

# ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	3229105
ToLID	<b>qqAelCypr9</b>
Species	Aelurillus cypriotus
Class	Arachnida
Order	Araneae

Genome Traits	Expected	Observed
Haploid size (bp)	3,993,831,373	3,929,230,577
Haploid Number	14 (source: ancestor)	11
Ploidy	2 (source: ancestor)	2
Sample Sex	XX	XX

## EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 8.8.Q69

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

- . Observed Haploid Number is different from Expected
- . Kmer completeness value is less than 90 for pri

### Curator notes

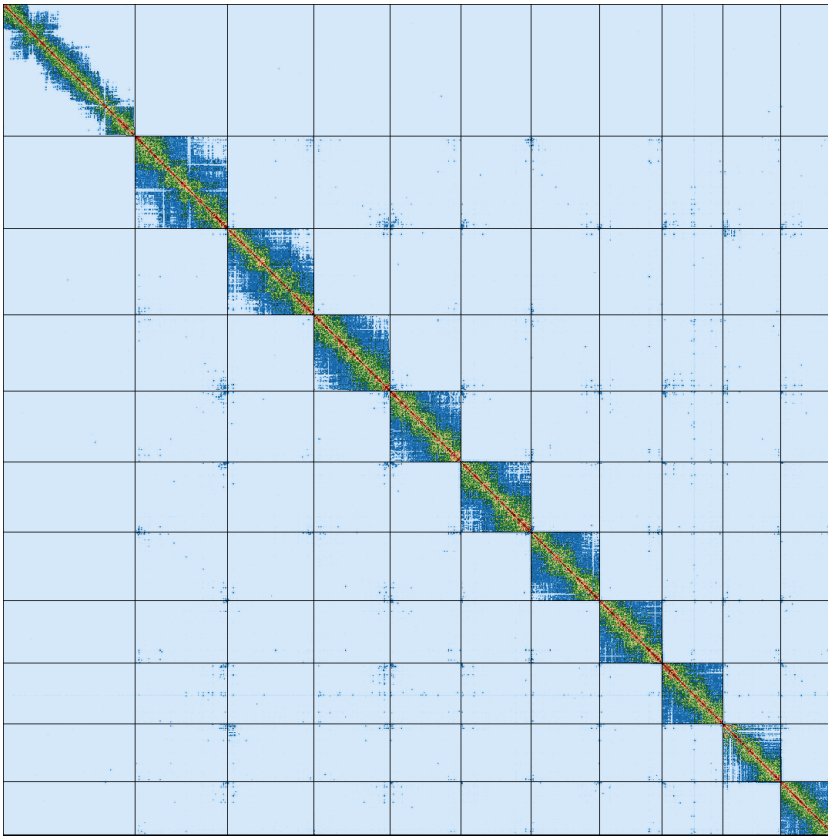
- . Interventions/Gb: 0.5
- . Contamination notes: "No contaminants were detected"
- . Other observations: "We have decided to curate the primary assembly for this species as it contained only four gaps and it is about four times as contiguous as each of the haps (hap1 and hap2 have 28 and 36 gaps respectively). The sample that was sequenced corresponded to an XX female while the HiC data came from a male. This helped us identify the X chromosome. We further confirmed the sex chromosome by alignment to other species within the same Dionycha clade."

# Quality metrics table

Metrics	Pre-curation pri	Curated pri
Total bp	3,929,230,377	3,929,230,577
GC %	29.16	29.16
Gaps/Gbp	0.76	1.02
Total gap bp	600	800
Scaffolds	51	51
Scaffold N50	335,564,643	333,985,199
Scaffold L50	5	5
Scaffold L90	10	10
Contigs	54	55
Contig N50	322,710,697	322,710,697
Contig L50	6	6
Contig L90	12	12
QV	69.4534	69.4534
Kmer compl.	78.8165	78.8165
BUSCO sing.	92.9%	92.9%
BUSCO dupl.	3.8%	3.8%
BUSCO frag.	1.5%	1.5%
BUSCO miss.	1.8%	1.8%

