp)	1,722,763,267	1,736,837,936
Haploid Number	28 (source: ancestor)	12
Ploidy	2 (source: ancestor)	4
Sample Sex	X0	unknown

## EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 7.8.Q63

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
- . Observed sex is different from Sample sex

### Curator notes

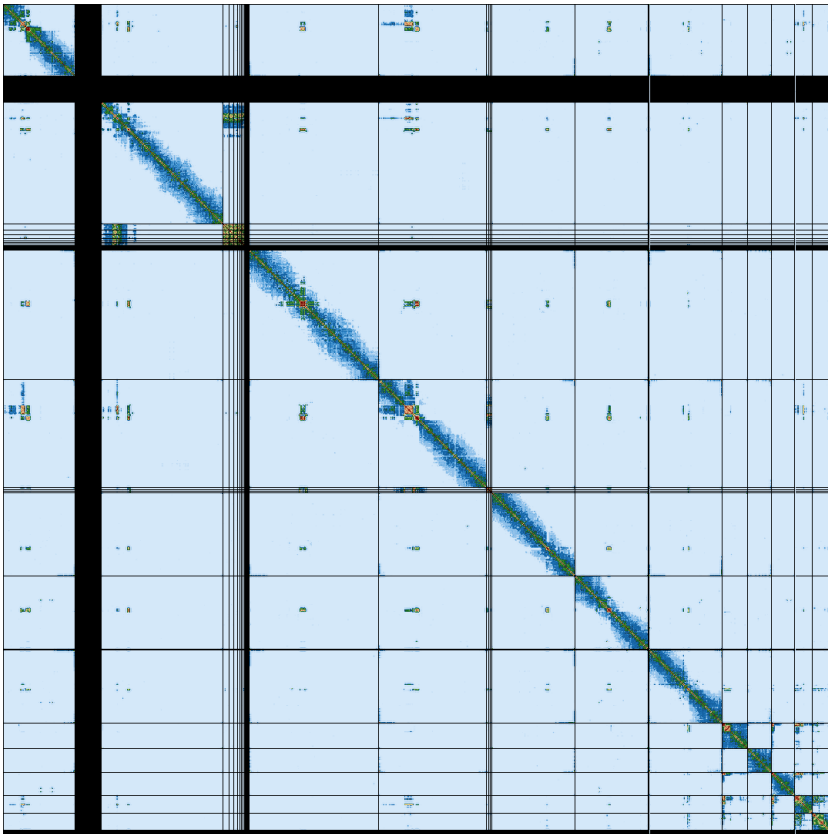
- . Interventions/Gb: 10
- . Contamination notes: "One contaminant (Spriochaetota -- 1.33 Mb) removed"
- . Other observations: "Curation made 2 cuts in contigs, 2 breaks at gaps and 13 joins"

# Quality metrics table

Metrics	Pre-curation pri	Curated pri
Total bp	1,743,793,236	1,736,837,936
GC %	36.44	36.43
Gaps/Gbp	2.29	8.64
Total gap bp	800	3,000
Scaffolds	586	573
Scaffold N50	96,336,705	173,203,730
Scaffold L50	5	4
Scaffold L90	18	12
Contigs	590	588
Contig N50	84,096,277	84,096,277
Contig L50	7	7
Contig L90	22	22
QV	63.3013	63.3319
Kmer compl.	92.3873	92.2663
BUSCO sing.	98.2%	98.0%
BUSCO dupl.	1.3%	1.3%
BUSCO frag.	0.2%	0.4%
BUSCO miss.	0.3%	0.3%

