ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	2689250
ToLID	**qqTroLibu4**
Species	Troglohyphantes liburnicus
Class	Arachnida
Order	Araneae

Genome Traits	Expected	Observed
Haploid size (bp)	1,160,633,276	1,358,755,034
Haploid Number	12 (source: ancestor)	0
Ploidy	2 (source: ancestor)	2
Sample Sex	unknown	unknown

EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 6.6.Q57

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

. Observed Haploid Number is different from Expected

. Not 90% of assembly in chromosomes for pri

Curator notes

. Interventions/Gb: 0
. Contamination notes: "60 sequences removed identrified as proteobacteria"
. Other observations: "Hi-C library failed, so a contig-level assembly was submitted"

Quality metrics table

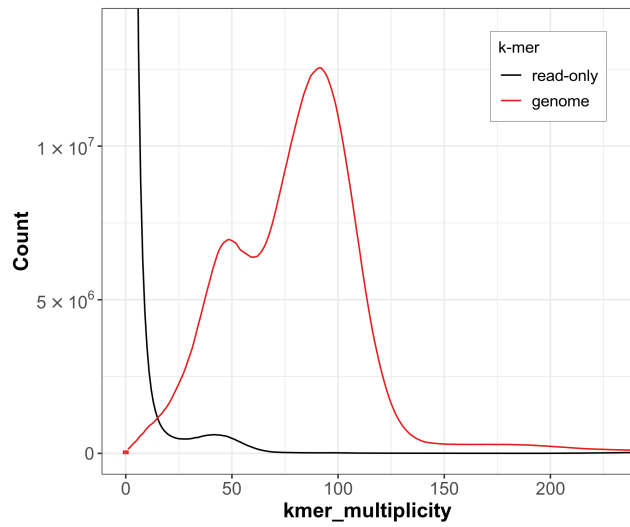| Metrics	Pre-curation pri	Curated pri
Total bp	1,358,755,034	1,358,755,034
GC %	32.09	32.09
Gaps/Gbp	0	0
Total gap bp	0	0
Scaffolds	1,951	1,951
Scaffold N50	2,770,517	2,770,517
Scaffold L50	148	148
Scaffold L90	539	539
Contigs	1,951	1,951
Contig N50	2,770,517	2,770,517
Contig L50	148	148
Contig L90	539	539
QV	57.721	57.721
Kmer compl.	96.8176	96.8176
BUSCO sing.	96.3%	96.3%
BUSCO dupl.	2.6%	2.6%
BUSCO frag.	0.4%	0.4%
BUSCO miss.	0.8%	0.8%

BUSCO: 6.0.0 (euk_genome_min, miniprot) / Lineage: araneae_odb12 (genomes:11, BUSCOs:3974)
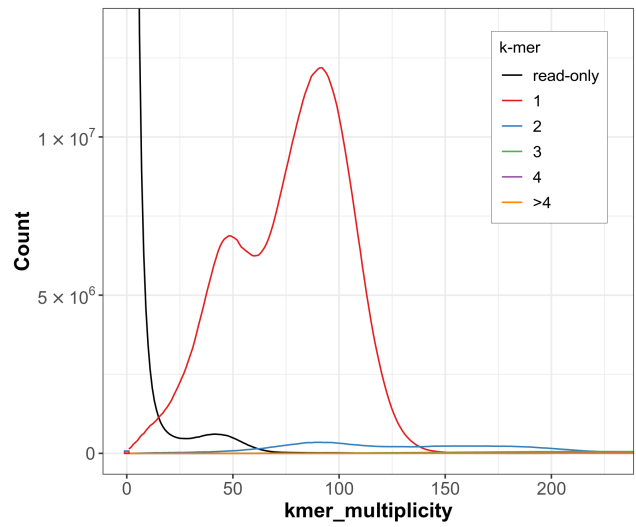
HiC contact map of curated assembly

pri HiC PNG is missing!

