

ERGA Assembly Report

v24.04.03_beta

Tags: ERGA-BGE

TxID	3139671
ToLID	qqTroGiro3
Species	Troglohyphantes giromettai
Class	Arachnida
Order	Araneae

Genome Traits	Expected	Observed
Haploid size (bp)	943,185,905	922,056,680
Haploid Number	12 (source: ancestor)	13
Ploidy	2 (source: ancestor)	2
Sample Sex	F	F

EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 6.7.Q54

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

- . Observed Haploid Number is different from Expected

Curator notes

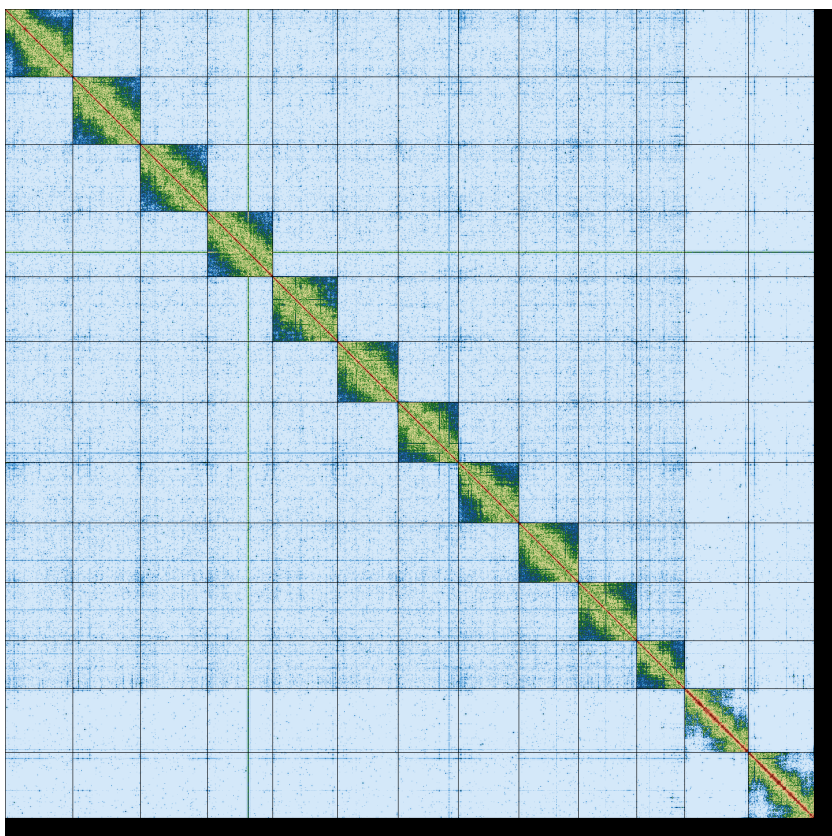
- . Interventions/Gb: 30
- . Contamination notes: "Contamination report for assembly labelled primary; Total length of scaffolds removed: 380,319 (0.0 %);Scaffolds removed: 14 (3.1 %);Largest scaffold removed: (64,442);FCS-GX contaminant species (number of scaffolds; total length of scaffolds):Pseudomonas spelaei, g-proteobacteria (11; 296,010);Pseudomonas sp. UBA7456, g-proteobacteria (1; 36,975);Pseudomonas tremae, g-proteobacteria (1; 32,468);Mitochondrion (1; 14,866)"
- . Other observations: "Hi-C was from a second individual (qqTroGiro14); X1 and X2 chromosomes were assigned based on syteny with GCA_963978545.1"

Quality metrics table

Metrics	Pre-curation pri	Curated pri
Total bp	922,631,568	922,056,680
GC %	31.63	31.62
Gaps/Gbp	275.3	280.89
Total gap bp	25,400	27,300
Scaffolds	449	436
Scaffold N50	71,148,236	70,533,125
Scaffold L50	7	7
Scaffold L90	12	12
Contigs	703	695
Contig N50	5,272,703	5,272,703
Contig L50	49	49
Contig L90	170	170
QV	54.1	54.1
Kmer compl.	99.62	99.63
BUSCO sing.	94.7%	94.7%
BUSCO dupl.	4.0%	4.0%
BUSCO frag.	0.3%	0.3%
BUSCO miss.	1.0%	1.0%

