

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	1342031
ToLID	icLarUrsu1
Species	Larinus ursus
Class	Insecta
Order	Coleoptera

Genome Traits	Expected	Observed
Haploid size (bp)	1,613,542,317	1,743,456,418
Haploid Number	19 (source: ancestor)	22
Ploidy	2 (source: ancestor)	2
Sample Sex	NA	NA

EBP metrics summary and curation notes

Obtained EBP quality metric for Pri: 7.7.Q62

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 Pri

Curator notes

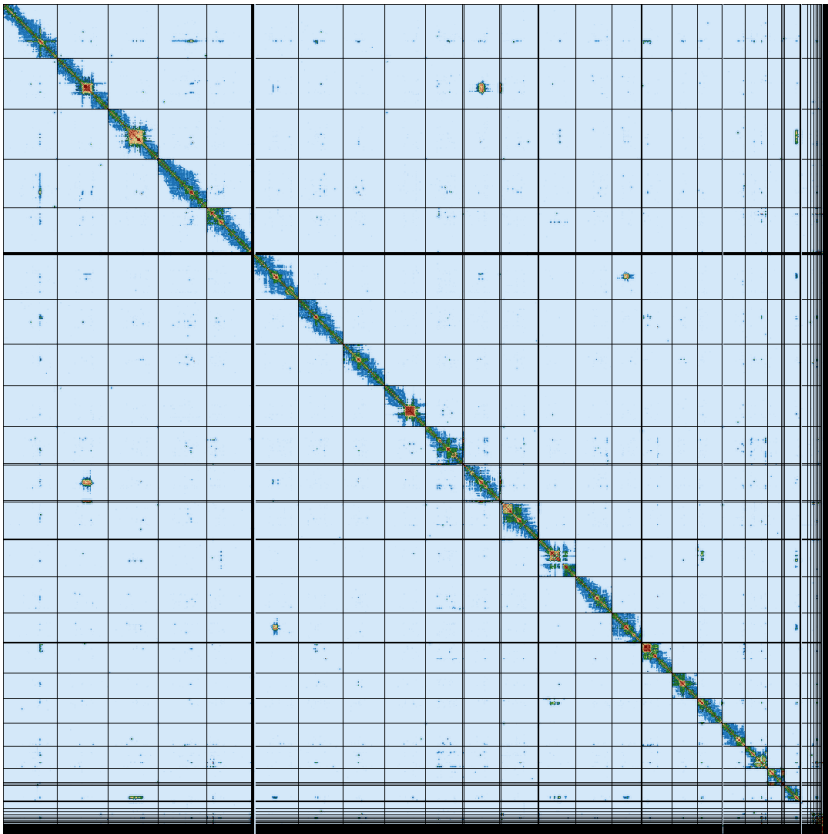
. Interventions/Gb: None
. Contamination notes: "Blobtoolkit detected no contamination."
. Other observations: "This assembly was obtained with Hifiasm from ONT data. Mitogenome was successfully assembled with FOAM. Curation made 23 cuts in contigs, 12 breaks at gaps and 35 joins. Eleven haplotig sequences, adding up a total of 35.2 Mb of sequence, were removed during curaton."

Quality metrics table

Metrics	Pre-curation Pri	Curated Pri
Total bp	1,778,658,397	1,743,456,418
GC %	35.31	35.32
Gaps/Gbp	20.8	34.41
Total gap bp	7,400	12,000
Scaffolds	179	168
Scaffold N50	86,794,555	86,231,057
Scaffold L50	9	9
Scaffold L90	22	20
Contigs	216	228
Contig N50	48,742,161	45,364,611
Contig L50	14	15
Contig L90	42	49
QV	62.4669	62.5343
Kmer compl.	79.8695	79.5824
BUSCO sing.	98.5%	98.8%
BUSCO dupl.	1.5%	1.2%
BUSCO frag.	0.0%	0.0%
BUSCO miss.	0.0%	0.0%

