ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	3237728
ToLID	**icRadStyx9**
Species	Radziella styx
Class	Insecta
Order	Coleoptera

Genome Traits	Expected	Observed
Haploid size (bp)	343,371,750	340,306,295
Haploid Number	11 (source: ancestor)	12
Ploidy	2 (source: ancestor)	2
Sample Sex	NA	XX

EBP metrics summary and curation notes

Obtained EBP quality metric for hap1: 5.7.Q61

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

. Observed Haploid Number is different from Expected
. Observed sex is different from Sample sex

. Kmer completeness value is less than 90 for hap1
. Assembly length loss > 3% for hap1
. More than 1000 gaps/Gbp for hap1
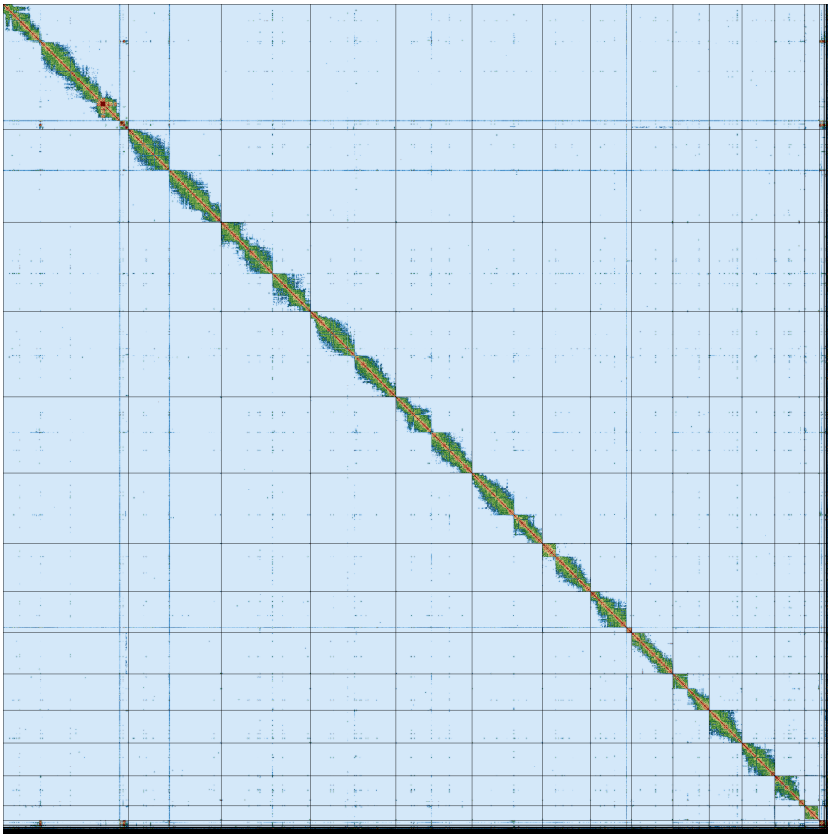. Not 90% of assembly in chromosomes for hap1

Curator notes

. Interventions/Gb: 66
. Contamination notes: "Contaminants were found and removed with the pipeline NCBI
FCS GX v Galaxy Version 0.5.5+galaxy1. Scaffolds that are flagged as contaminants by
BlobToolKit were confirmed with FCS output table and with contact in the map as
non-contaminants."
. Other observations: "Only one X chromosomes was found with alignement with close
relatives Leptodirus hochenwartii"

