

ERGA Assembly Report

v24.04.03_beta

Tags: ERGA-BGE

TxID	3056766
ToLID	iqAntSpin1
Species	<i>Antaxius spinibrachius</i>
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

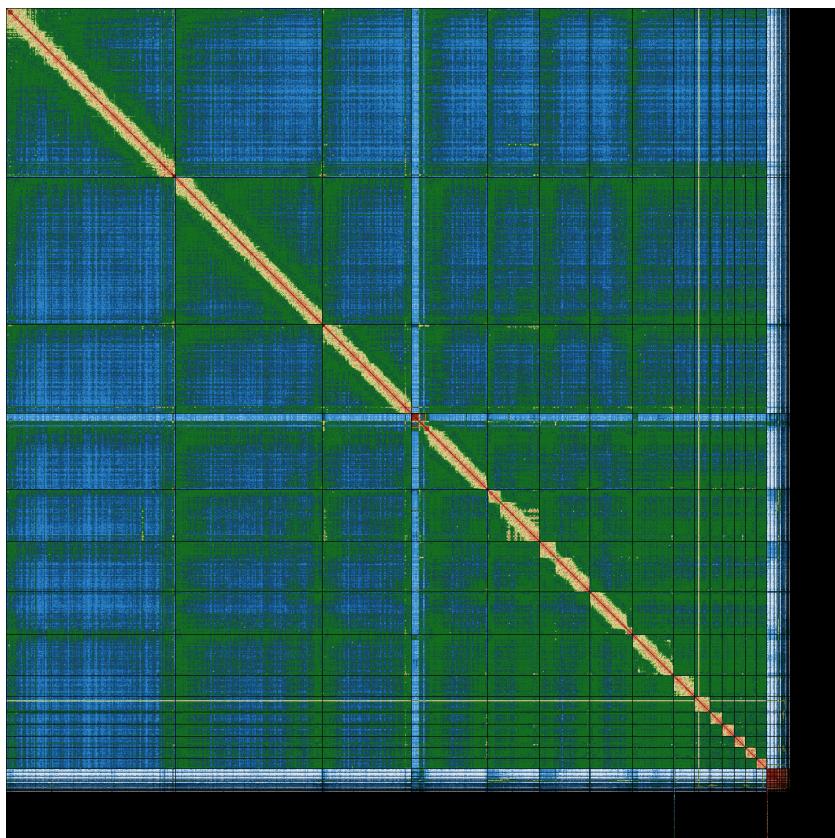
- . Interventions/Gb: 62
- . Contamination notes: "Contamination report for assembly labelled hap1; Total length of scaffolds removed: 1,493,926 (0.0 %); Scaffolds removed: 59 (4.8 %); Largest scaffold removed: (48,121); FCS-GX contaminant species (number of scaffolds; total length of scaffolds): Mitochondrion (59; 1,493,926)"
- . Other observations: "Hifiiasm 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 rearrangement 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%

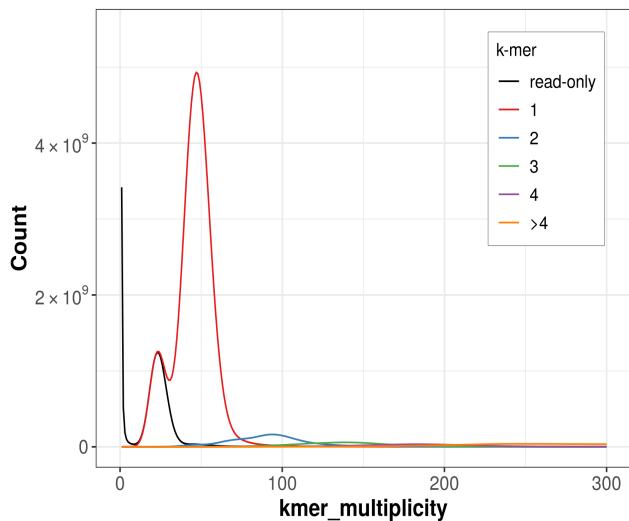
BUSCO 6.0.0 Lineage: insecta_odb10 (genomes:75, BUSCOs:1367)

HiC contact map of curated assembly

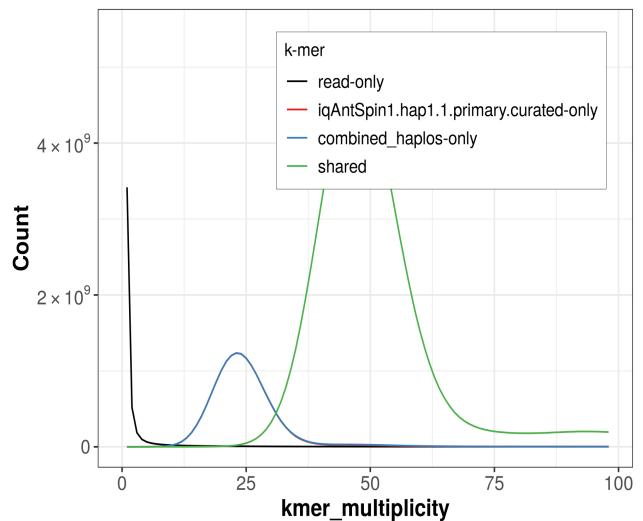


pri [LINK]

