

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	2721269
ToLID	qqStaHerc9
Species	<i>Stalagtia hercegovinensis</i>
Class	Arachnida
Order	Araneae

Genome Traits	Expected	Observed
Haploid size (bp)	2,285,618,970	2,806,615,544
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.Q63

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: "None"
- . Other observations: "Hi-C data showed no interactions, so a contig-level assembly was submitted. Approximately 60 sequences were identified as bacteria and removed"

Quality metrics table

Metrics	Pre-curation pri	Curated pri
Total bp	2,806,615,544	2,806,615,544
GC %	35.1	35.1
Gaps/Gbp	0	0
Total gap bp	0	0
Scaffolds	1,133	1,133
Scaffold N50	5,079,695	5,079,695
Scaffold L50	167	167
Scaffold L90	592	592
Contigs	1,133	1,133
Contig N50	5,079,695	5,079,695
Contig L50	167	167
Contig L90	592	592
QV	63.4485	63.4485
Kmer compl.	73.2506	73.2506
BUSCO sing.	91.1%	91.1%
BUSCO dupl.	6.4%	6.4%
BUSCO frag.	0.6%	0.6%
BUSCO miss.	1.9%	1.9%

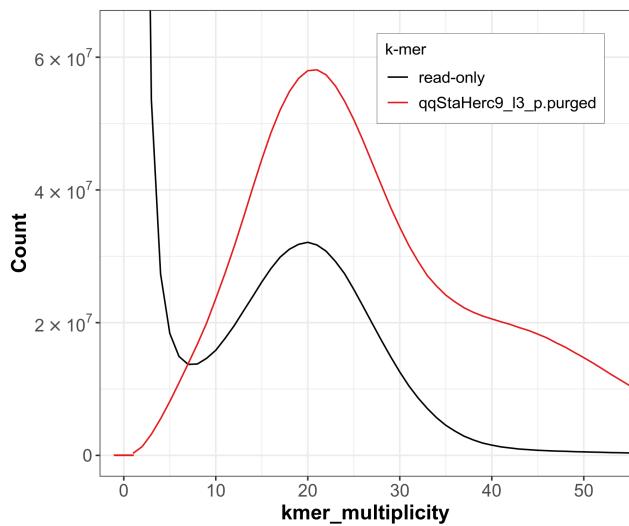
BUSCO: 6.0.0 (euk_genome_min, miniprot) / Lineage: arachnida_odb12 (genomes:34, BUSCOs:1123)

HiC contact map of curated assembly

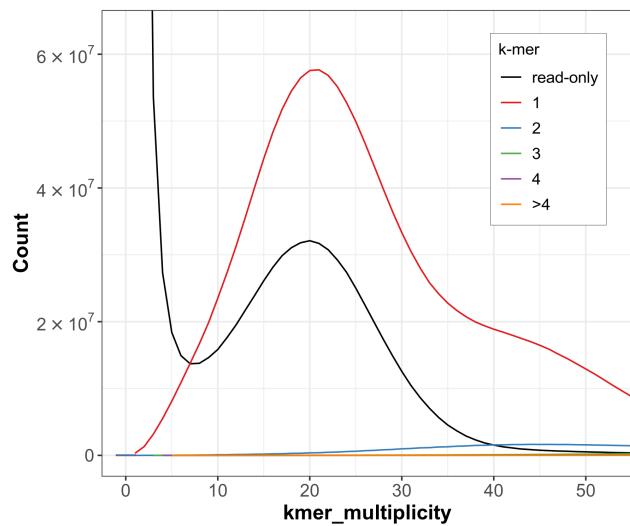
pri HiC PNG is missing!

pri File link is missing!

