ERGA Assembly Report
v24.10.15

Tags: ERGA-BGE

TxID	3139673
ToLID	**qqTroRobe1**
Species	Troglohyphantes roberti
Class	Arachnida
Order	Araneae

Genome Traits	Expected	Observed
Haploid size (bp)	846,580,222	804,890,129
Haploid Number	12 (source: ancestor)	0
Ploidy	2 (source: ancestor)	2
Sample Sex	NA	NA

EBP metrics summary and curation notes

Obtained EBP quality metric for hap1: 5.5.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
. 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. Despite the scaffolding the N50 was to low to procede with the curation."

Quality metrics table

| Metrics	Pre-curation hap1	Curated hap1
Total bp	804,890,129	804,890,129
GC %	31.8	31.8
Gaps/Gbp	0	0
Total gap bp	0	0
Scaffolds	11,418	11,418
Scaffold N50	102,548	102,548
Scaffold L50	2,356	2,356
Scaffold L90	7,720	7,720
Contigs	11,418	11,418
Contig N50	102,548	102,548
Contig L50	2,356	2,356
Contig L90	7,720	7,720
QV	50.4853	50.4853
Kmer compl.	70.4334	70.4334
BUSCO sing.	60.86%	60.86%
BUSCO dupl.	1.90%	1.90%
BUSCO frag.	4.75%	4.75%
BUSCO miss.	32.48%	32.48%

BUSCO: 5.8.0 (euk_genome_met, metaeuk) / Lineage: insecta_odb10 (genomes:10, BUSCOs:2934)
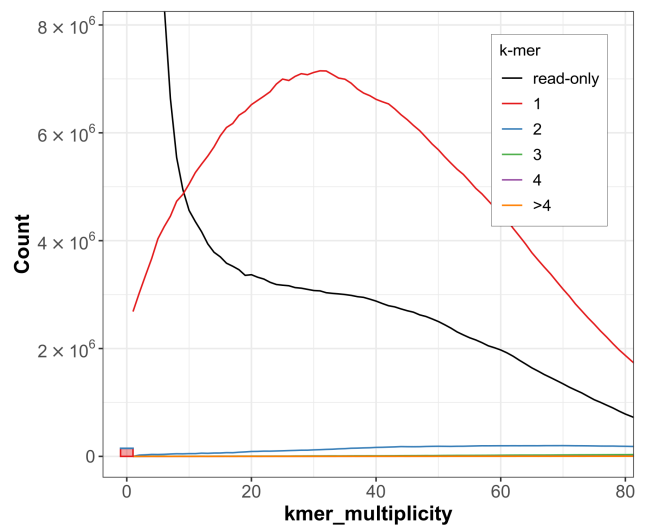
HiC contact map of curated assembly

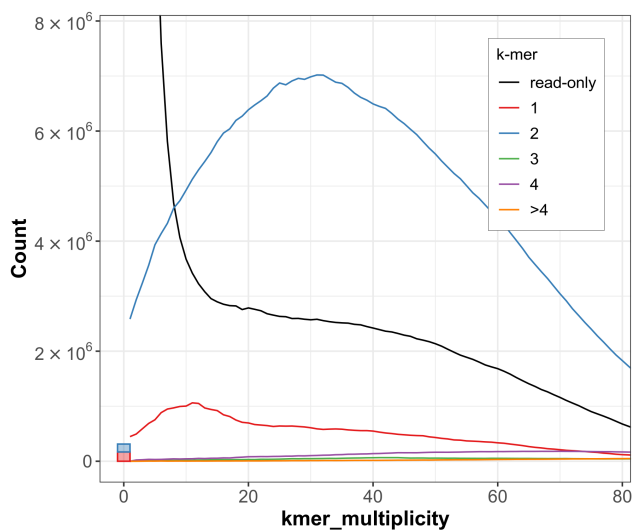**hap1** HiC PNG is missing!

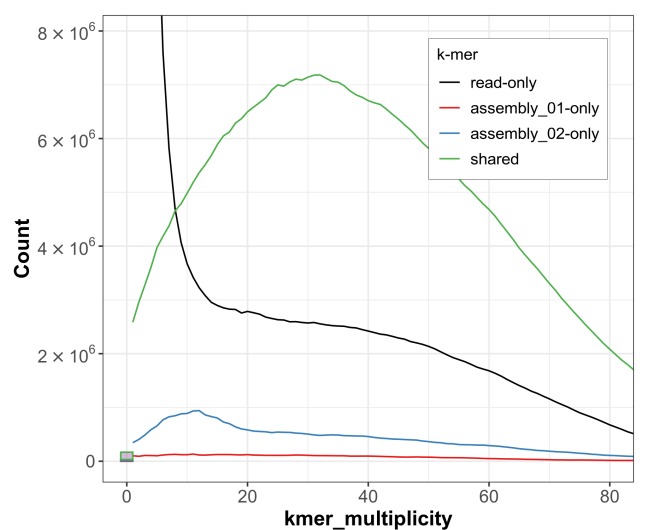**hap1** File link is missing!

