

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

| | |
|---------|---------------------------------|
| TxID | 1872043 |
| ToLID | qqFroFrut6 |
| Species | <i>Frontinellina frutetorum</i> |
| Class | Arachnida |
| Order | Araneae |

| Genome Traits | Expected | Observed |
|-------------------|-----------------------|---------------|
| Haploid size (bp) | 1,245,553,457 | 1,277,728,908 |
| Haploid Number | 12 (source: ancestor) | 14 |
| Ploidy | 2 (source: ancestor) | 2 |
| Sample Sex | Unknown | Unknown |

EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 6.7.Q59

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 collapsed
- More than 1000 gaps/Gbp for collapsed

Curator notes

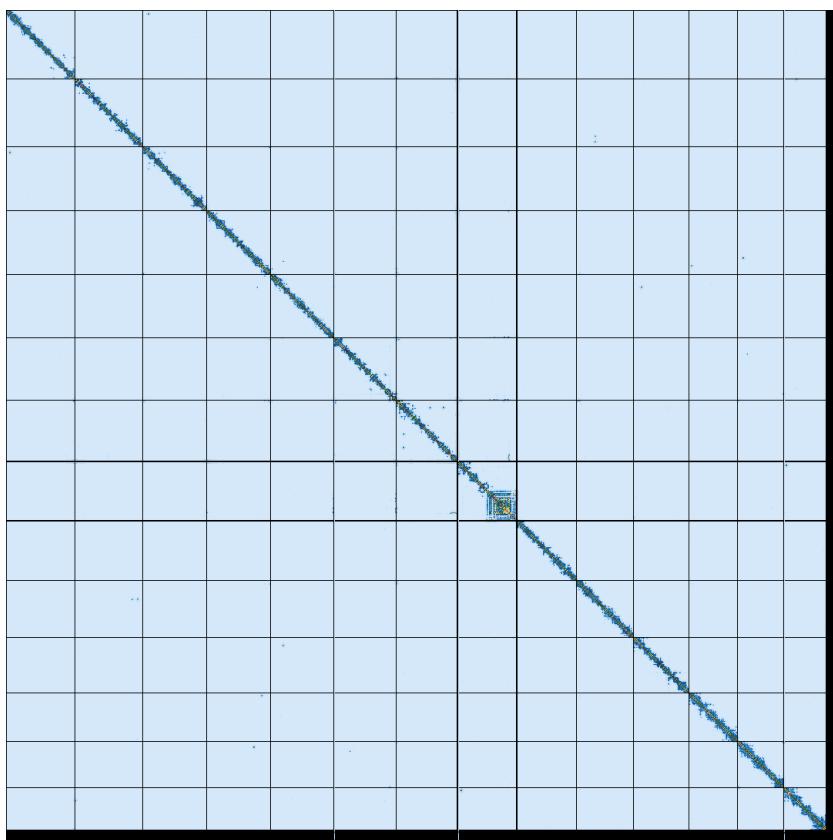
- Interventions/Gb: 46
- Contamination notes: ""
- Other observations: "The assembly of *Frontinellina frutetorum* (qqFroFrut6) is based on 35X PacBio data and Omni-C Hi-C data generated as part of the European Reference Genome Atlas (ERGA, <https://www.erga-biodiversity.eu/>) via the Biodiversity Genomics Europe project (BGE, <https://biodiversitygenomics.eu/>). The assembly process included the following steps: initial PacBio assembly generation with Hifiasm, removal of contaminant sequences using Context, removal of haplotypic duplications using purge_dups, and Hi-C-based scaffolding with YaHS. In total, 26 contigs were identified as contaminants (bacterial, archaeal, or viral), totaling 5.8 Mb (with the largest being 2.3Mb). Additionally, 1,178 regions totaling 69 Mb (with the largest being 1.1 Mb) were identified as haplotypic duplications and removed. The mitochondrial genome was assembled using OATK. Finally, the primary assembly was analyzed and manually improved using Pretext. During manual curation, 5 haplotypic regions were removed, totaling 2.3 Mb (with the largest being 0.74 Mb). Chromosome-scale scaffolds confirmed by Hi-C data were named in order of size "

