

# ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	49205
ToLID	<b>qqHyaLus11</b>
Species	Hyalomma lusitanicum
Class	Arachnida
Order	Ixodida

Genome Traits	Expected	Observed
Haploid size (bp)	1,828,234,218	1,814,221,550
Haploid Number	11 (source: ancestor)	18
Ploidy	2 (source: ancestor)	2
Sample Sex	X0	unknown

## EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 8.8.Q65

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

- . Observed Haploid Number is different from Expected
- . Observed sex is different from Sample sex
- . Kmer completeness value is less than 90 for pri

## Curator notes

- . Interventions/Gb: None
- . Contamination notes: "Analyses with FCS-GX and BTK did not detect contaminants in the assembly."
- . Other observations: "Our best assembly was haplotype 2 obtained with hifiasm. We will upload this assembly as a contig-level primary assembly to ENA. Contigs are large and almost chromosome level. However, we could not obtain a Hi-C library for this genome, so it was not scaffolded with YaHS or curated using Hi-C. We could not confirm if it is a T2T assembly due to the lack of close reference and telomere peaks at both ends of the largest scaffolds ( $\geq 16.7$  Mb). Illumina was used only to build a combined meryl database with the ONT and estimate genome-size. Mitogenome was not assembled."

## Quality metrics table

Metrics	Pre-curation pri	Curated pri
Total bp	1,814,221,550	1,814,221,550
GC %	46.53	46.53
Gaps/Gbp	0	0
Total gap bp	0	0
Scaffolds	59	59
Scaffold N50	153,563,811	153,563,811
Scaffold L50	5	5
Scaffold L90	13	13
Contigs	59	59
Contig N50	153,563,811	153,563,811
Contig L50	5	5
Contig L90	13	13
QV	65.2791	65.2791
Kmer compl.	78.2416	78.2416
BUSCO sing.	93.2%	93.2%
BUSCO dupl.	2.1%	2.1%
BUSCO frag.	2.1%	2.1%
BUSCO miss.	2.6%	2.6%

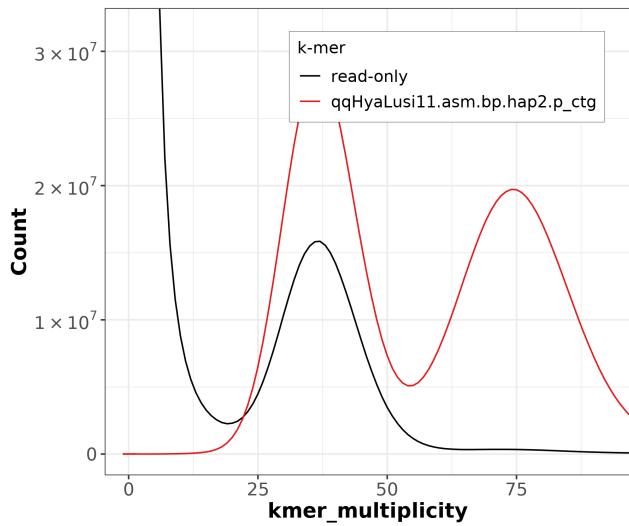
BUSCO: 5.4.0 (euk\_genome\_met, metaeuk) / Lineage: arachnida\_odb10 (genomes:10, BUSCOs:2934)

# HiC contact map of curated assembly

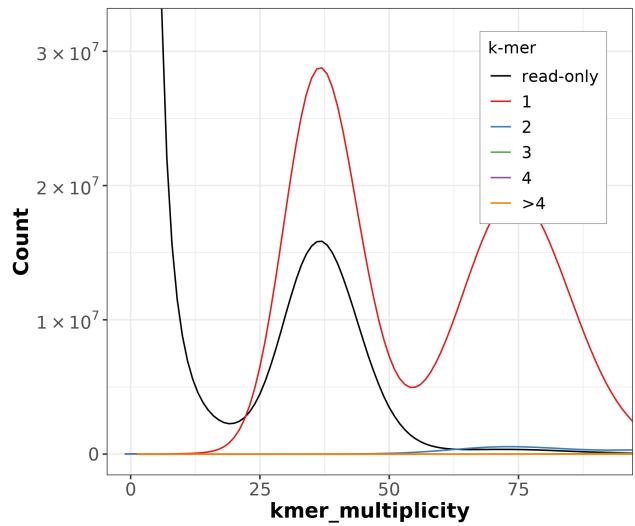
**pri** HiC PNG is missing!

**pri** File link is missing!

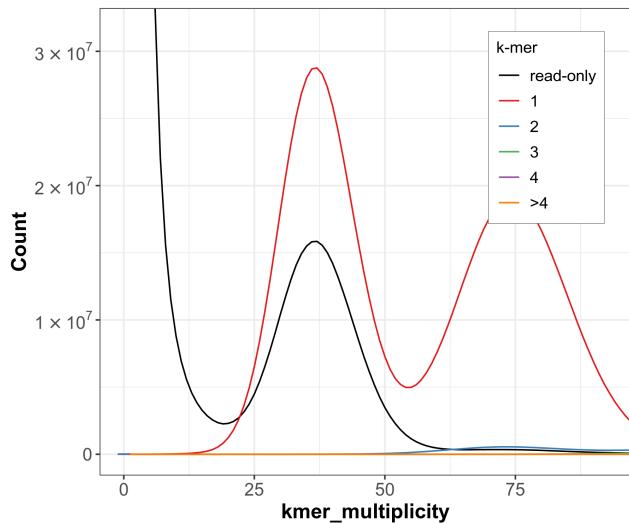
# K-mer spectra of curated assembly



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



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



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

# Post-curation contamination screening

## Data profile

	Data	ONT	Illumina
Coverage	98x		111x

## Assembly pipeline

```
- CLAWS pipeline
|_ ver: 2.2.0
|_ key param: NA
- Trim_galore
|_ ver: 0.6.7
|_ key param: --max_n 0
|_ key param: --gzip
|_ key param: -q 20
|_ key param: --paired
|_ key param: --retain_unpaired
- Filtlong
|_ ver: 0.2.1
|_ key param: --min_length 1000
|_ key param: --min_mean_q 90
|_ key param: --target_bases 140000000000
- Hifiasm
|_ ver: 0.24.0
|_ key param: --ont
```

## Curation pipeline

```
- Blobtoolkit DToL Nextflow Pipeline
|_ ver: 0.6
|_ key param: NA
- FCS-GX
|_ ver: 0.5.5
|_ key param: NA
```

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Date and time: 2026-02-23 15:00:31 CET