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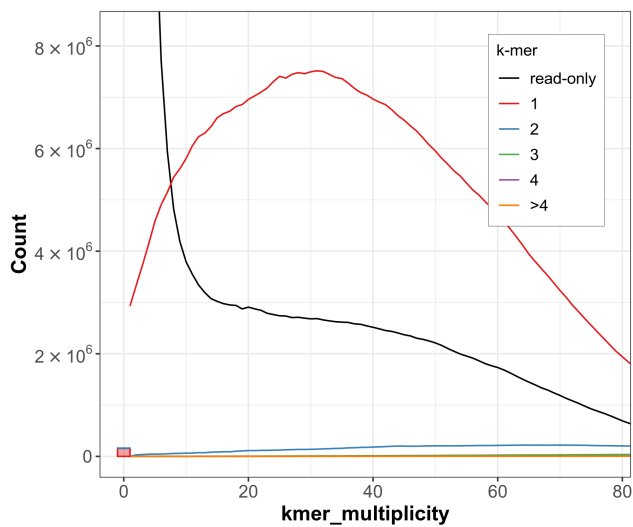
Distribution of k-mer counts per copy
numbers found in **assembly_02** (hapl.)

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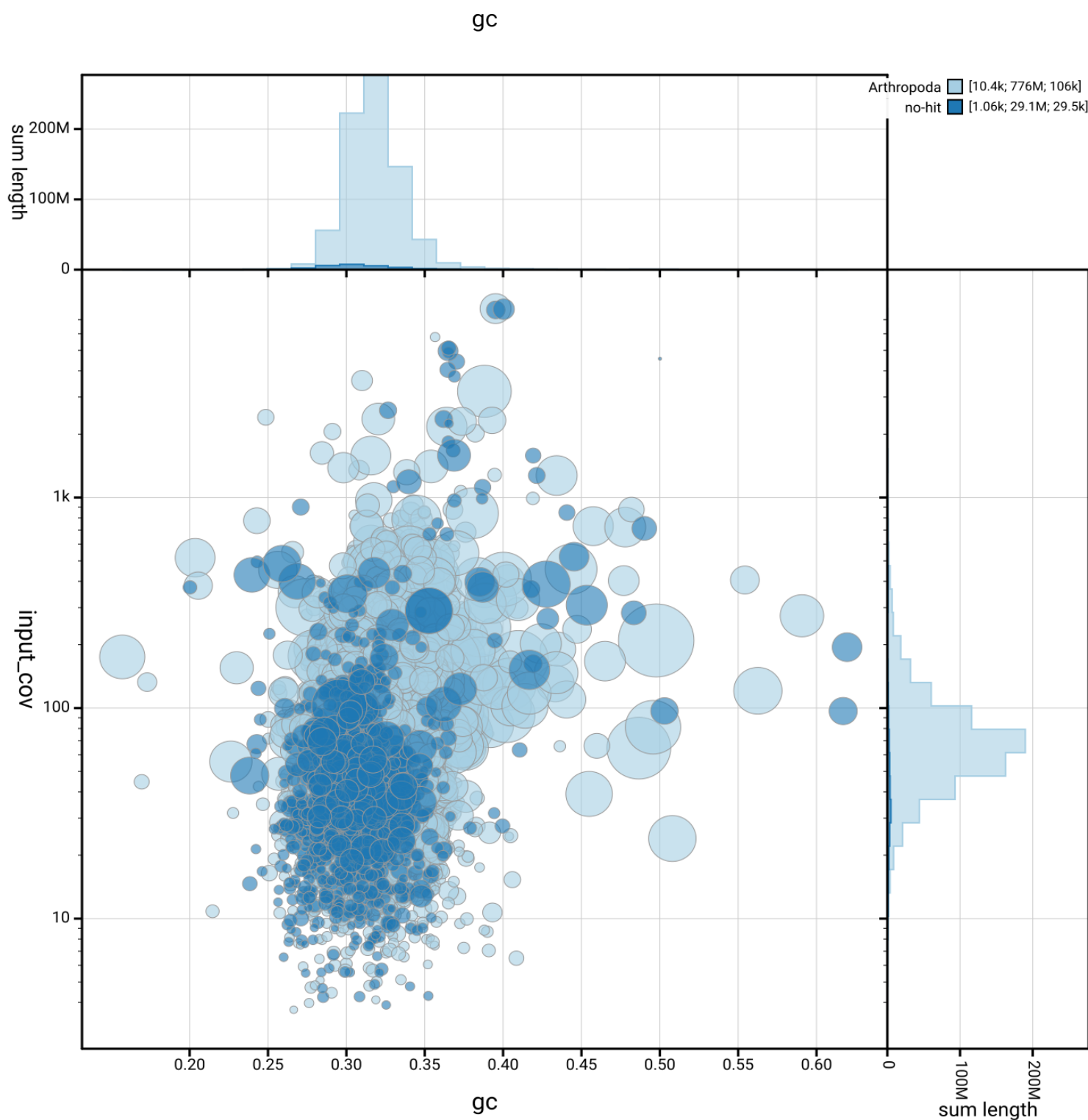numbers found in **assembly_01** (hapl.)

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	33.67x	56.28x

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 1.2a.2+galaxy3
    - |_ *key param:* VGP Galaxy workflow v 3.3

Curation pipeline

Invalid pipeline data format

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