

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	3139262
ToLID	qqRhoMag1
Species	<i>Rhode magnifica</i>
Class	Arachnida
Order	Araneae

Genome Traits	Expected	Observed
Haploid size (bp)	3,486,225,572	2,759,692,961
Haploid Number	11 (source: ancestor)	0
Ploidy	2 (source: ancestor)	2
Sample Sex	unknown	NA

EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 6.6.Q62

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

- . Observed Haploid size (bp) has >20% difference with Expected
- . Observed Haploid Number is different from Expected
- . Observed sex is different from Sample sex
- . Kmer completeness value is less than 90 for pri
- . BUSCO duplicated value is more than 5% for pri
- . Not 90% of assembly in chromosomes for pri

Curator notes

- . Interventions/Gb: None
- . Contamination notes: "60 sequences identified by fcs-gx as bacteria were removed"
- . Other observations: "Hi-C libraries for this species failed, so a contig-level assembly was made and submitted"

Quality metrics table

Metrics	Pre-curation pri	Curated pri
Total bp	2,759,692,961	2,759,692,961
GC %	35.32	35.32
Gaps/Gbp	0	0
Total gap bp	0	0
Scaffolds	2,824	2,824
Scaffold N50	2,704,898	2,704,898
Scaffold L50	309	309
Scaffold L90	1,069	1,069
Contigs	2,824	2,824
Contig N50	2,704,898	2,704,898
Contig L50	309	309
Contig L90	1,069	1,069
QV	62.1106	62.1106
Kmer compl.	82.8355	82.8355
BUSCO sing.	91.3%	91.3%
BUSCO dupl.	5.3%	5.3%
BUSCO frag.	1.5%	1.5%
BUSCO miss.	1.9%	1.9%

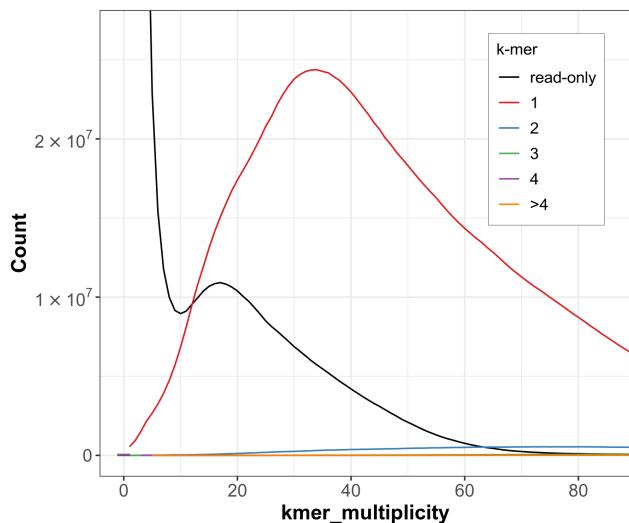
BUSCO: 6.0.0 (euk_genome_min, miniprot) / Lineage: arachnida_odb12 (genomes:34, BUSCOs:1123)

HiC contact map of curated assembly

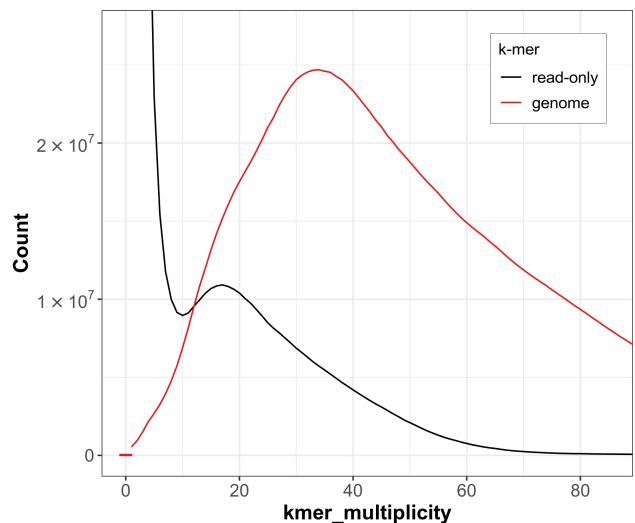
pri HiC PNG is missing!

pri File link is missing!