Quality metrics table

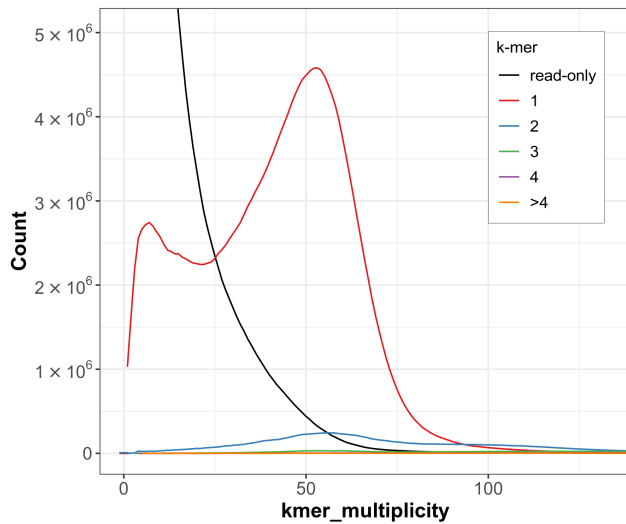| Metrics	Pre-curation hap1	Curated hap1
Total bp	357,343,292	340,306,295
GC %	31.22	31.11
Gaps/Gbp	1,603.5	1,939.43
Total gap bp	114,600	132,000
Scaffolds	182	72
Scaffold N50	16,428,764	28,715,623
Scaffold L50	9	5
Scaffold L90	21	13
Contigs	755	732
Contig N50	887,040	844,232
Contig L50	126	125
Contig L90	398	398
QV	61.2587	61.6149
Kmer compl.	88.5495	88.0818
BUSCO sing.	94.4%	96.6%
BUSCO dupl.	4.0%	1.7%
BUSCO frag.	0.7%	0.7%
BUSCO miss.	0.9%	1.1%

BUSCO: 5.8.0 (euk_genome_min, miniprot) / Lineage: insecta_odb10 (genomes:75, BUSCOs:1367)
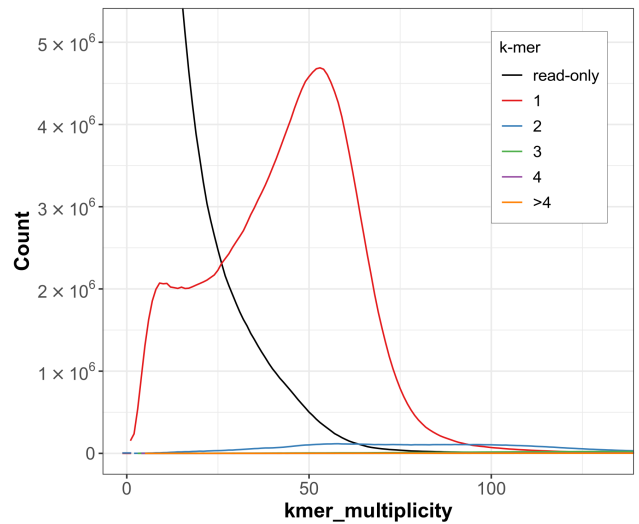
HiC contact map of curated assembly
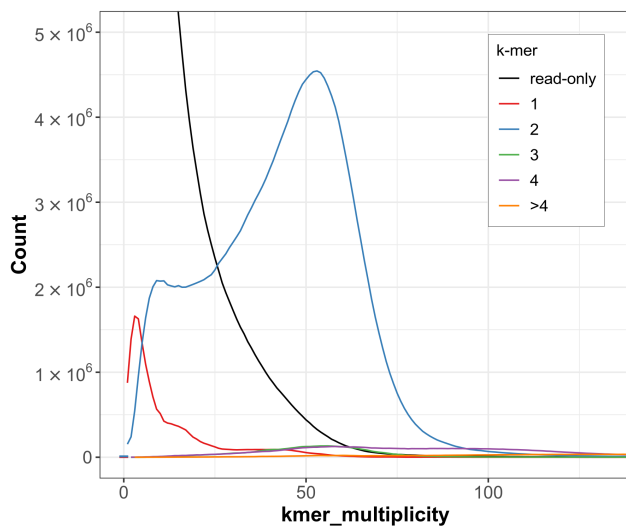

hap1 [LINK]

