

ERGA Assembly Report

v24.04.03_beta

Tags: ERGA-BGE

TxID	171369
ToLID	qcEupGros1
Species	<i>Eupolybothrus grossipes</i>
Class	Chilopoda
Order	Lithobiomorpha

Genome Traits	Expected	Observed
Haploid size (bp)	6,577,503,001	6,577,898,979
Haploid Number	20 (source: ancestor)	14
Ploidy	2 (source: ancestor)	2
Sample Sex	F	F

EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 6.8.Q65

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 pri

Curator notes

- . Interventions/Gb: 168
- . Contamination notes: "Contamination report for assembly labelled hap1; Total length of scaffolds removed: 665,591 (0.0 %); Scaffolds removed: 34 (1.6 %); Largest scaffold removed: (57,401); FCS-GX contaminant species (number of scaffolds; total length of scaffolds):: Rickettsia endosymbiont of Cimex lectularius, a-proteobacteria (2; 44,092); Rickettsia endosymbiont of Bradysia coprophila, a-proteobacteria (1; 57,401); Besnoitia besnoiti, alveolates (1; 9,369); Mitochondrion (30; 554,729); FCS-Adaptor (1; 38)"
- . Other observations: "Hifiasm assembly run in Hi-C phasing mode; The exact order and orientation of the contigs on chromosome 1 (813,203 - 818,222 Kbp) are unknown. The exact order and orientation of the contigs on chromosome 2 (22,884 - 28,304 & 89,329 - 103,1c81 Kbp) are unknown. The exact order and orientation of the contigs on chromosome 3 (548,024 - 553,243 & 665,056 - 669,473 Kbp) are unknown. The exact order and orientation of the contigs on chromosome 4 (359,929 - 371,974 & 389,840 - 400,880 & 663,049 - 668,667 Kbp) are unknown. The exact order and orientation of the contigs on chromosome 7 (275,015 - 280,435 Kbp) are unknown. The exact order and orientation of the contigs on chromosome 8 (50,988 - 55,806 Kbp) are unknown. The exact order and orientation of the contigs on chromosome 9 (271,804 - 275,216 Kbp) are unknown. The

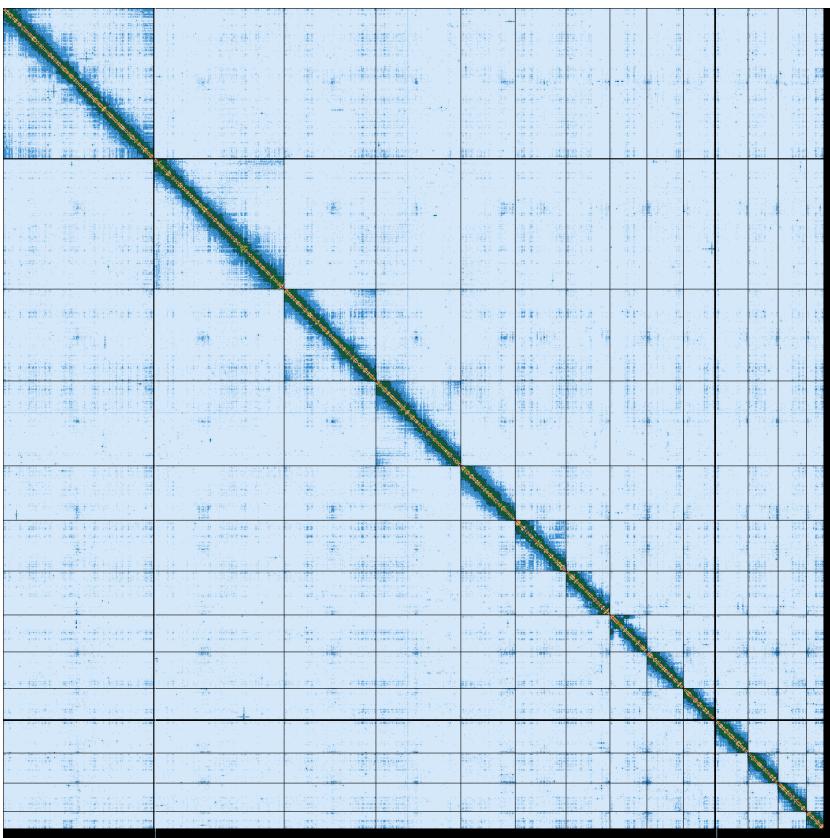
exact order and orientation of the contigs on chromosome 10 (64,638 - 75,679 Kbp) are unknown. The exact order and orientation of the contigs on chromosome 13 (176,451 - 181, 871 & g402,312 - 406,943 Kbp) are unknown"

