

# ERGA Assembly Report

v24.10.15

Tags: BGE [ INVALID TAG ]

TxID	3139678
ToLID	<b>q1AbsGiga1</b>
Species	<i>Absolonia gigantea</i>
Class	Collembola
Order	Poduromorpha

Genome Traits	Expected	Observed
Haploid size (bp)	357,714,307	453,403,575
Haploid Number	5 (source: ancestor)	0
Ploidy	2 (source: ancestor)	2
Sample Sex	NA	NA

## EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 6.6.Q60

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
- . Kmer completeness value is less than 90 for pri
- . Not 90% of assembly in chromosomes for pri

## Curator notes

- . Interventions/Gb: None
- . Contamination notes: "60 sequences totalling 3Mb were identified as proteobacteria by fcs-gx and removed"
- . Other observations: "Hi-C library failed for this species. A contig-level assembly is submitted after purging and decontamination."

## Quality metrics table

Metrics	Pre-curation pri	Curated pri
Total bp	453,403,575	453,403,575
GC %	35.85	35.85
Gaps/Gbp	0	0
Total gap bp	0	0
Scaffolds	491	491
Scaffold N50	3,310,077	3,310,077
Scaffold L50	37	37
Scaffold L90	162	162
Contigs	491	491
Contig N50	3,310,077	3,310,077
Contig L50	37	37
Contig L90	162	162
QV	60.6246	60.6246
Kmer compl.	84.5474	84.5474
BUSCO sing.	94.3%	94.3%
BUSCO dupl.	3.4%	3.4%
BUSCO frag.	1.3%	1.3%
BUSCO miss.	1.0%	1.0%

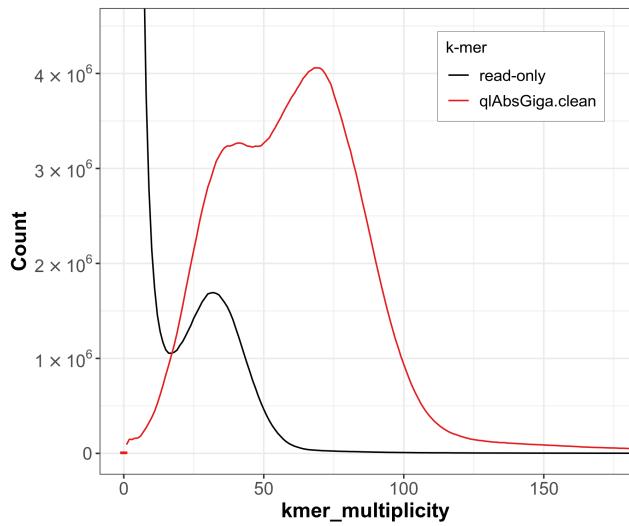
BUSCO: 6.0.0 (euk\_genome\_min, miniprot) / Lineage: arthropoda\_odb12 (genomes:76, BUSCOs:1667)

# HiC contact map of curated assembly

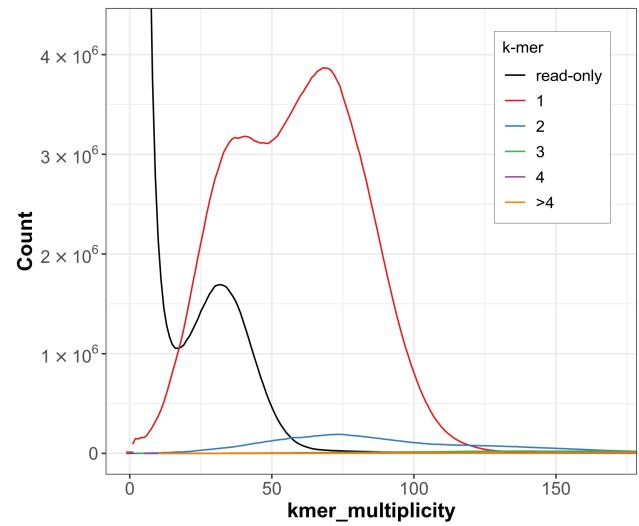
**pri** HiC PNG is missing!

