

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

| | |
|---------|-------------------|
| TxID | 2883604 |
| ToLID | qqEusFeti1 |
| Species | Euscorpius feti |
| Class | Arachnida |
| Order | Scorpiones |

| Genome Traits | Expected | Observed |
|-------------------|-----------------------|---------------|
| Haploid size (bp) | 4,312,354,347 | 4,371,788,358 |
| Haploid Number | 35 (source: ancestor) | 33 |
| Ploidy | 2 (source: ancestor) | 2 |
| Sample Sex | unknown | unknown |

EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 7.8.Q67

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

- . Observed Haploid Number is different from Expected
- . BUSCO single copy value is less than 90% for pri
- . BUSCO duplicated value is more than 5% for pri

Curator notes

. Interventions/Gb: 8

. Contamination notes: "The BTK pipeline detected 1 contaminant scaffold (scaffold_136) in the pre-curated assembly. However this scaffold was kept, as it is a false positive containing 1 arachnida_odb10 Complete BUSCO and contacts strongly with a chromosome (scaffold_31 or SUPER_32 in curated assembly). For this report, we just show the blob plot of the precurated assembly, actually the only difference with the curated is the number of total scaffolds (184 instead of 187 after curation)."

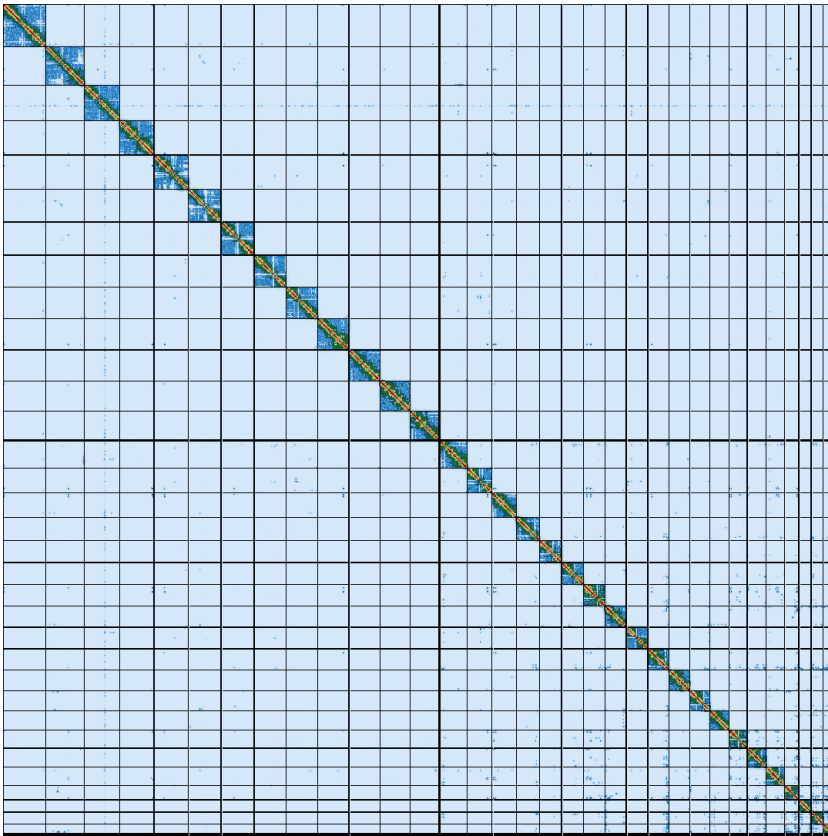
. Other observations: "Our best genome assembly was obtained running hifiiasm with the Hi-C phasing option and then scaffolding the primary assembly with YaHS. Although the sequenced specimen was a female, during curation we could not detect the sex chromosomes. In fact, the lack of distinguishable sex chromosomes is consistent with previous studies in the Euscorpius genus (10.15671/HJBC.2019.269). Regarding to the mitochondrial genome, this was assembled with FOAM into a single circular contig of 15,340 bp."

Quality metrics table

| Metrics | Pre-curation pri | Curated pri |
|--------------|---------------------|----------------|
| Total bp | 4,371,786,958 | 4,371,788,358 |
| GC % | 36.59 | 36.59 |
| Gaps/Gbp | 16.7 | 18.3 |
| Total gap bp | 14,600 | 16,000 |
| Scaffolds | 187 | 184 |
| Scaffold N50 | 158,507,893 | 151,694,389 |
| Scaffold L50 | 12 | 13 |
| Scaffold L90 | 28 | 28 |
| Contigs | 260 | 264 |
| Contig N50 | 88,203,554 | 81,262,035 |
| Contig L50 | 17 | 18 |
| Contig L90 | 54 | 55 |
| QV | 67.4071 | 67.4071 |
| Kmer compl. | 97.6951 | 97.6951 |
| BUSCO sing. | 88.7% | 88.7% |
| BUSCO dupl. | 8.3% | 8.3% |
| BUSCO frag. | 1.3% | 1.3% |
| BUSCO miss. | 1.7% | 1.7% |