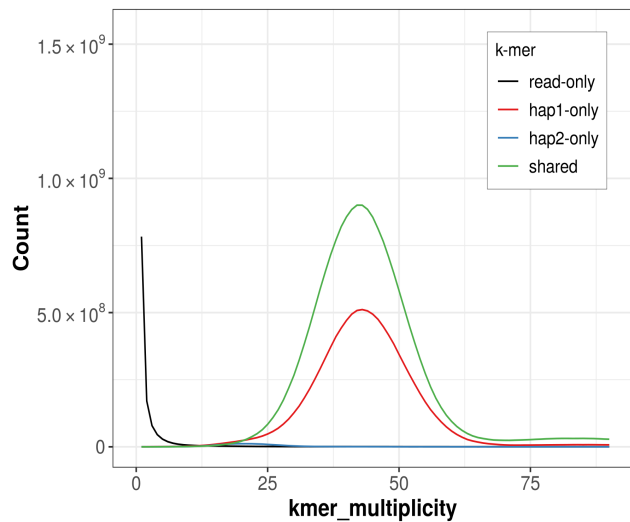
BUSCO 6.0.0 Lineage: arthropoda_odb10 (genomes:90, BUSCOs:1013)

HiC contact map of curated assembly

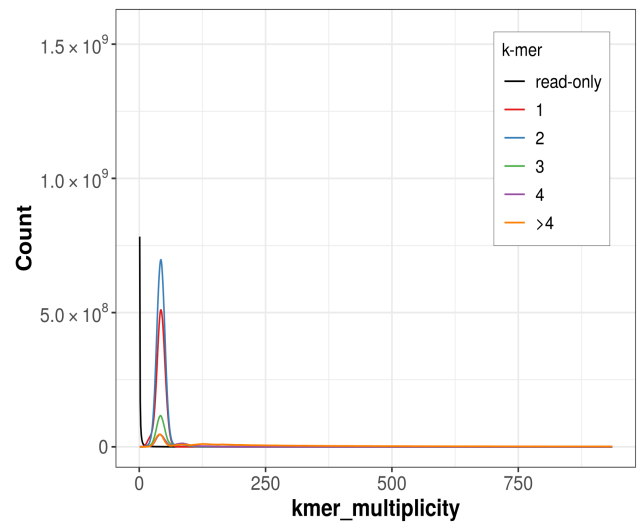


pri [\[LINK\]](#)

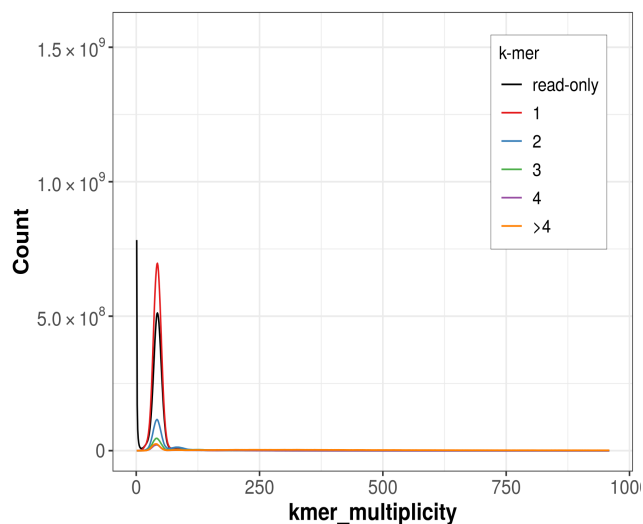
K-mer spectra of curated assembly



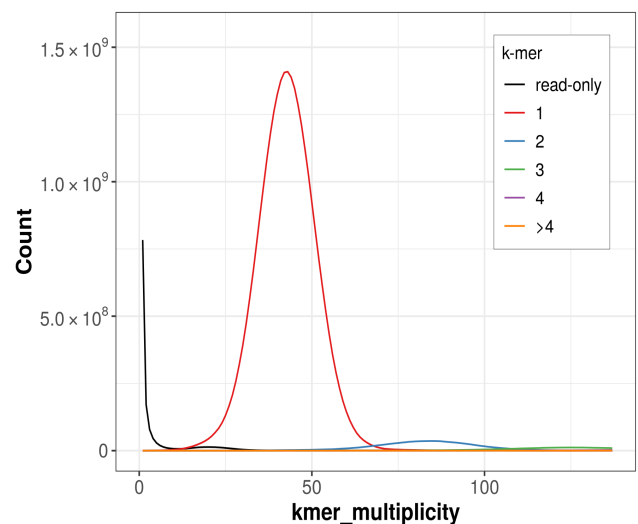
Distribution of k-mer counts coloured by their presence in reads/assemblies



Distribution of k-mer counts per copy numbers found in asm (dipl.)