K-mer spectra of curated assembly

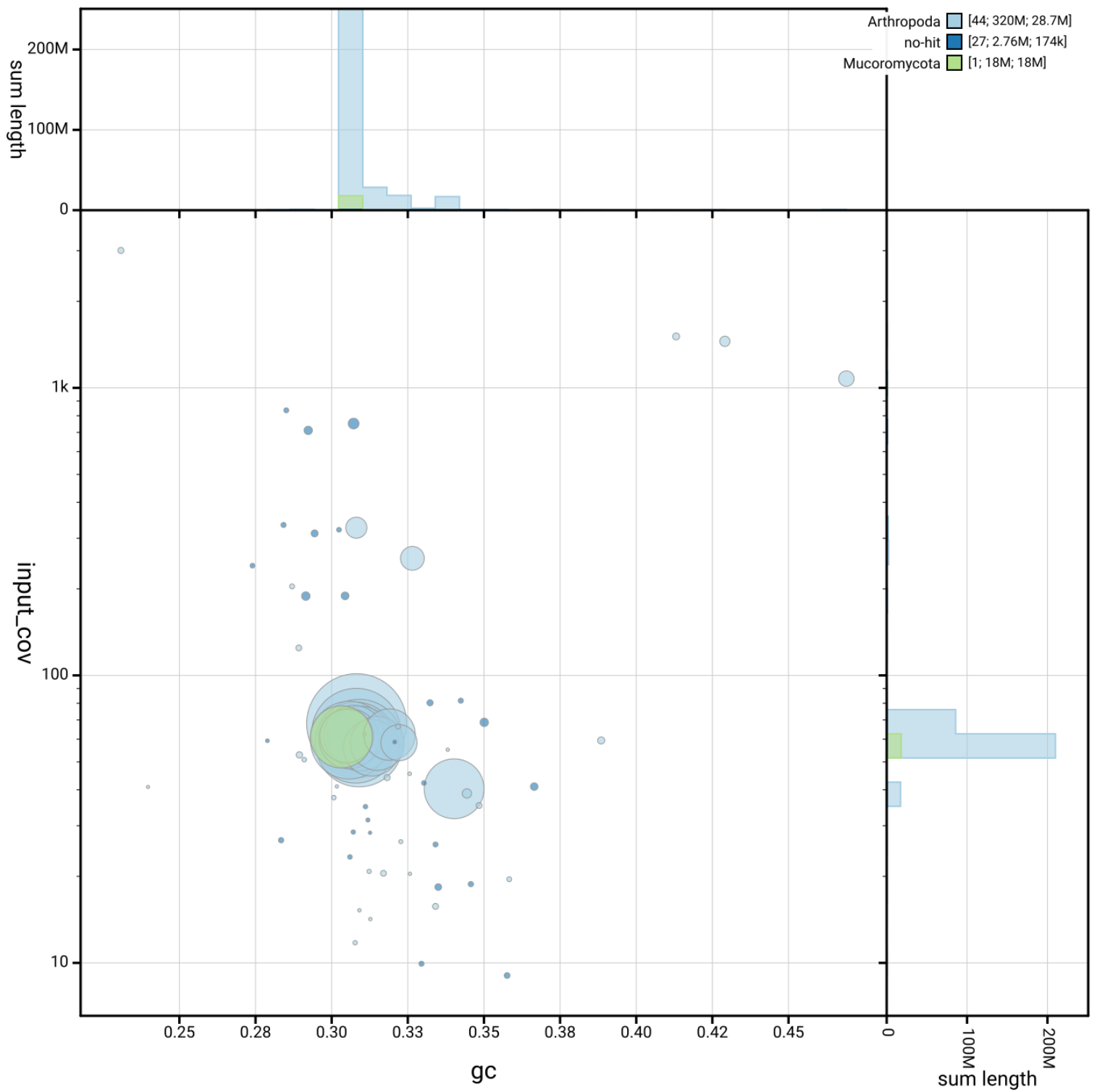Distribution of k-mer counts per copy numbers found in **assembly_02** (hapl.)

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	25.79x	40.10x

Assembly pipeline

- **Hifiasm**
    - |_ *ver:* Galaxy Version 0.24.0+galaxy0
    - |_ *key param:* VGP Galaxy workflow VGP3 v 0.2.8
- **purge_dups**
    - |_ *ver:* Galaxy Version 1.2.6+galaxy0
    - |_ *key param:* VGP Galaxy workflow VGP6 v 0.5
- **YaHS**
    - |_ *ver:* Galaxy Version 1.2a.2+galaxy2
    - |_ *key param:* VGP Galaxy workflow VGP8 v 1.4

Curation pipeline

- **PretextMap**
    - |_ *ver:* Galaxy Version 0.1.9+galaxy1
    - |_ *key param:* VGP workflow VGP PretextMap generation v2
- **HiGlass**
    - |_ *ver:* 1.0
    - |_ *key param:* NA
- **PretextView**
    - |_ *ver:* 1.0.0
    - |_ *key param:* NA

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