K-mer spectra of curated assembly

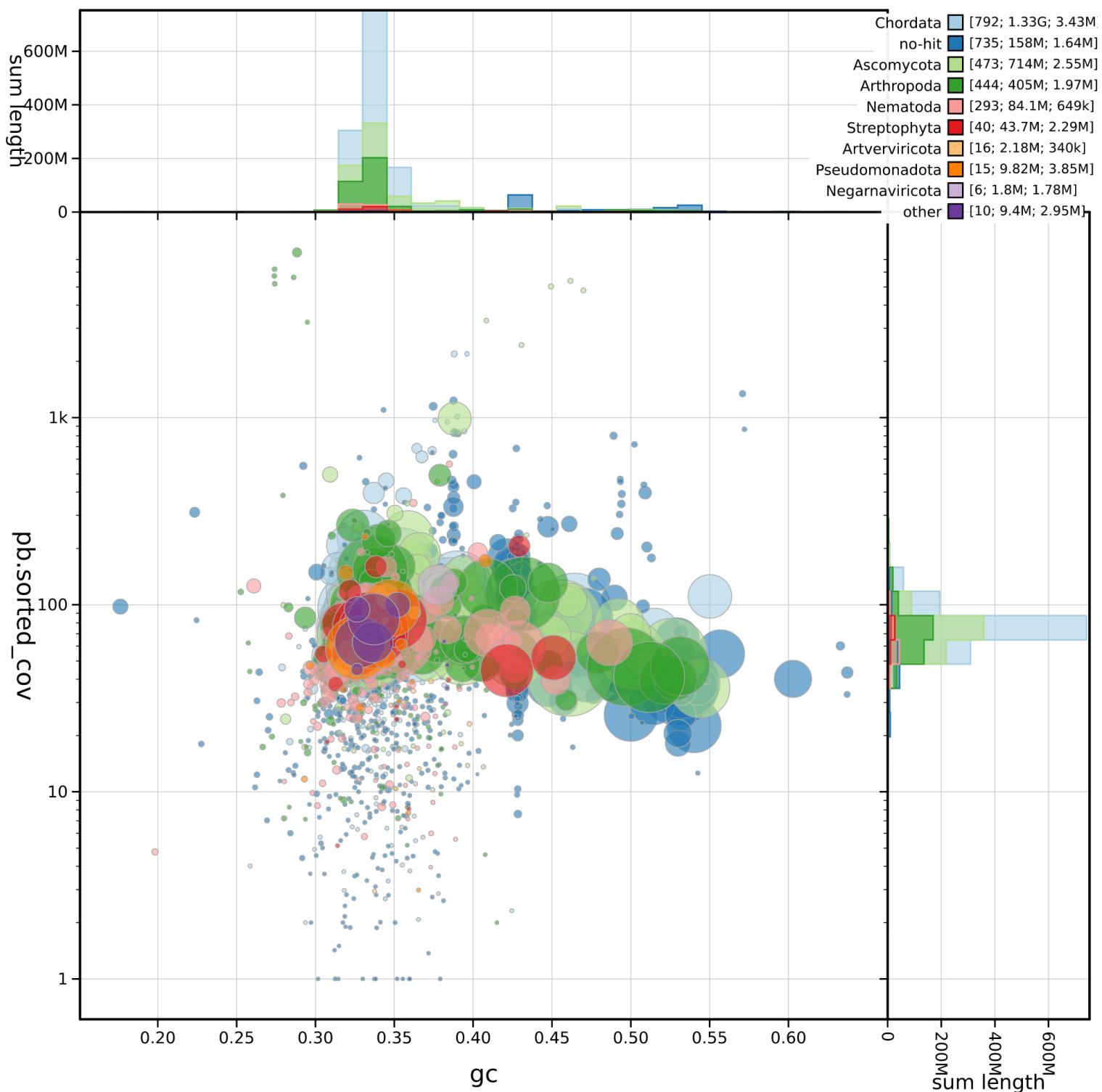


Distribution of k-mer counts per copy numbers found in asm



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

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
Coverage	37

Assembly pipeline

- **HiFiasm**
 - |_ ver: 0.25.0
 - |_ key param: NA
- **purge-dups**
 - |_ ver: 1.2.6
 - |_ key param: NA
- **fcs-gx**
 - |_ ver: 0.5.0
 - |_ key param: NA

Curation pipeline

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Date and time: 2026-02-19 14:09:00 CET