K-mer spectra of curated assembly

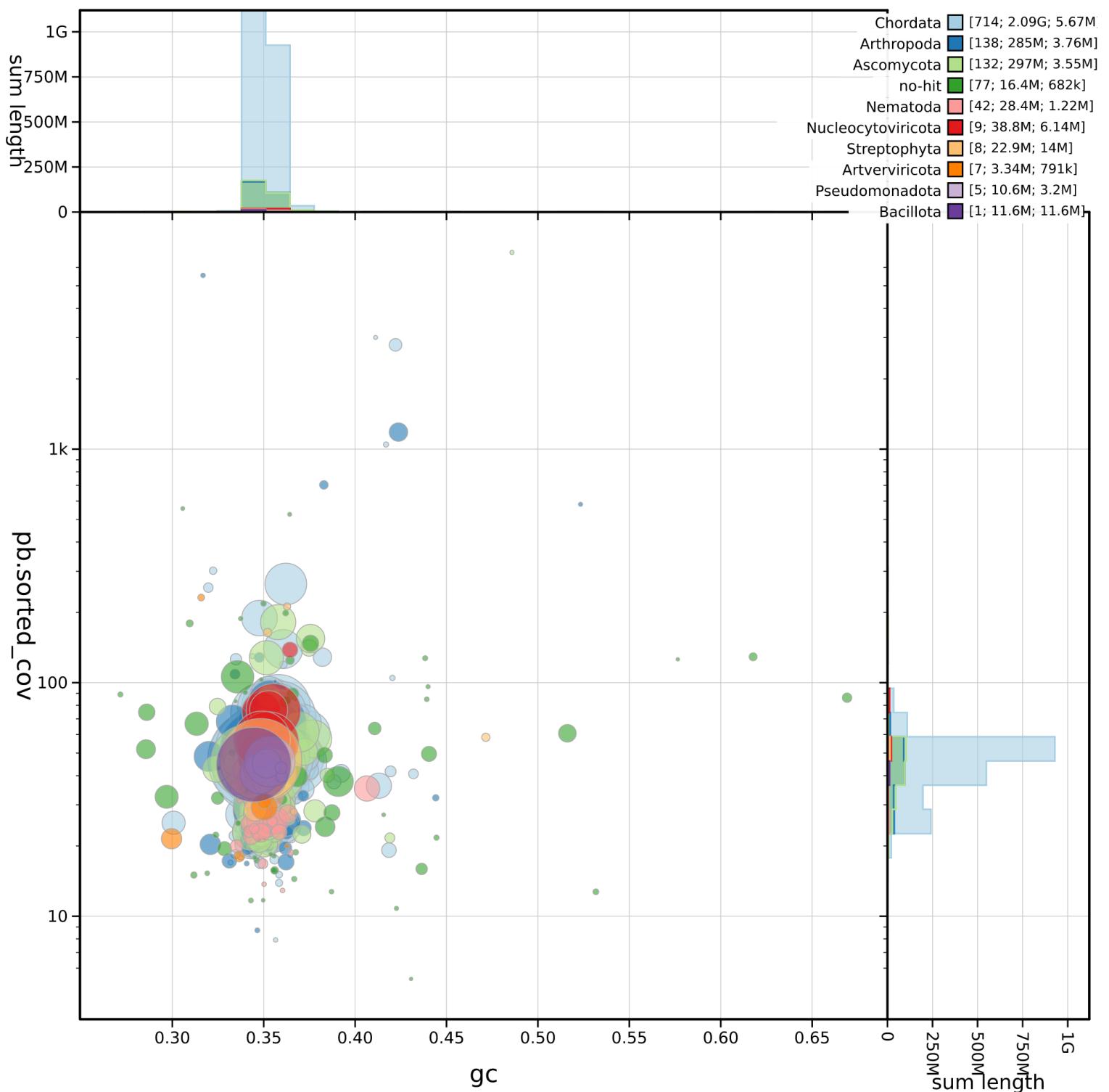


Distribution of k-mer counts coloured by their presence in reads/assemblies



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
Coverage	40

Assembly pipeline

```
- hifiasm
  |_ ver: 0.25.0
  |_ key param: NA
- purge-dups
  |_ ver: 1.2.6
  |_ key param: NA
```

Curation pipeline

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Date and time: 2026-02-18 13:55:39 CET