

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	618066
ToLID	icLucTetr
Species	Lucanus tetraodon
Class	Insecta
Order	Coleoptera

Genome Traits	Expected	Observed
Haploid size (bp)	360,638,005	337,598,709
Haploid Number	11 (source: ancestor)	14
Ploidy	2 (source: ancestor)	2
Sample Sex	XY	XY

EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 6.7.Q39

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

- . Observed Haploid Number is different from Expected
- . QV value is less than 40 for collapsed
- . Kmer completeness value is less than 90 for collapsed
- . Assembly length loss > 3% for collapsed

Curator notes

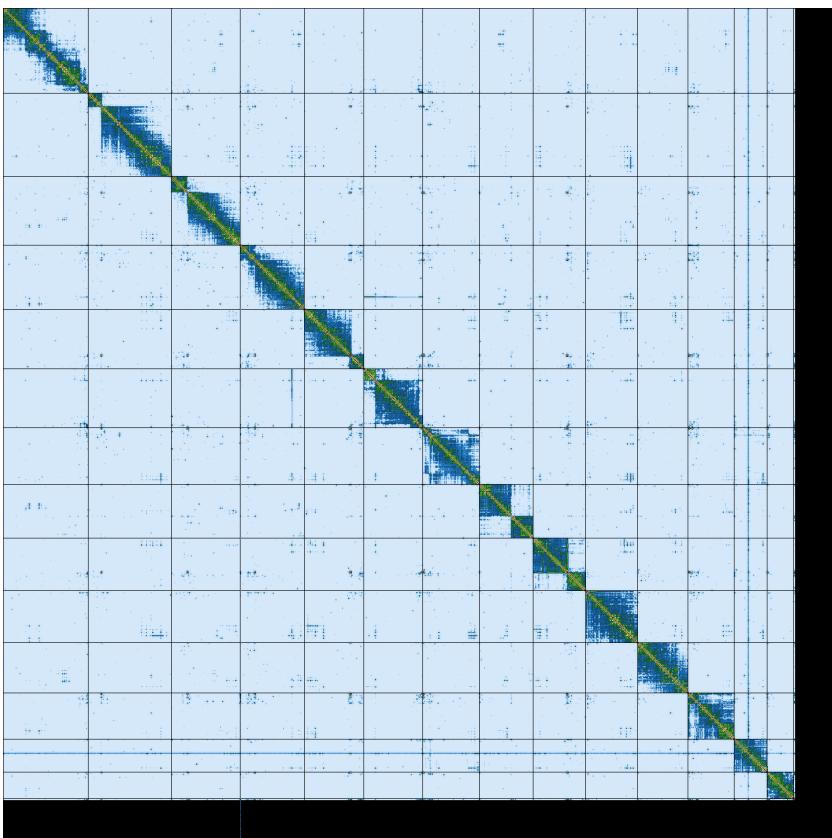
- . Interventions/Gb: 386
- . Contamination notes: "No contaminants were detected."
- . Other observations: "The assembly of species Lucanus tetraodon (icLucTetr) is based on 150X long read ONT data and 85X Arima Hi-C data generated as part of the European Reference Genome Atlas (ERGA, <https://www.erga-biodiversity.eu/>) via the Biodiversity Genomics Europe project (BGE, <https://biodiversitygenomics.eu/>). The assembly process included the following steps: ONT reads shorter than 3 kb were filtered out, thus the remaining reads were assembled using Necat with polishing performed using NextPolish. Contigs were subsequently filtered with purge_dups to remove haplotigs and obtain a more accurate, non-redundant assembly. Scaffolding was performed by aligning Hi-C reads to the purged contigs using the Omni-C mapping pipeline, followed by YaHS for scaffold construction. Contamination was checked using BlobTools, and no contaminants were detected. The scaffolds were processed through sanger_tol/curationpretext pipeline to generate the contact map, which was manually improved using PretextView. 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	362,404,194	337,598,709
GC %	35.67	35.66
Gaps/Gbp	711.91	995.26
Total gap bp	25,800	47,400
Scaffolds	356	249
Scaffold N50	18,996,966	23,875,370
Scaffold L50	8	6
Scaffold L90	28	13
Contigs	614	585
Contig N50	1,875,229	1,983,884
Contig L50	51	47
Contig L90	211	190
QV	39.8955	39.6757
Kmer compl.	86.6829	84.6071
BUSCO sing.	91.0%	94.9%
BUSCO dupl.	5.2%	0.7%
BUSCO frag.	1.3%	1.3%
BUSCO miss.	2.5%	3.0%

