

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	49205
ToLID	qqHyaLusi11
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 is a T2T assembly due to the lack of close reference and telomere peaks at both ends of the largest scaffolds (≥ 16.7 Mb). Illumina was used only to build a combined mer1 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%

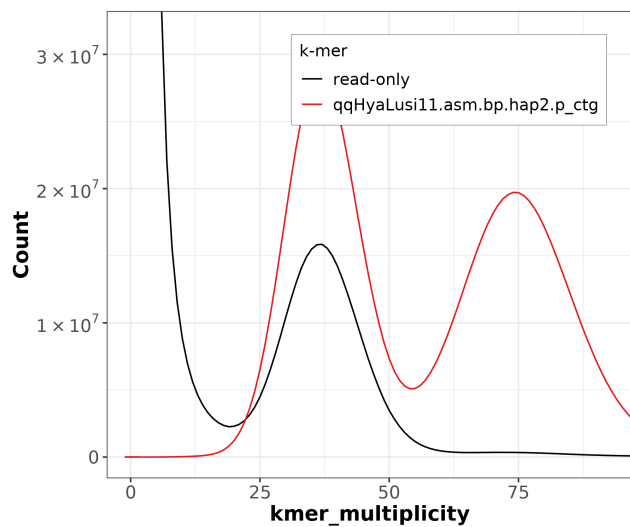
BUSCO: 5.4.0 (euk_genome_met, metaeuk) / Lineage: arachnida_odb10 (genomes:10, BUSCOs:2934)

HiC contact map of curated assembly

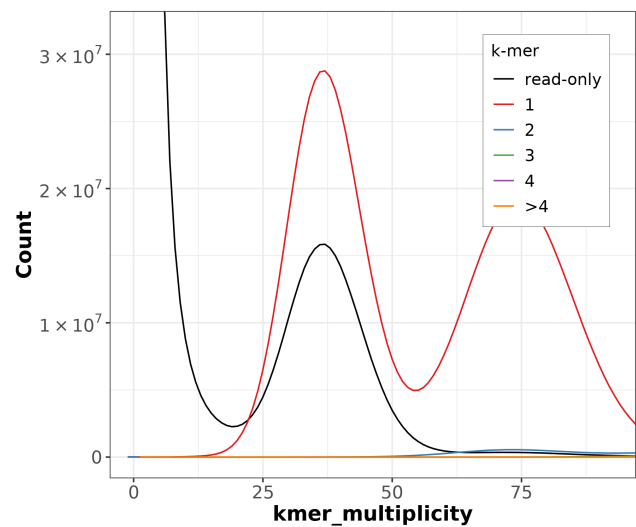
pri HiC PNG is missing!

pri File link is missing!

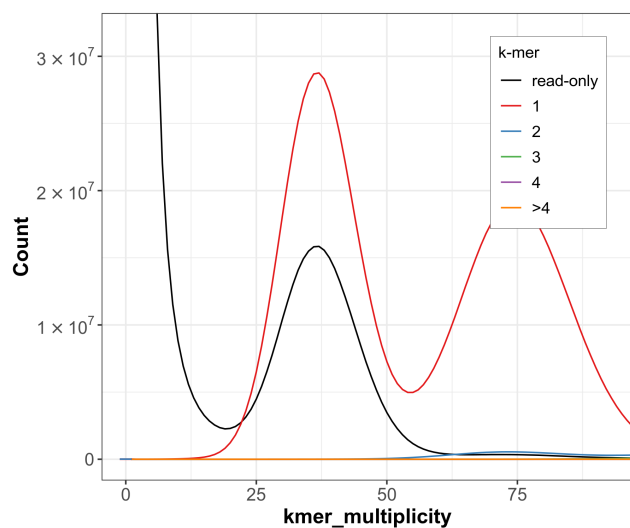
K-mer spectra of curated assembly



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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