

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	2770602
ToLID	qqRhoAspi1
Species	Rhode aspinifera
Class	Arachnida
Order	Araneae

Genome Traits	Expected	Observed
Haploid size (bp)	1,767,830,687	1,568,305,066
Haploid Number	11 (source: ancestor)	0
Ploidy	2 (source: ancestor)	2
Sample Sex	NA	NA

EBP metrics summary and curation notes

Obtained EBP quality metric for hap1: 4.4.Q50

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 hap1
- . BUSCO single copy value is less than 90% for hap1
- . Not 90% of assembly in chromosomes for hap1

Curator notes

- . Interventions/Gb: NA
- . Contamination notes: "Contaminants were not removed as it was difficult to define their correct assignation as contaminants."
- . Other observations: "This is a contig level assembly. The contig N50 was too low, and it was decided not to proceed with scaffolding."

Quality metrics table

Metrics	Pre-curation hap1	Curated hap1
Total bp	1,568,305,066	1,568,305,066
GC %	33.94	33.94
Gaps/Gbp	0	0
Total gap bp	0	0
Scaffolds	22,497	22,497
Scaffold N50	99,051	99,051
Scaffold L50	4,947	4,947
Scaffold L90	15,354	15,354
Contigs	22,497	22,497
Contig N50	99,051	99,051
Contig L50	4,947	4,947
Contig L90	15,354	15,354
QV	50.8942	50.8942
Kmer compl.	80.7202	80.7202
BUSCO sing.	73.1%	73.1%
BUSCO dupl.	4.9%	4.9%
BUSCO frag.	6.2%	6.2%
BUSCO miss.	15.8%	15.8%

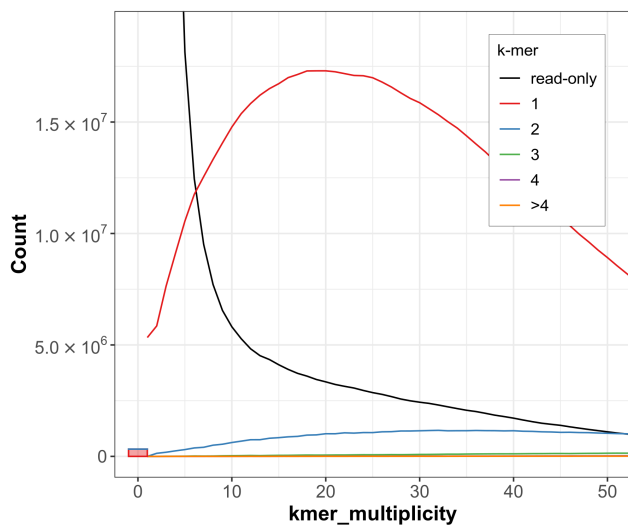
BUSCO: 5.8.0 (euk_genome_min, miniprot) / Lineage: arachnida_odb10 (genomes:10, BUSCOs:2934)

HiC contact map of curated assembly

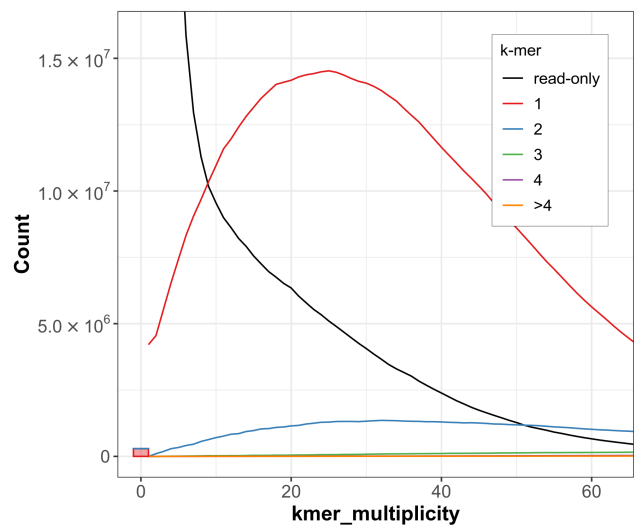
hap1 HiC PNG is missing!

hap1 File link is missing!