**pri** File link is missing!

# K-mer spectra of curated assembly

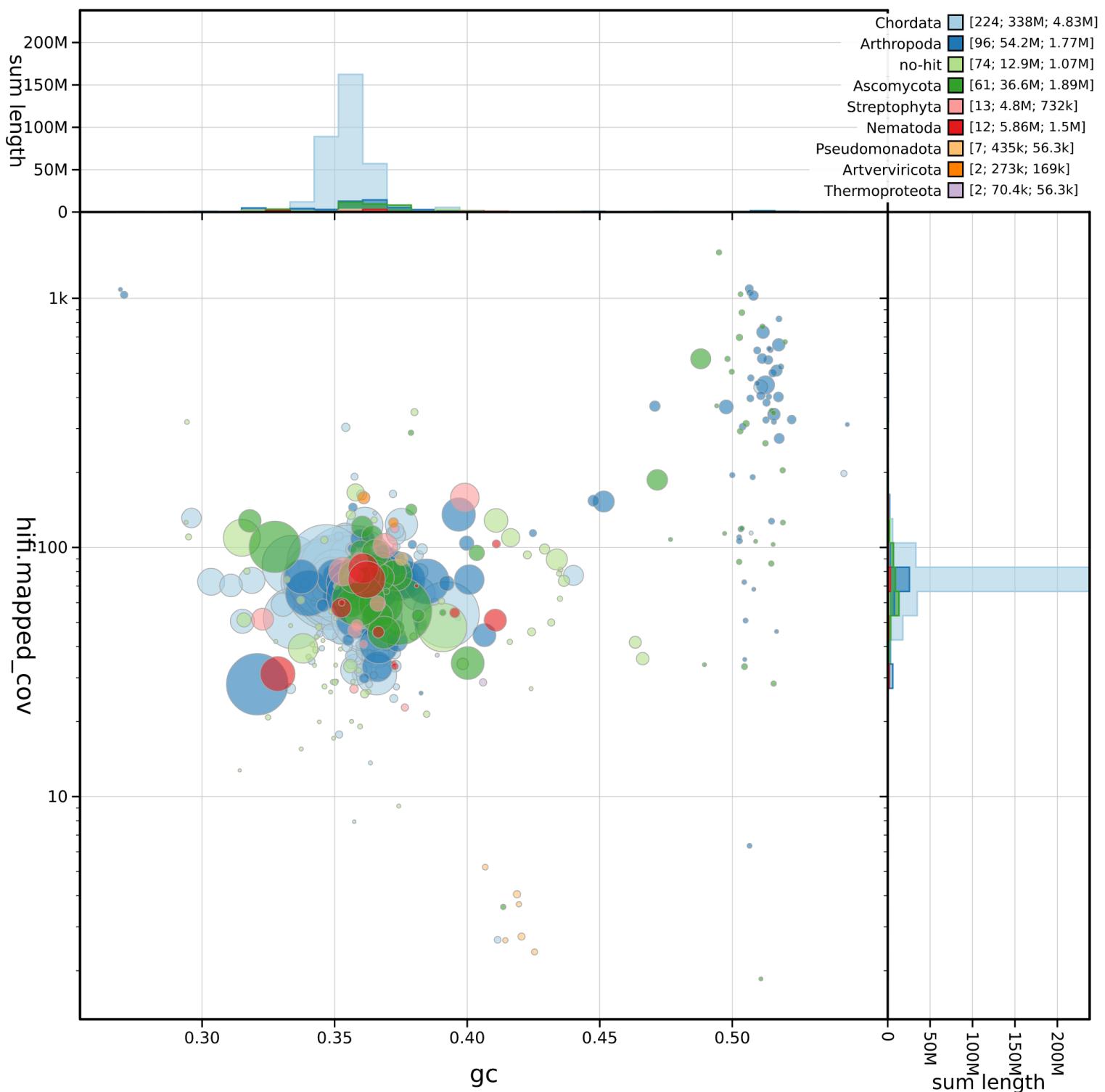


Distribution of k-mer counts coloured by their presence in reads/assemblies



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	HiFi
Coverage	50	

## Assembly pipeline

```
- hifiasm
  |_ ver: 0.24.0
  |_ key param: NA
- purge-dups
  |_ ver: 1.2.6
  |_ key param: NA
- fcs
  |_ ver: 0.5.4
  |_ key param: NA
```

## Curation pipeline

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Date and time: 2026-01-22 10:53:02 CET