Quality metrics table

| Metrics | Pre-curation collapsed | Curated collapsed |
|--------------|------------------------|-------------------|
| Total bp | 1,280,409,366 | 1,277,728,908 |
| GC % | 31.85 | 31.85 |
| Gaps/Gbp | 1,017.64 | 1,005.69 |
| Total gap bp | 143,400 | 145,100 |
| Scaffolds | 333 | 239 |
| Scaffold N50 | 92,665,346 | 93,533,890 |
| Scaffold L50 | 7 | 7 |
| Scaffold L90 | 13 | 13 |
| Contigs | 1,603 | 1,524 |
| Contig N50 | 1,922,386 | 1,922,386 |
| Contig L50 | 196 | 196 |
| Contig L90 | 706 | 704 |
| QV | 59.9252 | 59.9331 |
| Kmer compl. | 76.2769 | 76.2178 |
| BUSCO sing. | 93.7% | 93.9% |
| BUSCO dupl. | 1.1% | 0.9% |
| BUSCO frag. | 3.3% | 3.2% |
| BUSCO miss. | 1.9% | 1.9% |

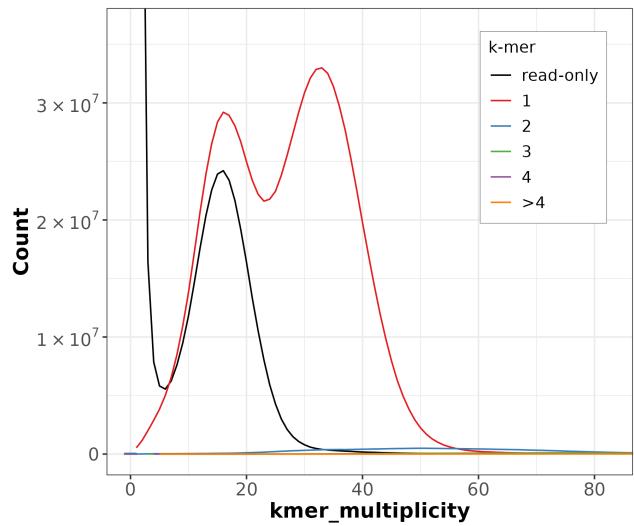
BUSCO: 5.8.2 (euk_genome_met, metaeuk) / Lineage: araneae_odb12 (genomes:11, BUSCOs:3974)

HiC contact map of curated assembly

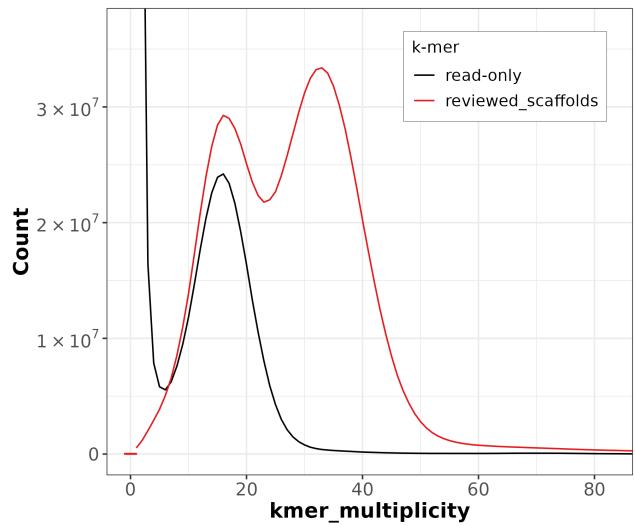


collapsed [\[LINK\]](#)

