

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	3139638
ToLID	qqBarKorc1
Species	Barusia korculana
Class	Arachnida
Order	Araneae

Genome Traits	Expected	Observed
Haploid size (bp)	589,543,170	681,386,728
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: 6.6.Q60

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 duplicated value is more than 5% for hap1
- . Not 90% of assembly in chromosomes for hap1

Curator notes

- . Interventions/Gb: NA
- . Contamination notes: "Contaminants were first removed with NCBI FCS and then with a diamond and Blobtoolkit identification. Only the scaffold that were confirmed as contaminant were removed"
- . Other observations: "This is a contig level assembly. The production of the HiC reads failed so there is no scaffolding for this species."

Quality metrics table

Metrics	Pre-curation hap1	Curated hap1
Total bp	681,386,728	681,386,728
GC %	32.68	32.68
Gaps/Gbp	0	0
Total gap bp	0	0
Scaffolds	1,257	1,257
Scaffold N50	1,015,877	1,015,877
Scaffold L50	192	192
Scaffold L90	683	683
Contigs	1,257	1,257
Contig N50	1,015,877	1,015,877
Contig L50	192	192
Contig L90	683	683
QV	60.2279	60.2279
Kmer compl.	85.1283	85.1283
BUSCO sing.	90.8%	90.8%
BUSCO dupl.	5.5%	5.5%
BUSCO frag.	1.6%	1.6%
BUSCO miss.	2.1%	2.1%

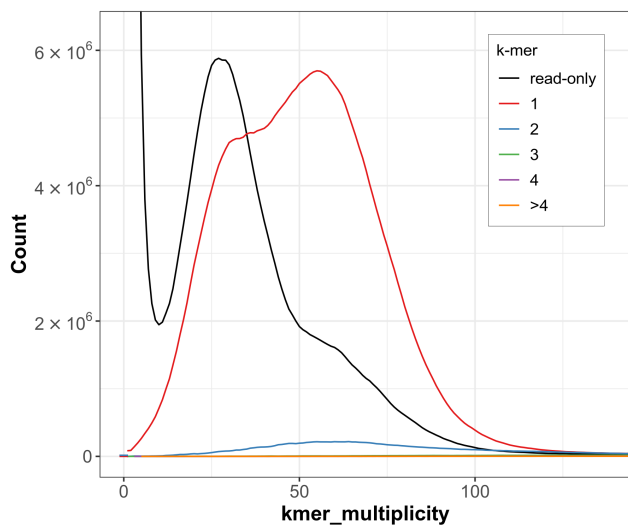
BUSCO: 5.8.0 (euk_genome_met, metaeuk) / Lineage: arachnida_odb10 (genomes:10, BUSCOs:2934)

HiC contact map of curated assembly

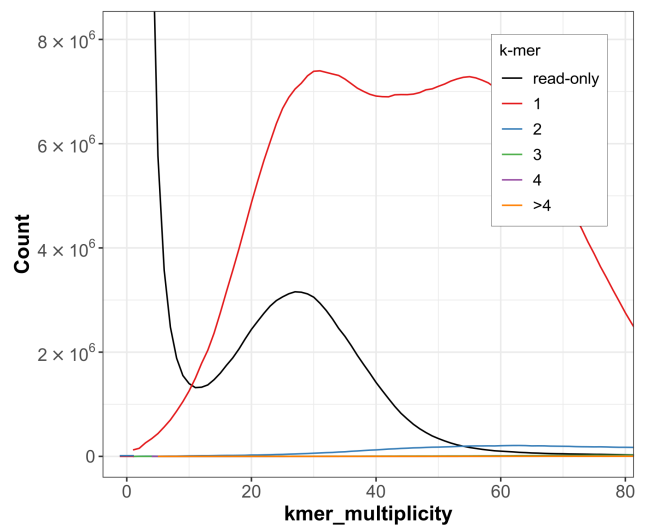
hap1 HiC PNG is missing!

hap1 File link is missing!