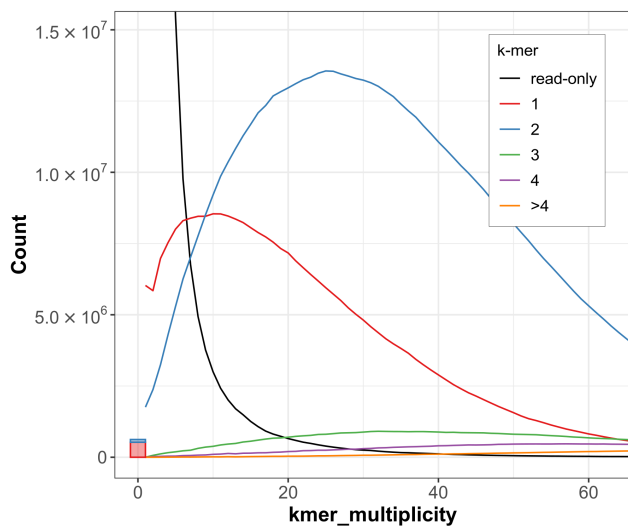
K-mer spectra of curated assembly



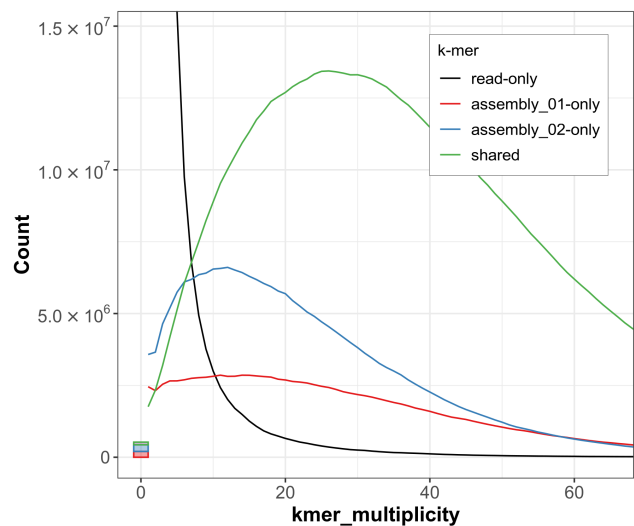
Distribution of k-mer counts per copy numbers found in **assembly_02** (hapl.)



Distribution of k-mer counts per copy numbers found in **assembly_01** (hapl.)

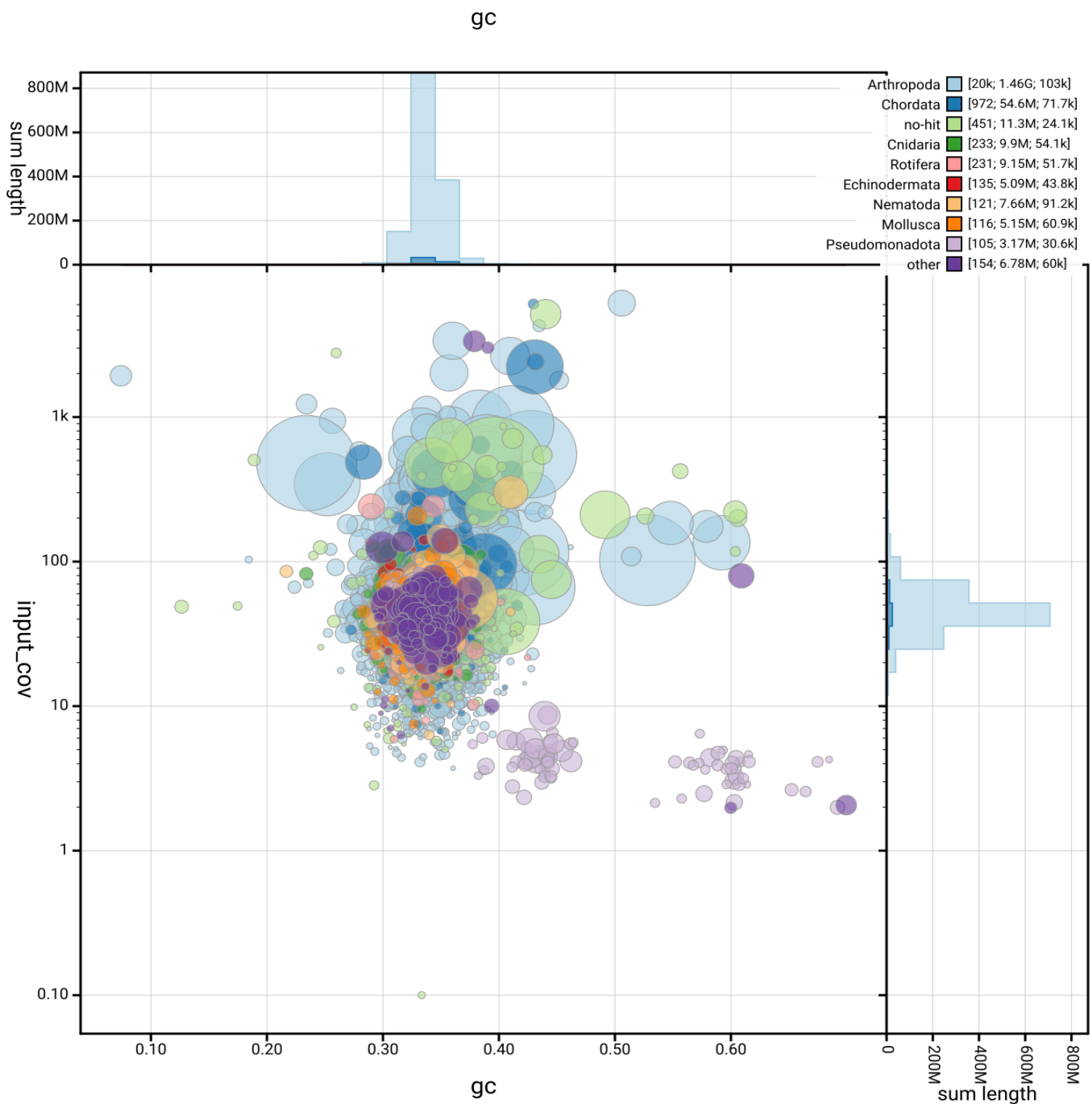


Distribution of k-mer counts per copy numbers found in **asm** (dipl.)



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

Post-curation contamination screening



hap1. 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	HiFi
Coverage	26.70x

Assembly pipeline

- **Hifiasm**
 - |_ *ver*: Galaxy Version 0.25.0+galaxy0
 - |_ *key param*: VGP Galaxy workflow VGP3 v 0.3.4
- **purge_dups**
 - |_ *ver*: Galaxy Version 1.2.6+galaxy0
 - |_ *key param*: VGP Galaxy workflow VGP6 v 0.10.4

Curation pipeline

Invalid pipeline data format

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