K-mer spectra of curated assembly

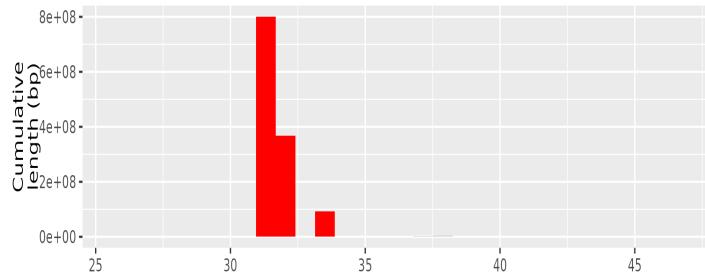


Distribution of k-mer counts per copy numbers found in asm

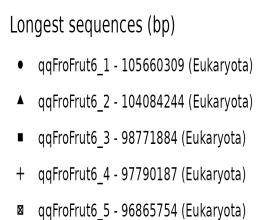
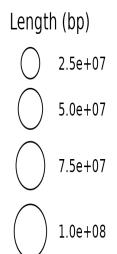
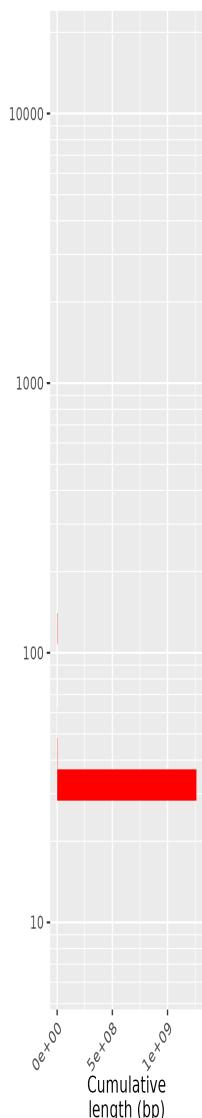
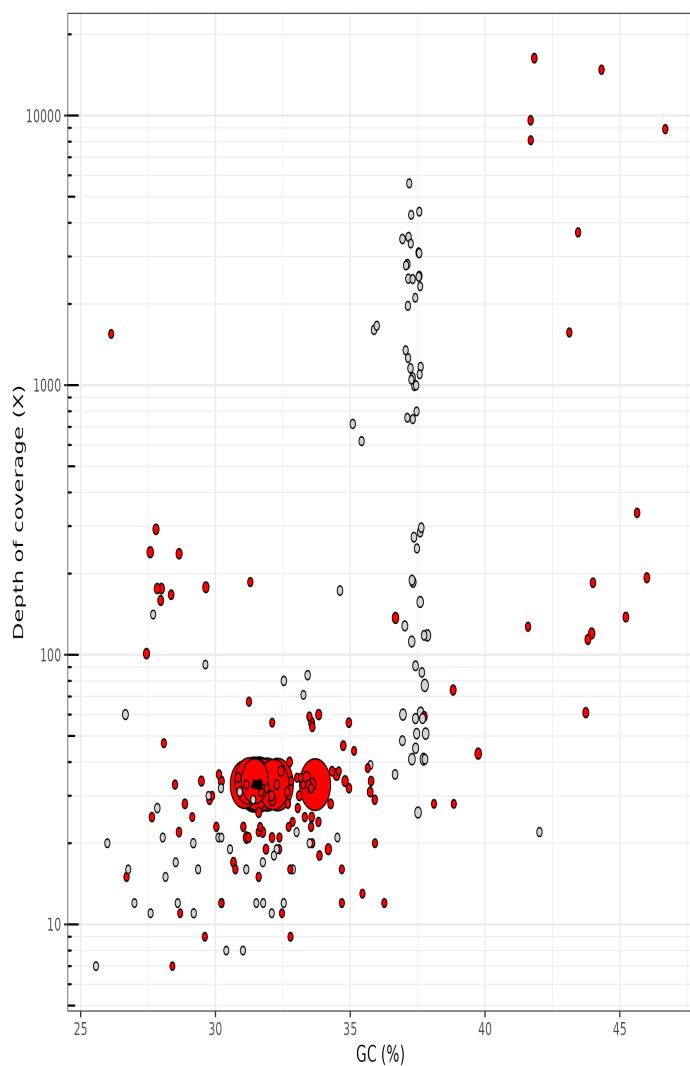


Distribution of k-mer counts coloured by their presence in reads/assemblies

Post-curation contamination screening



TAPAs summary Graph



collapsed. 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 | Long reads | Omnic |
|----------|------------|-------|
| Coverage | 35 | 271 |

Assembly pipeline

- **Hifiasm**
 - |_ ver: 0.19.5-r593
 - |_ key param: NA
- **purge_dups**
 - |_ ver: 1.2.5
 - |_ key param: NA
- **YaHS**
 - |_ ver: 1.2
 - |_ key param: NA

Curation pipeline

- **PretextMap**
 - |_ ver: 0.1.9
 - |_ key param: NA
- **PretextView**
 - |_ ver: 0.2.5
 - |_ key param: NA

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Date and time: 2025-09-25 08:32:39 CEST