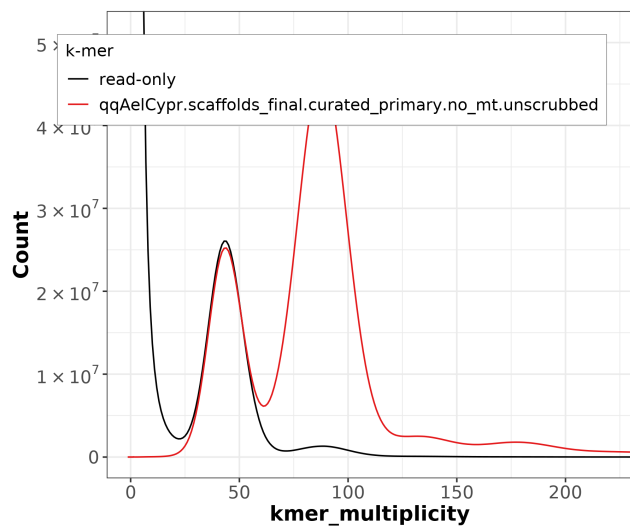
BUSCO: 5.5.0 (euk\_genome\_met, metaeuk) / Lineage: arthropoda\_odb10 (genomes:90, BUSCOs:1013)

# HiC contact map of curated assembly

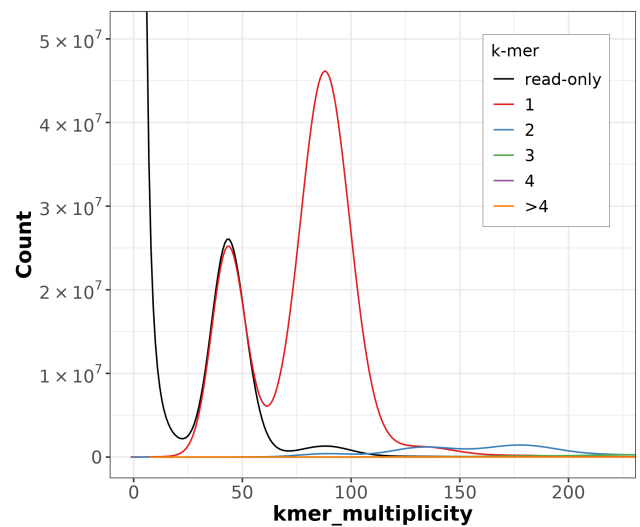


pri [\[LINK\]](#)

