

# ERGA Assembly Report

v24.04.03\_beta

Tags: ERGA-BGE

TxID	3056766
ToLID	<b>iqAntSpin1</b>
Species	Antaxius spinibrachius
Class	Insecta
Order	Orthoptera

Genome Traits	Expected	Observed
Haploid size (bp)	5,159,417,685	5,179,441,024
Haploid Number	15 (source: ancestor)	15
Ploidy	2 (source: ancestor)	2
Sample Sex	F	F

## EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 7.8.Q68

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

### Curator notes

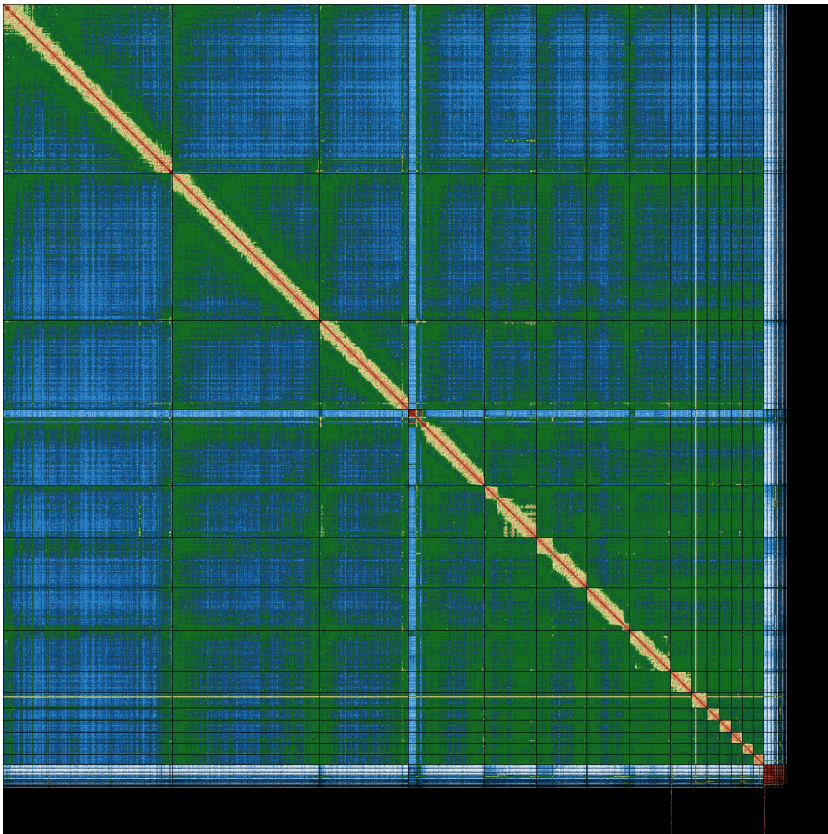
. Interventions/Gb: 62  
. Contamination notes: "Contamination report for assembly labelled hap1; Total length of scaffolds removed: 1,493,926 (0.0 %); Scaffolds removed: 59 (4.8 %); Largest scaffold removed: (48,121); FCS-GX contaminant species (number of scaffolds; total length of scaffolds): Mitochondrion (59; 1,493,926)"  
. Other observations: "Hifiasm assembly run in Hi-C phasing mode; The exact order and orientation of the contigs on chromosome 4 (393.6-410.3 Mbp)m chromosome 3 (515.5-521.2 Mbp) and chromosome 1 (4.0-10.8 and 1043-end Mbp) is unknown. The sample was homogametous. No X chromosome was assigned, as comparator X were ambiguous. Chromosome 8 shows a heterologous rearrangment from 52.6-174.7 Mbp to 250 Mbp."