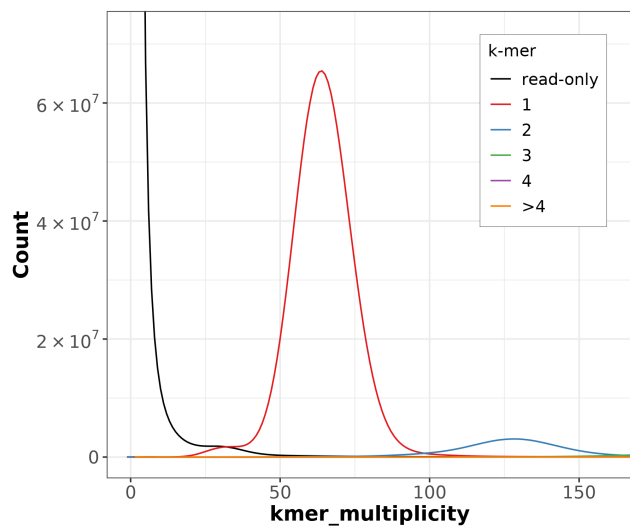
BUSCO: 5.5.0 (euk_genome_met, metaeuk) / Lineage: arachnida_odb10 (genomes:10, BUSCOs:2934)

HiC contact map of curated assembly

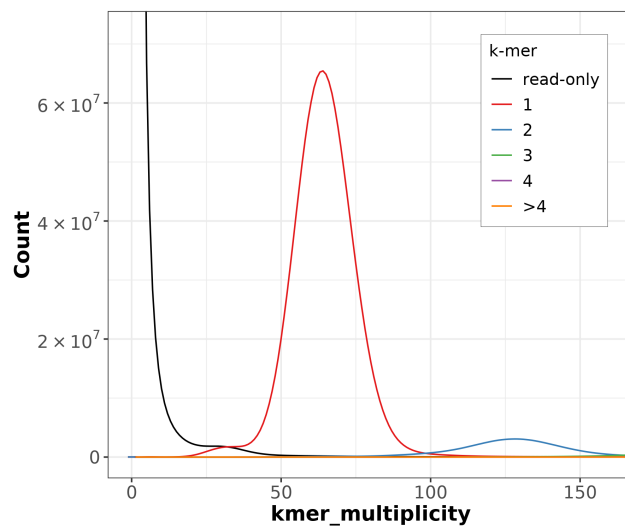


pri [\[LINK\]](#)