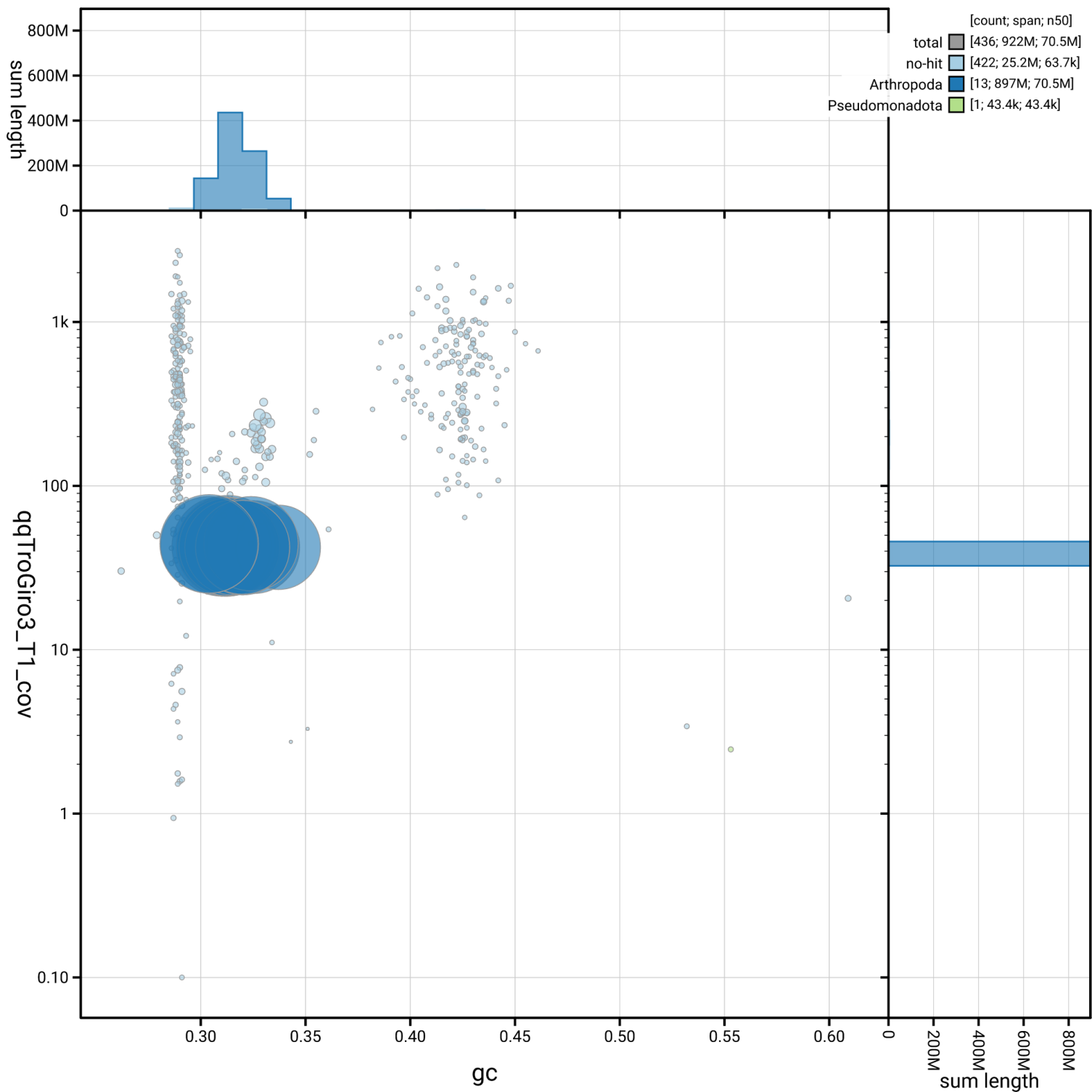


Distribution of k-mer counts per copy numbers found in **hap2** (hapl.)



Distribution of k-mer counts per copy numbers found in **hap1** (hapl.)

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	42x	297x

Assembly pipeline

- **hifiasm**
 - |_ *ver*: 0.19.8-r603
 - |_ *key param*: --primary
- **yahs**
 - |_ *ver*: 1.2.2
 - |_ *key param*: NA

Curation pipeline

- **hifiasm**
 - |_ *ver*: 0.19.8-r603
 - |_ *key param*: --primary
- **yahs**
 - |_ *ver*: 1.2.2
 - |_ *key param*: NA
- **TreeVal**
 - |_ *ver*: 1.2.1
 - |_ *key param*: NA

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Date and time: 2025-08-18 16:49:14 CEST