# Quality metrics table

Metrics	Pre-curation pri	Curated pri
Total bp	5,234,029,028	5,179,441,024
GC %	39.95	40.04
Gaps/Gbp	124	134.38
Total gap bp	64,900	82,200
Scaffolds	1,226	1,026
Scaffold N50	210,465,830	473,558,889
Scaffold L50	7	4
Scaffold L90	42	14
Contigs	1,875	1,722
Contig N50	45,506,000	45,506,000
Contig L50	34	34
Contig L90	200	183
QV	68.3	68.6
Kmer compl.	99.46	99.46
BUSCO sing.	95.1%	95.0%
BUSCO dupl.	4.1%	4.2%
BUSCO frag.	0.1%	0.1%
BUSCO miss.	0.7%	0.7%

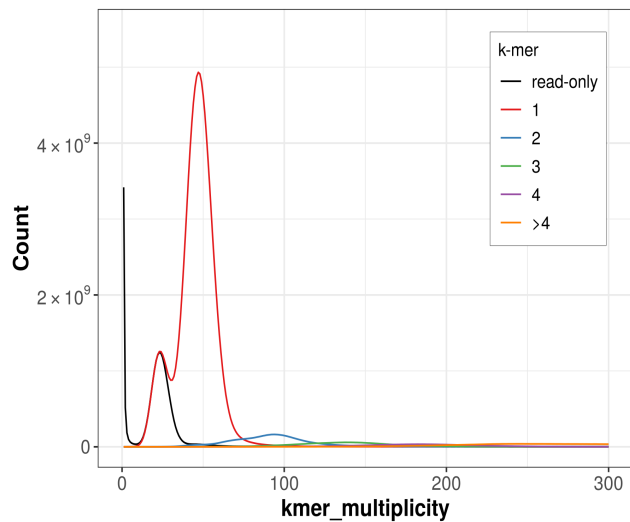
BUSCO 6.0.0 Lineage: insecta\_odb10 (genomes:75, BUSCOs:1367)

# HiC contact map of curated assembly

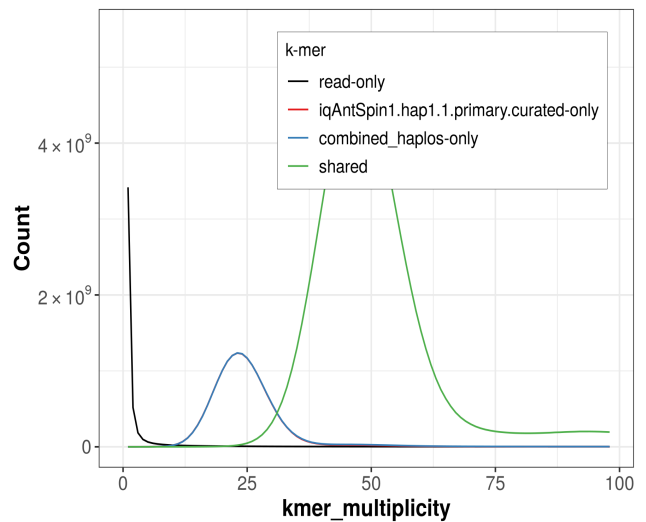


pri [\[LINK\]](#)

