ERGA Assembly Report
v24.10.15

Tags: ERGA-BGE

TxID	3139652
ToLID	**qqHisBide1**
Species	Histopona bidens
Class	Arachnida
Order	Araneae

Genome Traits	Expected	Observed
Haploid size (bp)	3,417,256,072	3,137,991,485
Haploid Number	22 (source: ancestor)	0
Ploidy	2 (source: ancestor)	2
Sample Sex	NA	NA

EBP metrics summary and curation notes

Obtained EBP quality metric for hap1: 5.6.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
. More than 1000 gaps/Gbp for hap1
. Not 90% of assembly in chromosomes for hap1

Curator notes

. Interventions/Gb: NA
. Contamination notes: "Decontamination was performed with NCBI FCS that removed 40 scaffold of protobacteria. Diamond and blobtools identified a lot of contaminants, and were not removed due to uncertainty."
. Other observations: "This is a contig level assembly. Despite scaffolding the N50 was to low to perform curation"

Quality metrics table

| Metrics	Pre-curation hap1	Curated hap1
Total bp	3,137,991,485	3,137,991,485
GC %	32.84	32.84
Gaps/Gbp	7,632.27	7,632.27
Total gap bp	2,395,000	2,395,000
Scaffolds	5,223	5,223
Scaffold N50	2,332,351	2,332,351
Scaffold L50	371	371
Scaffold L90	1,899	1,899
Contigs	29,173	29,173
Contig N50	117,545	117,545
Contig L50	8,411	8,411
Contig L90	23,478	23,478
QV	50.5869	50.5869
Kmer compl.	77.848	77.848
BUSCO sing.	85.6%	85.6%
BUSCO dupl.	3.5%	3.5%
BUSCO frag.	2.4%	2.4%
BUSCO miss.	8.5%	8.5%

BUSCO: 5.8.0 (euk_genome_min, miniprot) / Lineage: arachnida_odb10 (genomes:10, BUSCOs:2934)
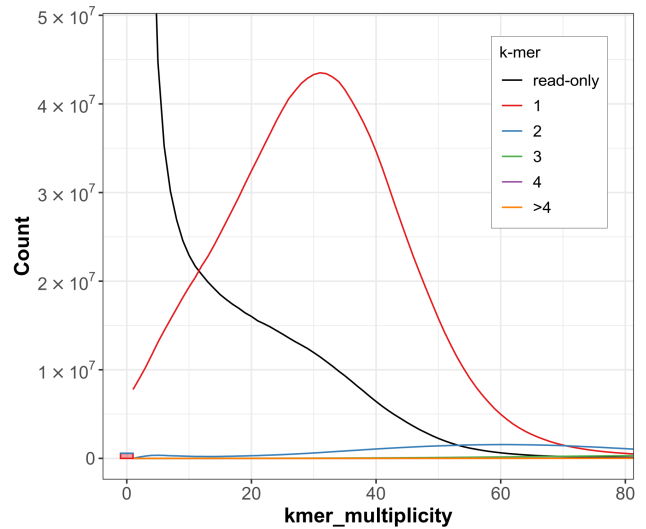
HiC contact map of curated assembly

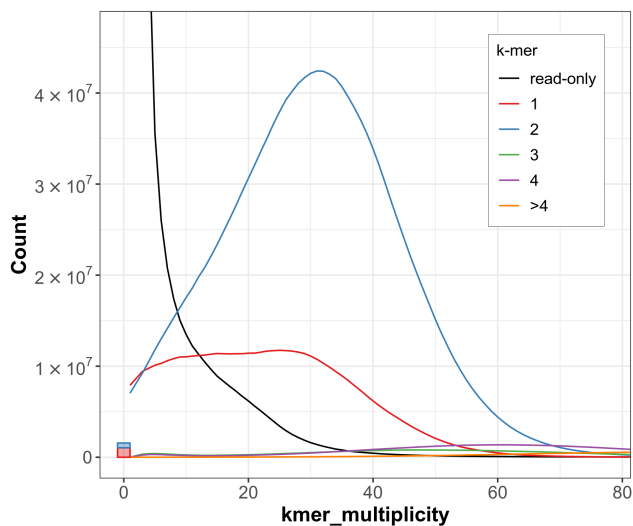**hap1** HiC PNG is missing!

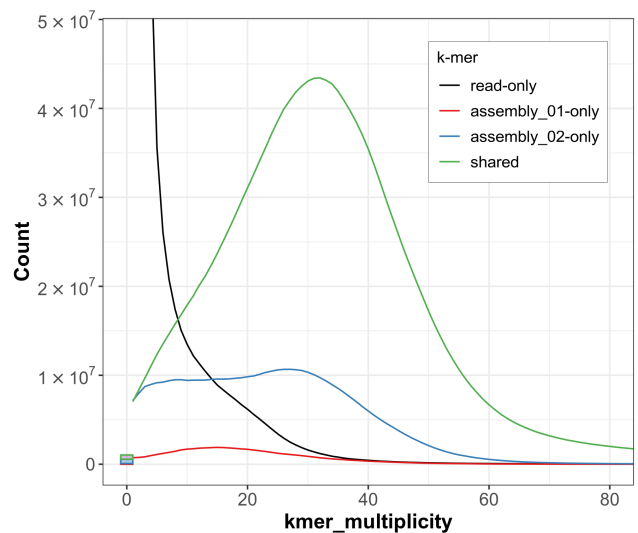**hap1** File link is missing!