Quality metrics table

Metrics	Pre-curation pri	Curated pri
Total bp	6,709,770,180	6,577,898,979
GC %	40.61	40.63
Gaps/Gbp	543.68	575.26
Total gap bp	364,800	419,138
Scaffolds	2,106	1,445
Scaffold N50	653,174,762	669,113,179
Scaffold L50	4	4
Scaffold L90	13	12
Contigs	5,754	5,229
Contig N50	3,308,181	3,235,202
Contig L50	604	609
Contig L90	2,143	2,108
QV	65.4	65.6
Kmer compl.	99.09	73.59
BUSCO sing.	96.8%	96.9%
BUSCO dupl.	1.6%	1.5%
BUSCO frag.	0.2%	0.4%
BUSCO miss.	1.4%	1.2%

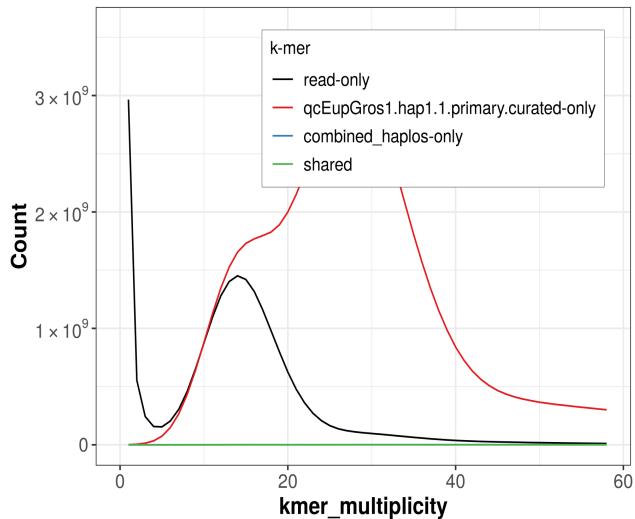
BUSCO 6.0.0 Lineage: arthropoda_odb10 (genomes:90, BUSCOs:1013)

HiC contact map of curated assembly

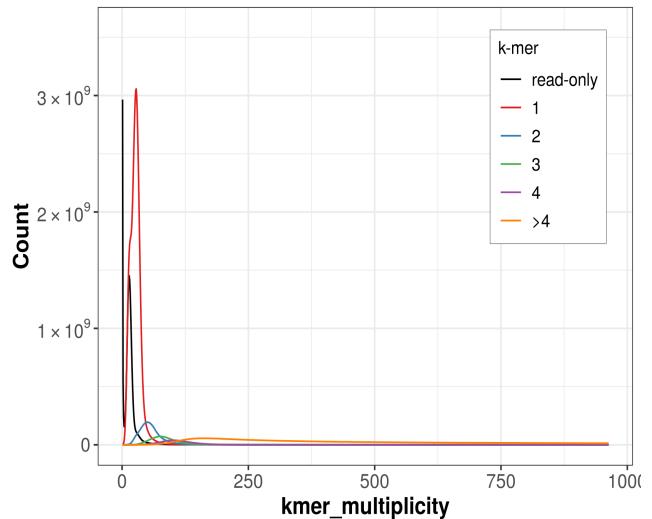


pri [LINK]