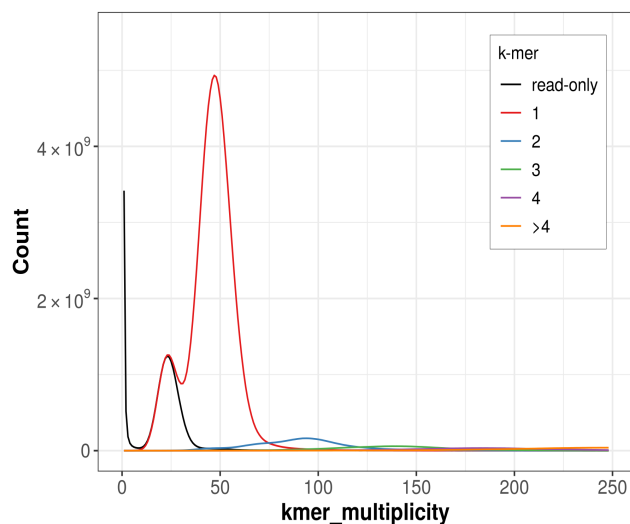
# K-mer spectra of curated assembly



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

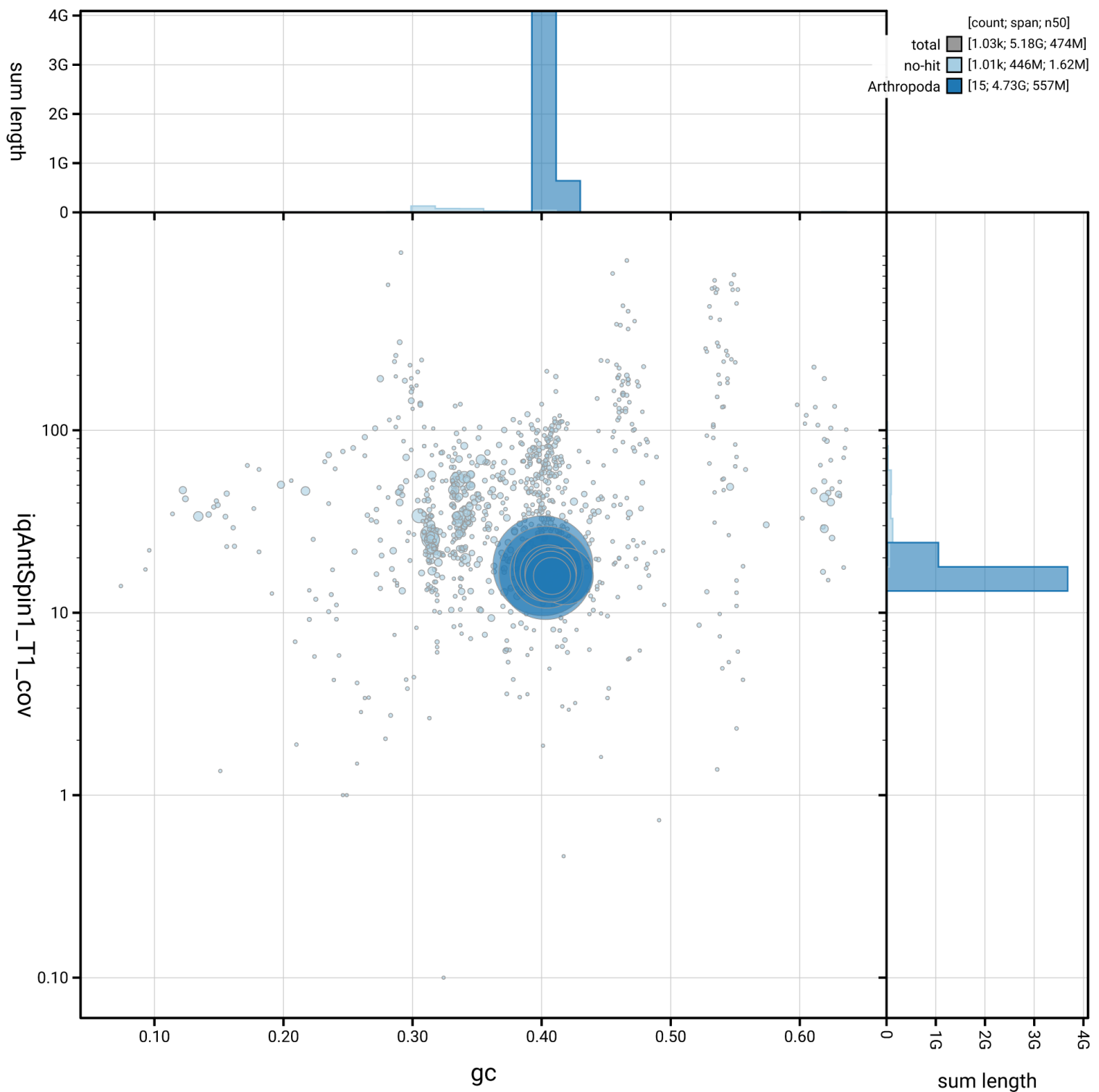


Distribution of k-mer counts coloured by their presence in reads/assemblies



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	PacBio HiFi	Arima v2
Coverage	46x	492x

# Assembly pipeline

- **hifiasm**
  - |\_ *ver*: 0.25.0-r726
  - |\_ *key param*: --h1/--h2
- **yahs**
  - |\_ *ver*: 1.2.2
  - |\_ *key param*: NA

# Curation pipeline

- **hifiasm**
  - |\_ *ver*: 0.25.0-r726
  - |\_ *key param*: --h1/--h2
- **yahs**
  - |\_ *ver*: 1.2.2
  - |\_ *key param*: NA
- **TreeVal**
  - |\_ *ver*: 1.2.1
  - |\_ *key param*: NA

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