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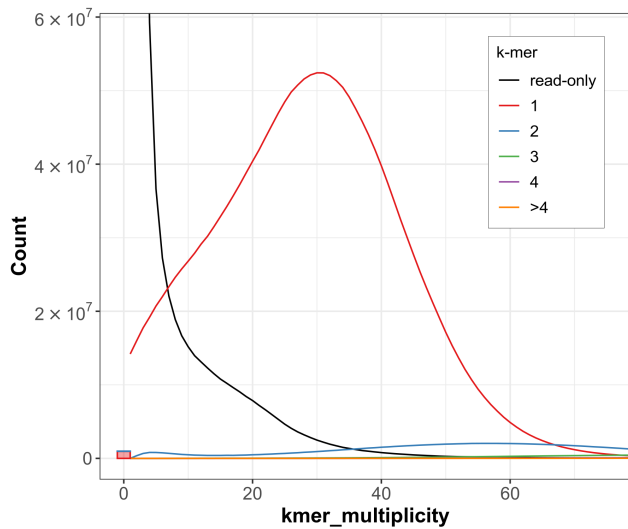
Distribution of k-mer counts per copy numbers found in **assembly_02** (hapl.)

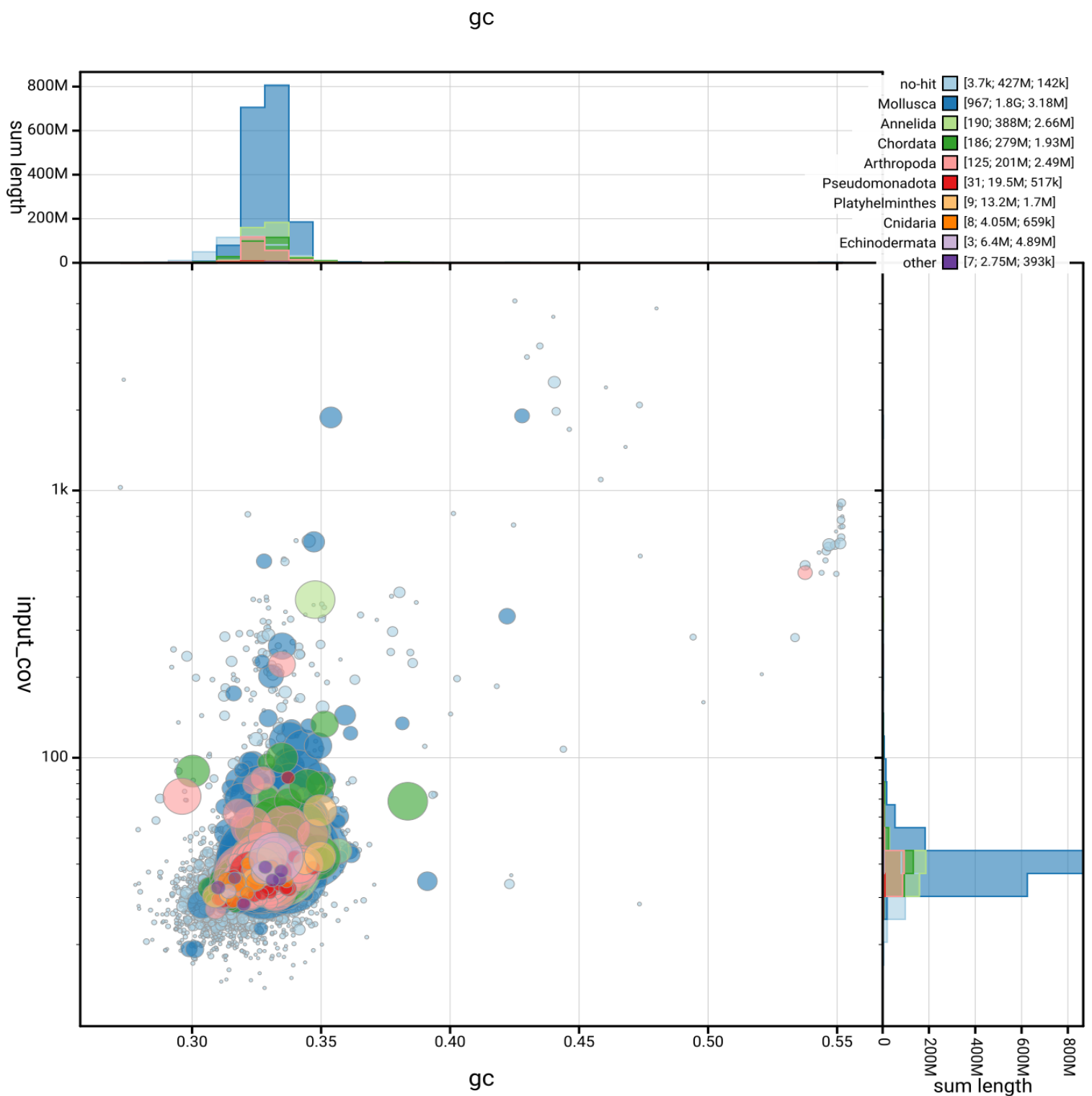Distribution of k-mer counts per copy numbers found in **assembly_01** (hapl.)

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	HiC
Coverage	33.59x	46.64x

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
- **YaHS**
    |_ *ver:* Galaxy Version 1.2s.2+galaxy3
    |_ *key param:* VGP Galaxy workflow VGP8 v 3.3

Curation pipeline

Invalid pipeline data format

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