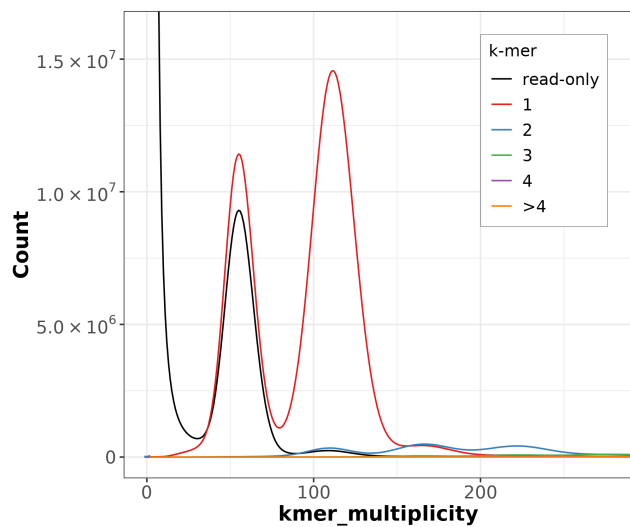
BUSCO: 6.0.0 (euk_genome_min, miniprot) / Lineage: insecta_odb10 (genomes:75, BUSCOs:1367)

HiC contact map of curated assembly

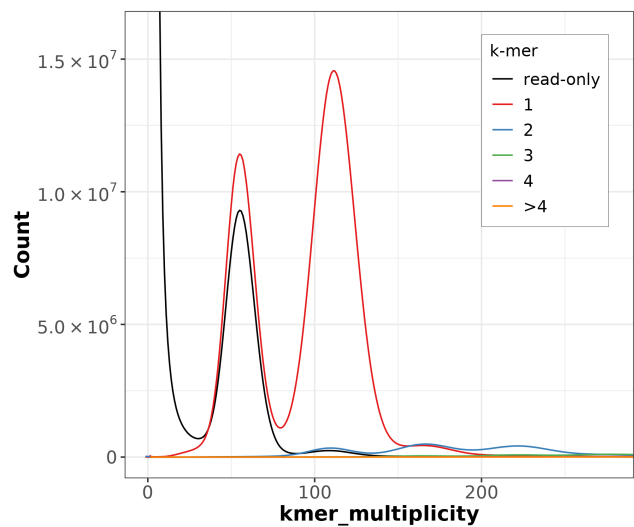


Pri [\[LINK\]](#)