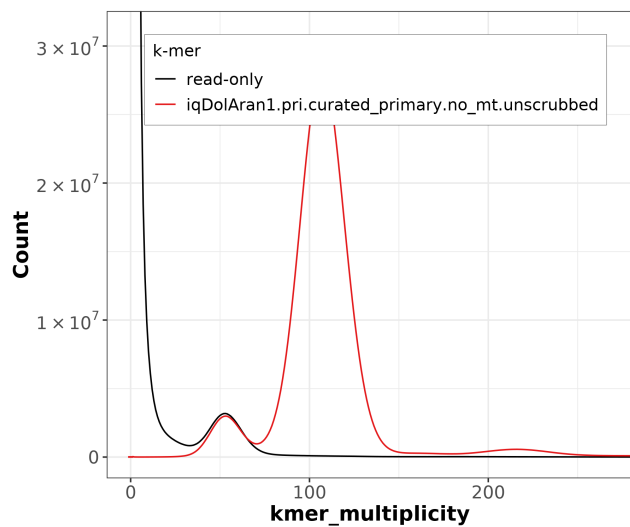
BUSCO: 5.5.0 (euk\_genome\_met, metaeuk) / Lineage: insecta\_odb10 (genomes:75, BUSCOs:1367)

# HiC contact map of curated assembly

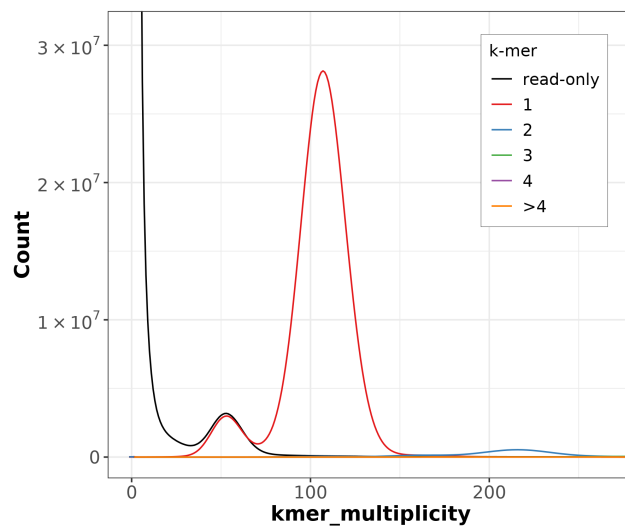


pri [\[LINK\]](#)