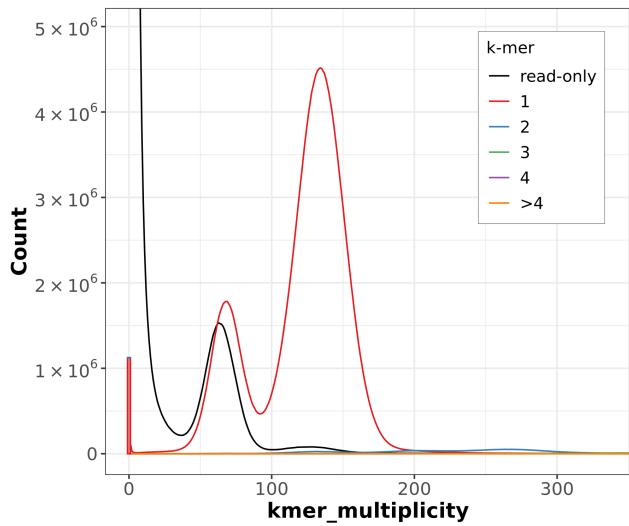
BUSCO: 6.0.0 (euk_genome_aug, augustus) / Lineage: polyphaga_odb12 (genomes:60, BUSCOs:4010)

HiC contact map of curated assembly

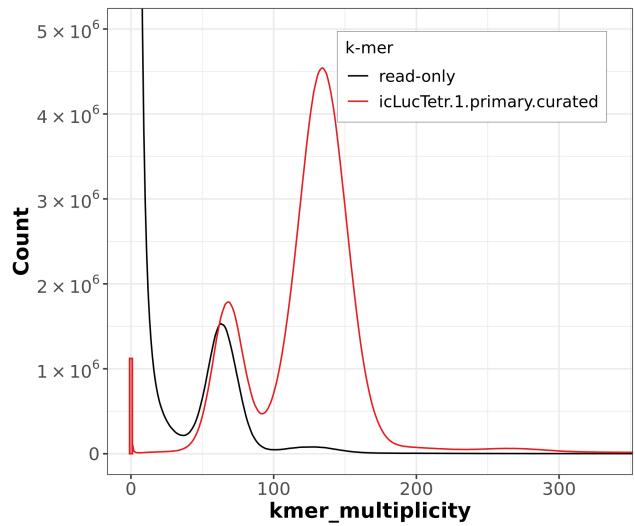


collapsed [\[LINK\]](#)