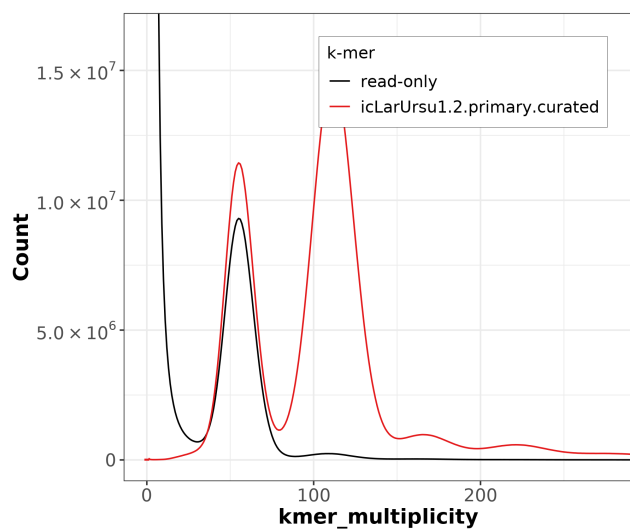
K-mer spectra of curated assembly



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

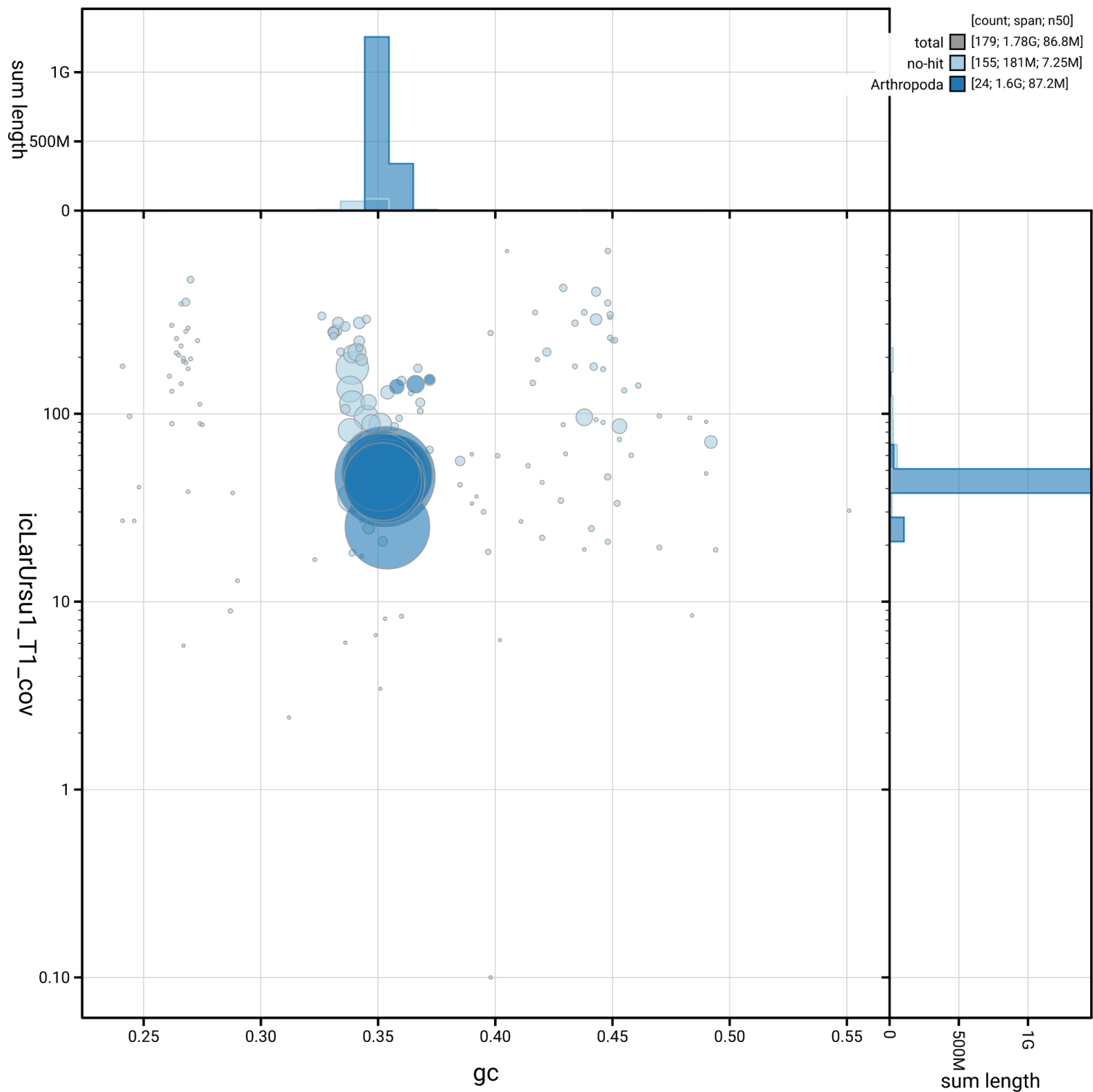


Distribution of k-mer counts per copy numbers found in asm



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	Omni-C
Coverage	42	83	61

Assembly pipeline

- **CLAWS**
 - |_ *ver*: v2.3.0
 - |_ *key param*: NA
- **Filtlong**
 - |_ *ver*: v0.2.1
 - |_ *key param*: --minlen 1000
 - |_ *key param*: --min_mean_q 80
- **Hifiasm**
 - |_ *ver*: 0.24.0
 - |_ *key param*: --ont
 - |_ *key param*: --telo-m AAATAACCC
- **Yahs**
 - |_ *ver*: 1.2a
 - |_ *key param*: -mq 10
 - |_ *key param*: --no-contig-ec
- **FOAM**
 - |_ *ver*: 0.5
 - |_ *key param*: NA

Curation pipeline

- **Blobtoolkit Nextflow pipeline**
 - |_ *ver*: 0.6
 - |_ *key param*: NA
- **PretextViewAI**
 - |_ *ver*: 1.0.5
 - |_ *key param*: NA

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