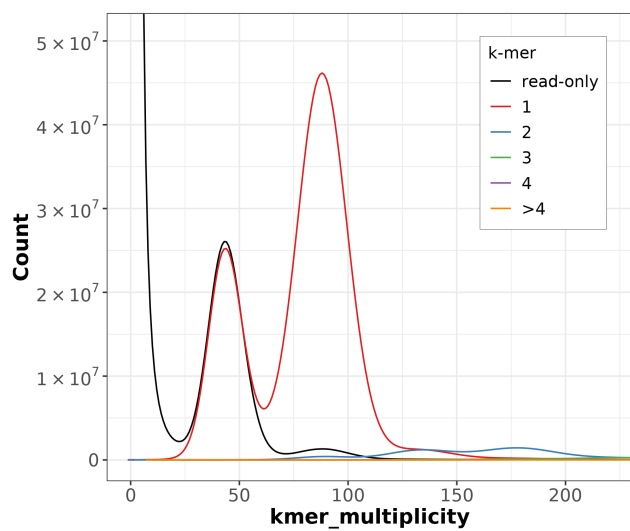
# K-mer spectra of curated assembly



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

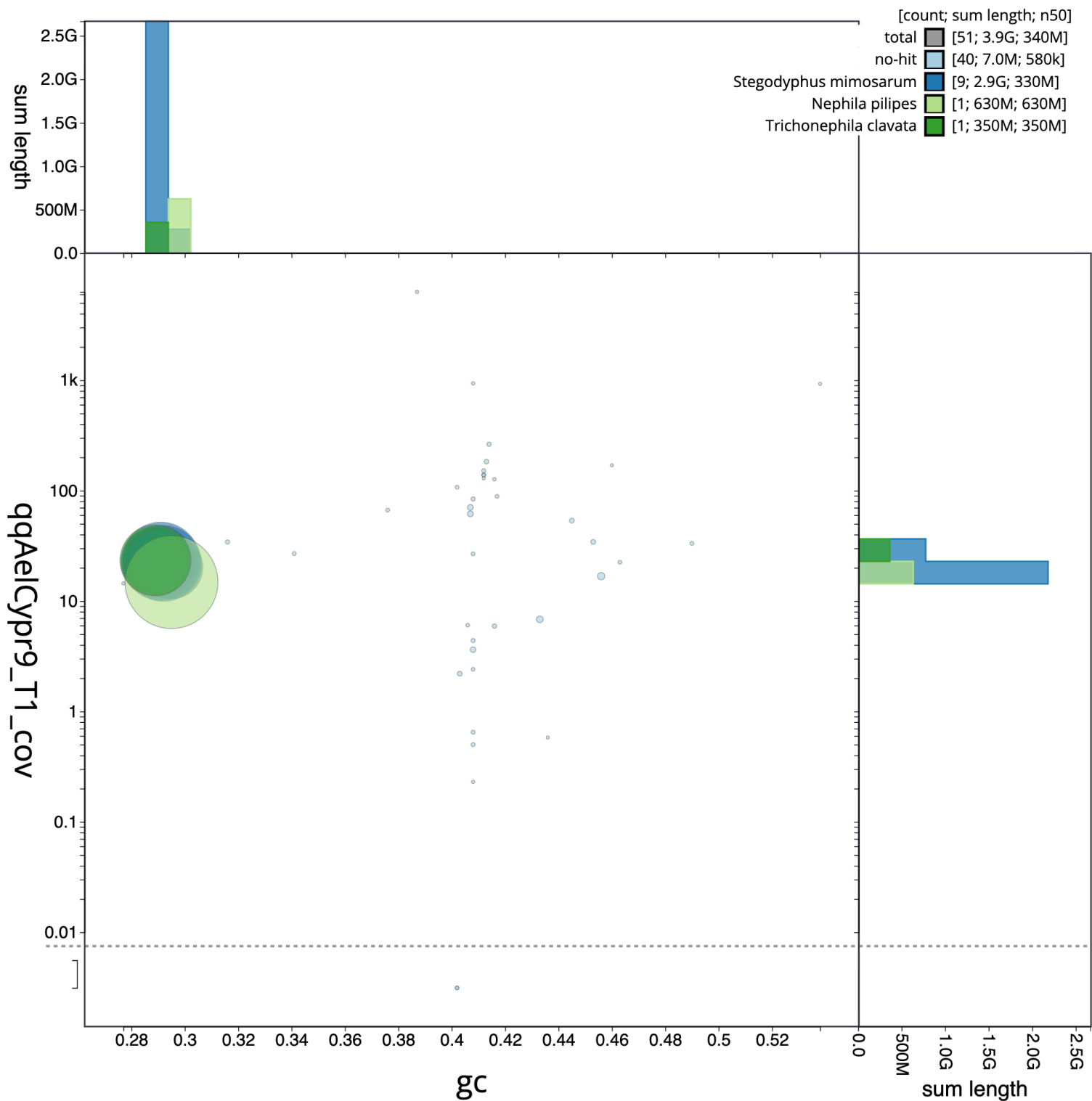


Distribution of k-mer counts per copy numbers found in asm



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	OmniC
Coverage	54x	62x

## Assembly pipeline

- **hifiasm**
  - |\_ *ver*: 0.24.0-r702
  - |\_ *key param*: NA
- **YaHS**
  - |\_ *ver*: 1.2a
  - |\_ *key param*: NA
- **CLAWS**
  - |\_ *ver*: 2.3
  - |\_ *key param*: NA

## Curation pipeline

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

Submitter: Francisco Camara

Affiliation: CNAG Barcelona

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