K-mer spectra of curated assembly



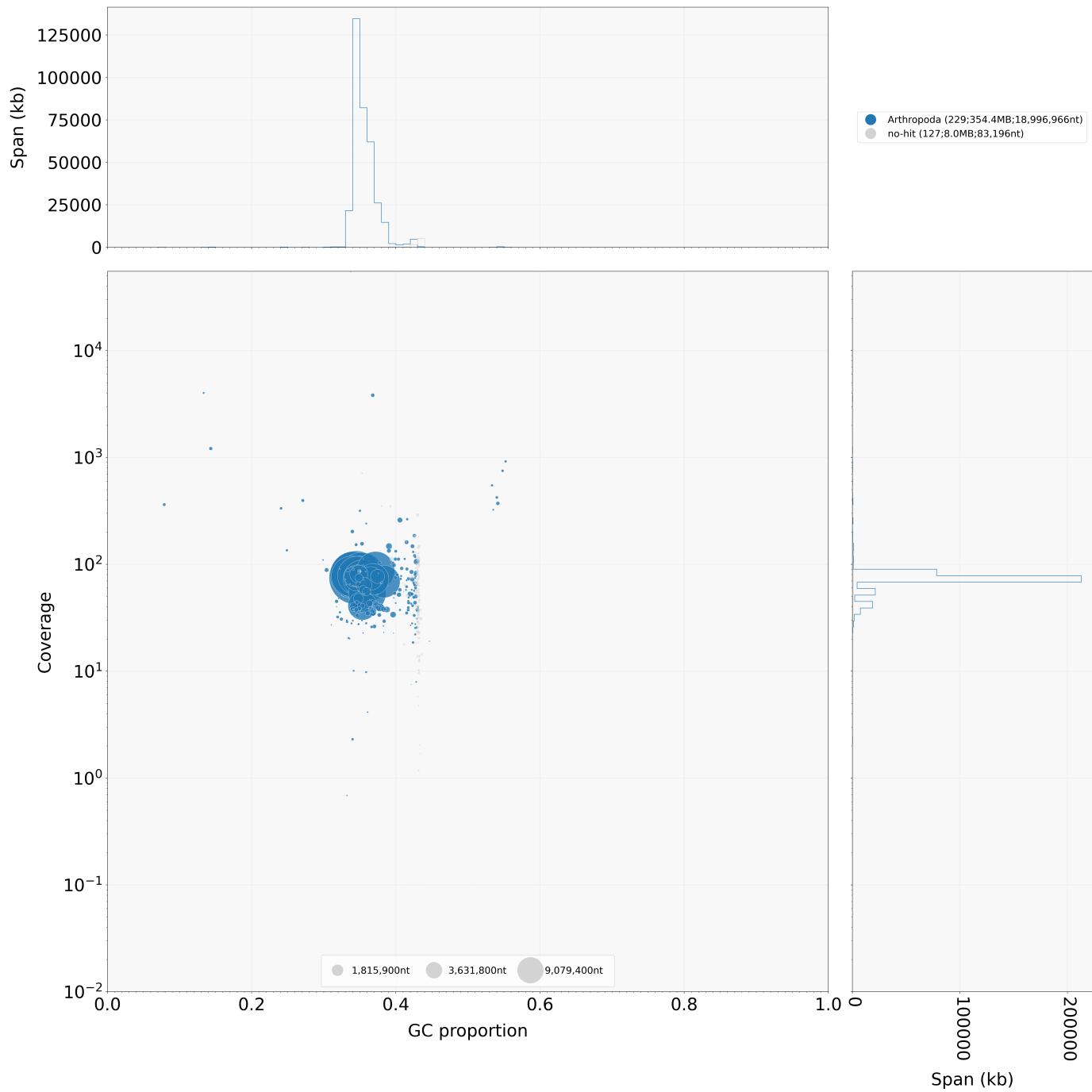
Distribution of k-mer counts per copy numbers found in asm



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

Post-curation contamination screening

filename.blobDB.json.bestsum.phylum.p8.span.100.blobplot.bam0



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	ONT	Arima HiC
Coverage	150	85	

Assembly pipeline

- **Necat**
 - |_ ver: 0.0.1
 - |_ key param: NA
- **purge_dups**
 - |_ ver: 1.2.5
 - |_ key param: NA
- **YaHS**
 - |_ ver: 1.2.2
 - |_ key param: NA

Curation pipeline

- **sanger-tol/curationpretext**
 - |_ ver: 1.5.0
 - |_ key param: NA
- **PretextView**
 - |_ ver: 1.0.5
 - |_ key param: NA

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