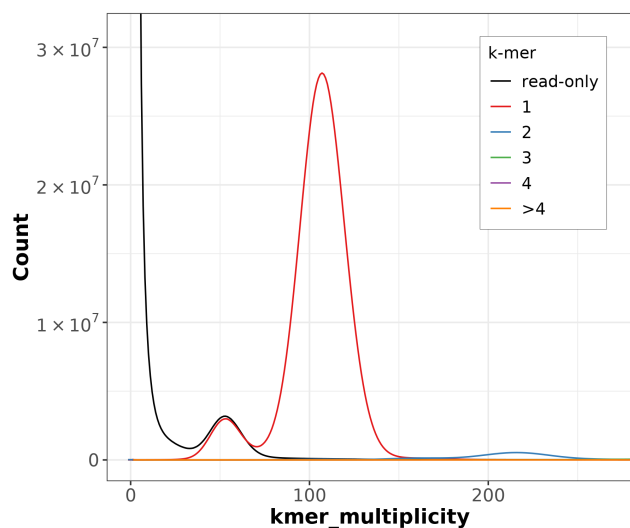
# K-mer spectra of curated assembly



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

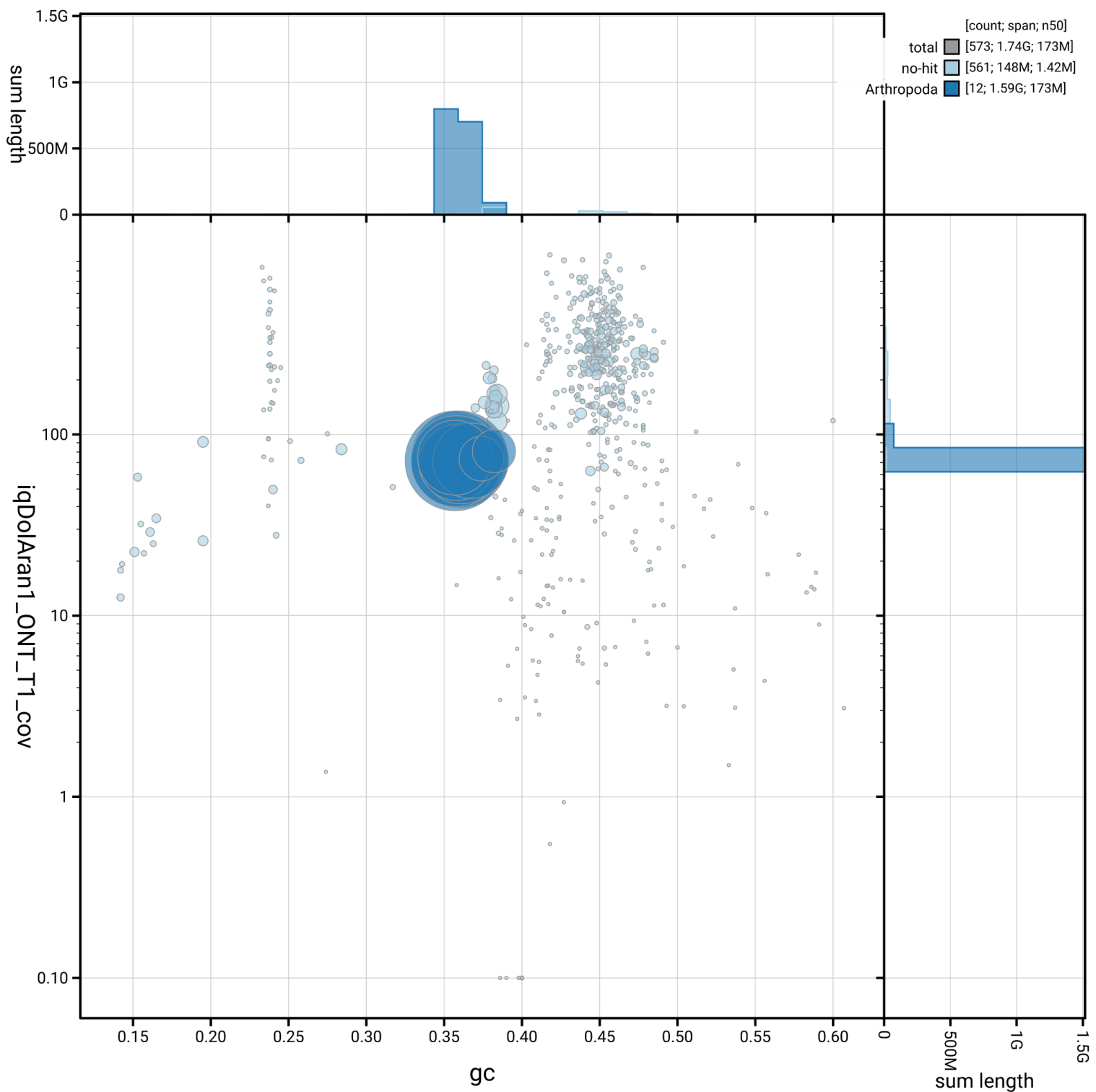


Distribution of k-mer counts per copy numbers found in asm



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	Illumina	Omni-C
Coverage	71x	56x	63x

# Assembly pipeline

- **Filtlong**
  - |\_ *ver*: 0.2.1
  - |\_ *key param*: --min\_length 1000 --min\_mean\_q 80
- **Hifiasm**
  - |\_ *ver*: 0.24.0
  - |\_ *key param*: --telo-m AACCT"
- **YaHS**
  - |\_ *ver*: 1.2a
  - |\_ *key param*: --no-contig-ec
- **CLAWS pipeline**
  - |\_ *ver*: 2.3.0
  - |\_ *key param*: NA
- **Blobtoolkit Nextflow pipeline (latest)**
  - |\_ *ver*: 0.6
  - |\_ *key param*: NA
- **FOAM pipeline**
  - |\_ *ver*: 0.5
  - |\_ *key param*: NA
- **mitos**
  - |\_ *ver*: 2.1.3
  - |\_ *key param*: NA

# Curation pipeline

- **GRIT\_Rapid**
  - |\_ *ver*: 2.0
  - |\_ *key param*: NA
- **PretextViewAI**
  - |\_ *ver*: 1.0.4
  - |\_ *key param*: NA

Submitter: Tyler Alioto

Affiliation: CNAG

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