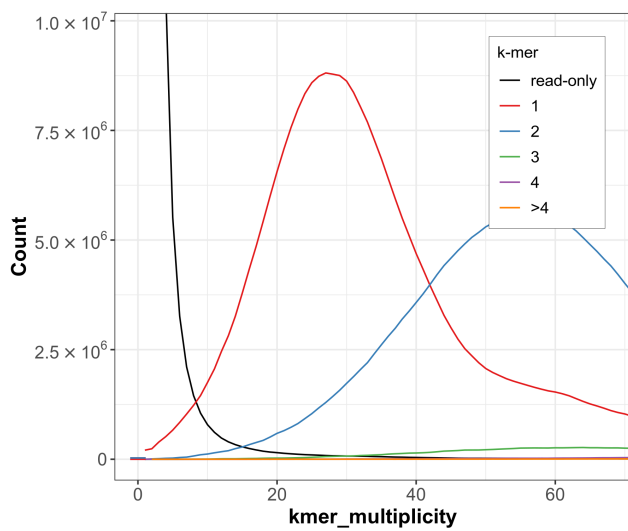
K-mer spectra of curated assembly



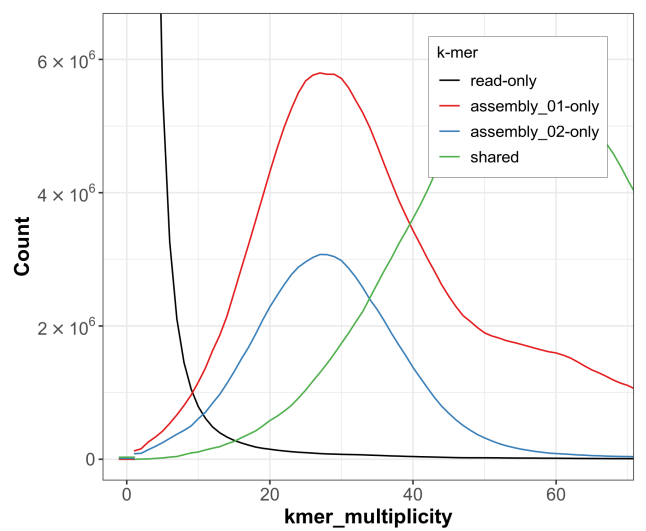
Distribution of k-mer counts per copy numbers found in **assembly_02** (hapl.)



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

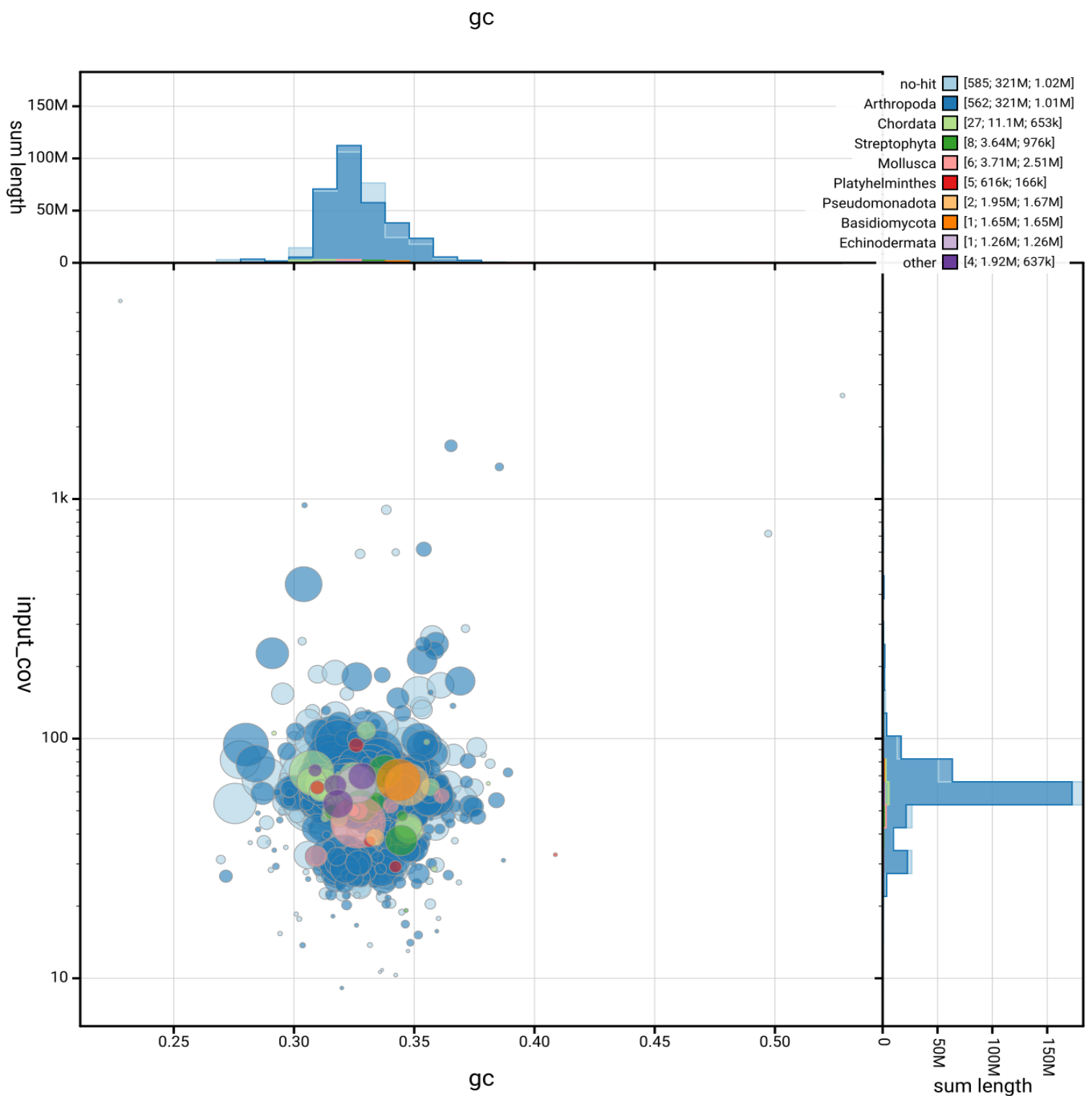


Distribution of k-mer counts per copy numbers found in **asm** (dipl.)



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	17.55x

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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