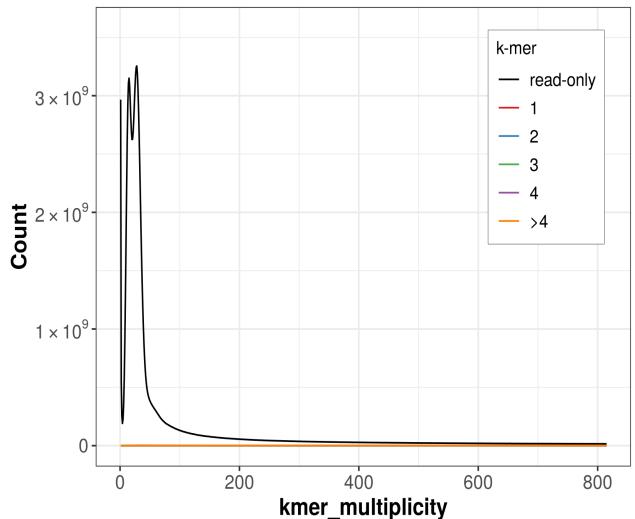
K-mer spectra of curated assembly



Distribution of k-mer counts coloured by their presence in reads/assemblies

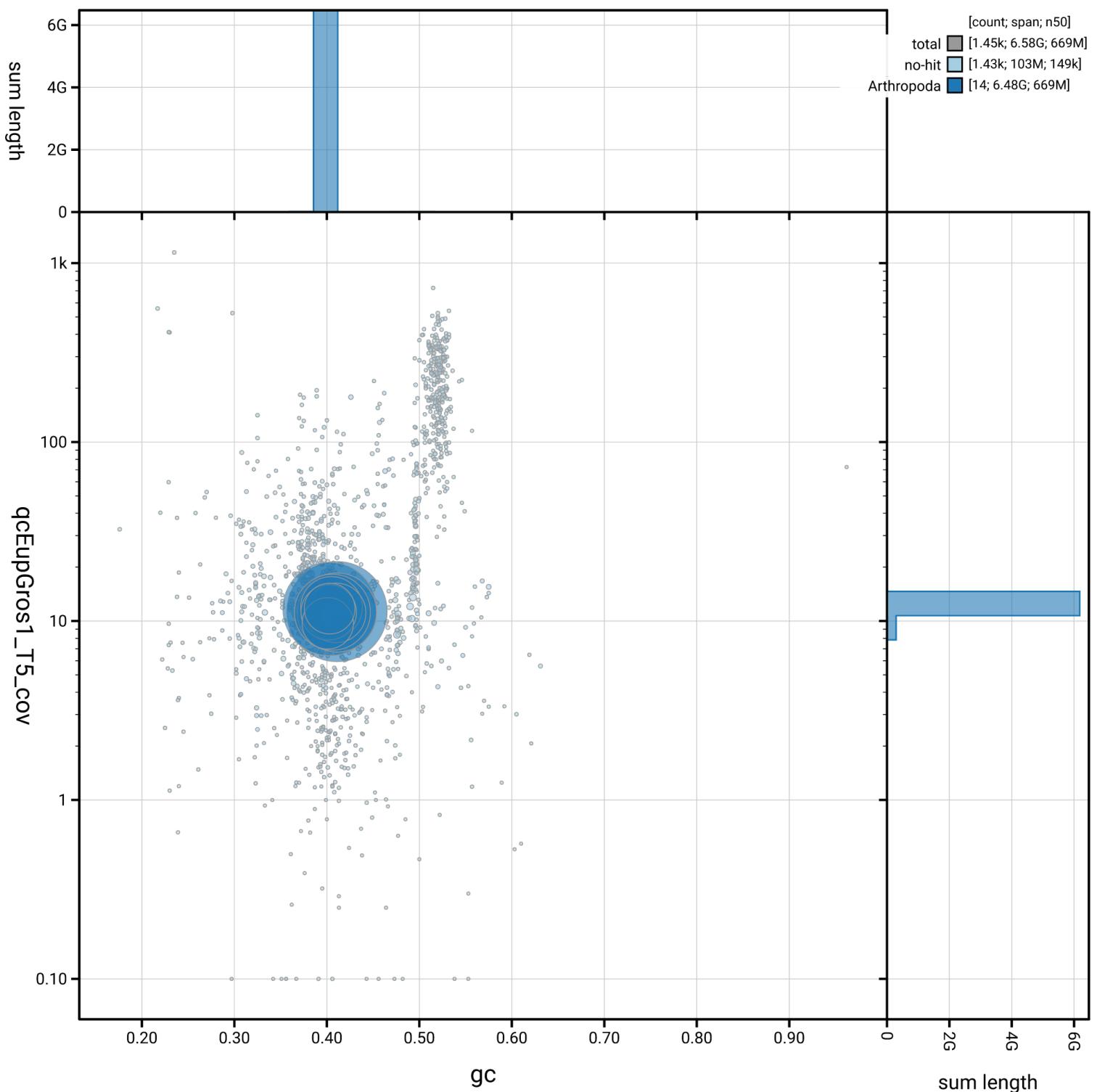


Distribution of k-mer counts per copy numbers found in asm



Distribution of k-mer counts per copy numbers found in asm

Post-curation contamination screening



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	PacBio HiFi	Arima v2
Coverage	27x	26x

Assembly pipeline

```
- hifiasm
  |_ ver: 0.25.0-r726
  |_ key param: --h1/--h2
- yahs
  |_ ver: 1.2.2
  |_ key param: NA
```

Curation pipeline

```
- hifiasm
  |_ ver: 0.25.0-r726
  |_ key param: --h1/--h2
- yahs
  |_ ver: 1.2.2
  |_ key param: NA
- TreeVal
  |_ ver: 1.2.1
  |_ key param: NA
```

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Date and time: 2026-01-29 13:50:10 CET