pri File link is missing!
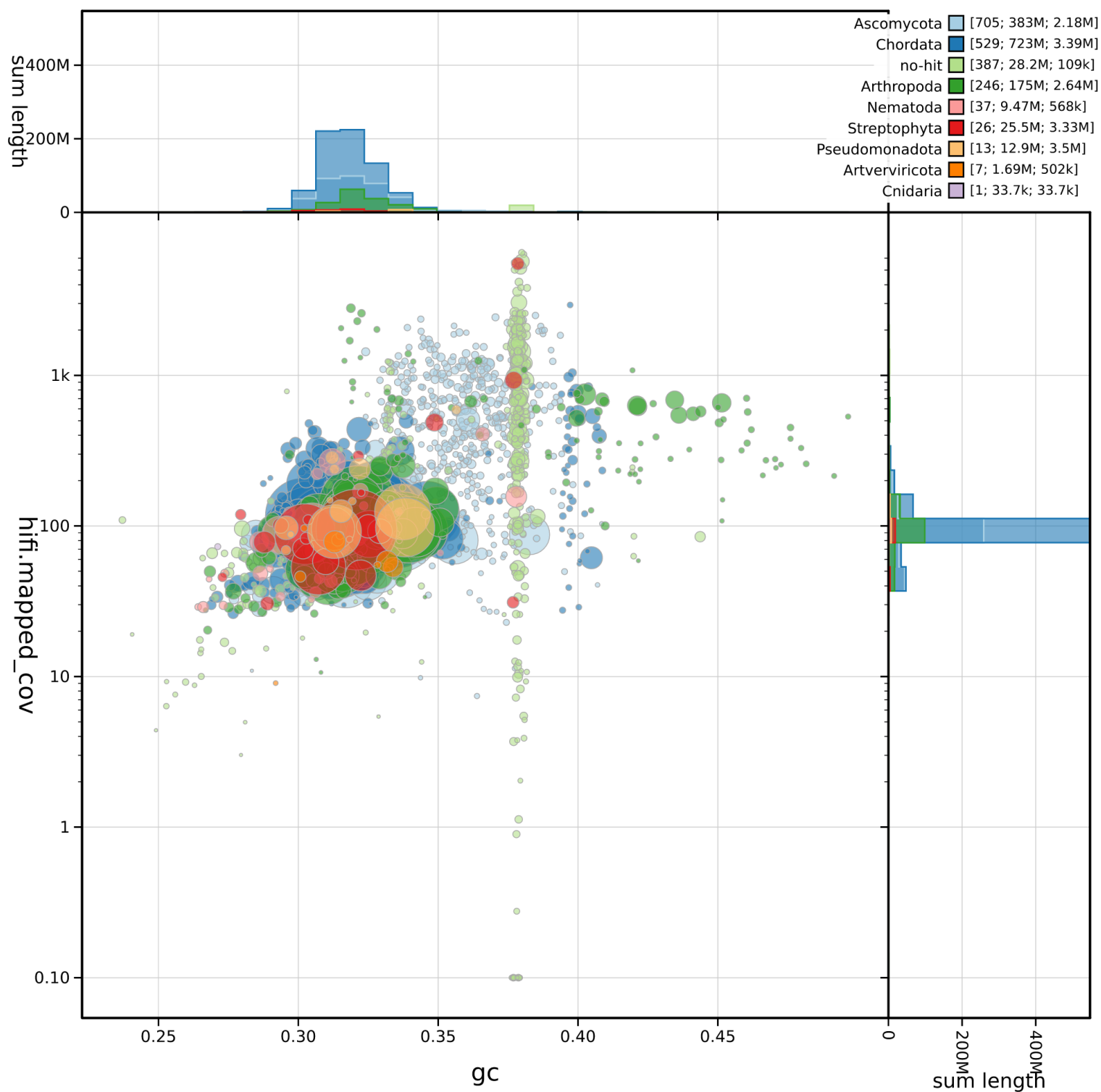
K-mer spectra of curated assembly

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

Ascomycota		[705; 383M; 2.18M]
Chordata		[529; 723M; 3.39M]
no-hit		[387; 28.2M; 109k]
Arthropoda		[246; 175M; 2.64M]
Nematoda		[37; 9.47M; 568k]
Streptophyta		[26; 25.5M; 3.33M]
Pseudomonadota		[13; 12.9M; 3.5M]
Artverviricota		[7; 1.69M; 502k]
Cnidaria		[1; 33.7k; 33.7k]

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	92

Assembly pipeline

- **HiFiasm**
  |_ *ver:* 0.25.0
  |_ *key param:* NA
- **purge-dups**
  |_ *ver:* 1.2.6
  |_ *key param:* NA
- **fcs-gx**
  |_ *ver:* 0.5.4
  |_ *key param:* NA

Curation pipeline

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