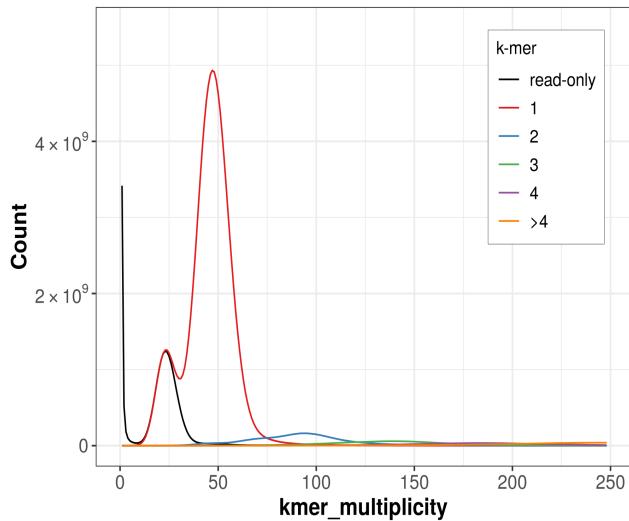
K-mer spectra of curated assembly



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

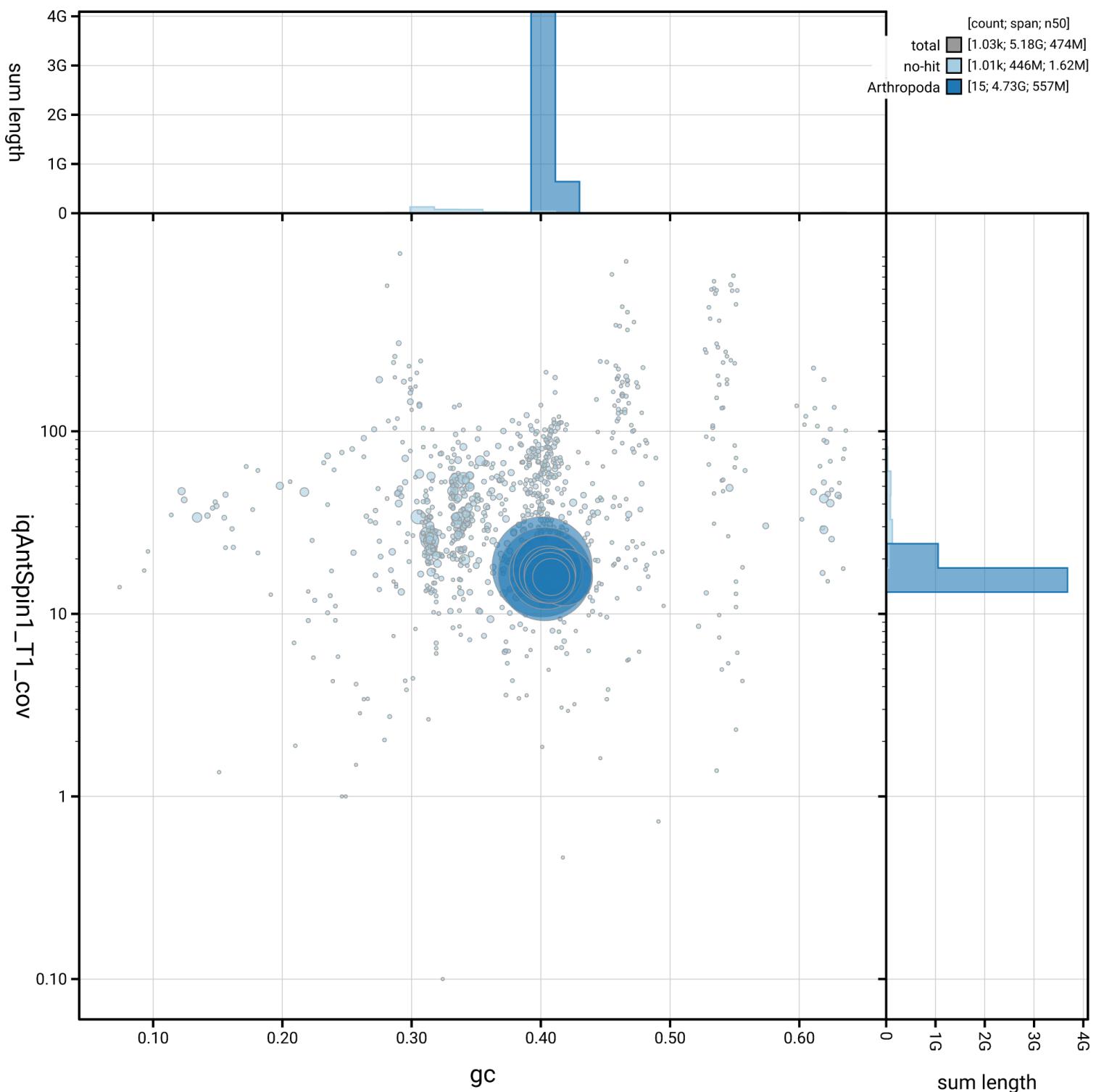


Distribution of k-mer counts coloured by their presence in reads/assemblies



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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Date and time: 2026-02-02 11:14:37 CET