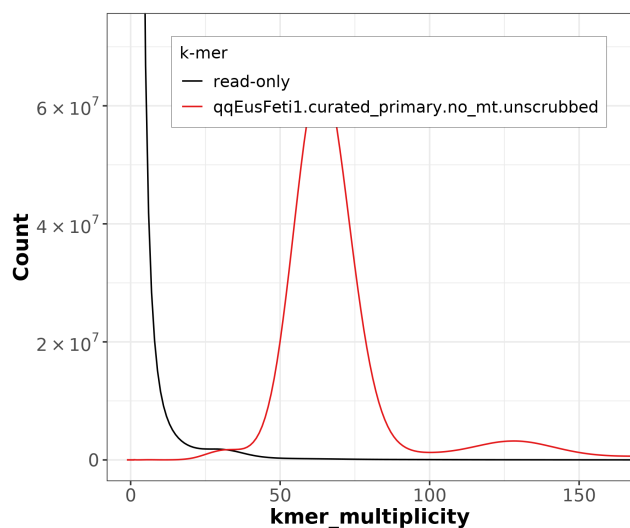
K-mer spectra of curated assembly



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

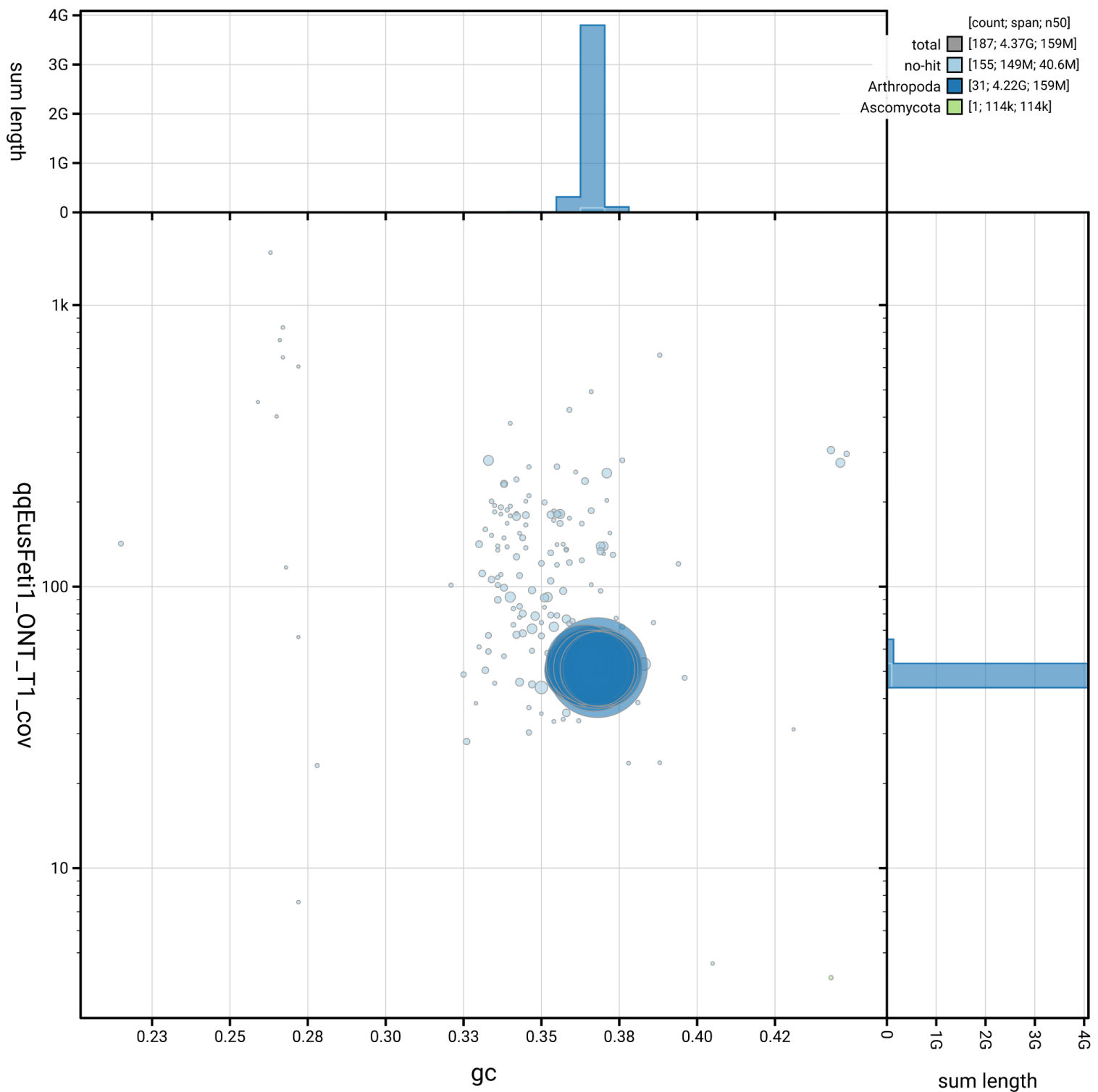


Distribution of k-mer counts per copy numbers found in asm



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

Post-curation contamination screening



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 | ONT | Illumina | OmniC |
|----------|-----|----------|-------|
| Coverage | 64x | 22x | 82x |

Assembly pipeline

- **CLAWS pipeline**
 - |_ ver: 2.2.0 and 2.3.0
 - |_ key param: NA
- **Trim_galore**
 - |_ ver: 0.6.7
 - |_ key param: NA
- **Filtlong**
 - |_ ver: 0.2.1
 - |_ key param: NA
- **flye**
 - |_ ver: 2.9.1
 - |_ key param: NA
- **nextdenovo**
 - |_ ver: 2.5.0
 - |_ key param: NA
- **hifiasm**
 - |_ ver: 0.24.0
 - |_ key param: NA
- **hypo**
 - |_ ver: 1.0.3
 - |_ key param: NA
- **purge_dups**
 - |_ ver: 1.2.6
 - |_ key param: NA
- **YaHS**
 - |_ ver: 1.2a
 - |_ key param: NA
- **Blobtoolkit Nextflow pipeline (latest)**
 - |_ ver: 0.6
 - |_ key param: NA
- **FOAM pipeline**
 - |_ ver: 0.5
 - |_ key param: NA
- **mitos**
 - |_ ver: 2.1.3
 - |_ key param: NA

Curation pipeline

- **PretextViewAI**
 - |_ ver: 1.0.3
 - |_ key param: NA

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