

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	1342031
ToLID	icLarUrs1
Species	Larinus ursus
Class	Insecta
Order	Coleoptera

Genome Traits	Expected	Observed
Haploid size (bp)	1,613,542,317	1,753,491,222
Haploid Number	19 (source: ancestor)	21
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

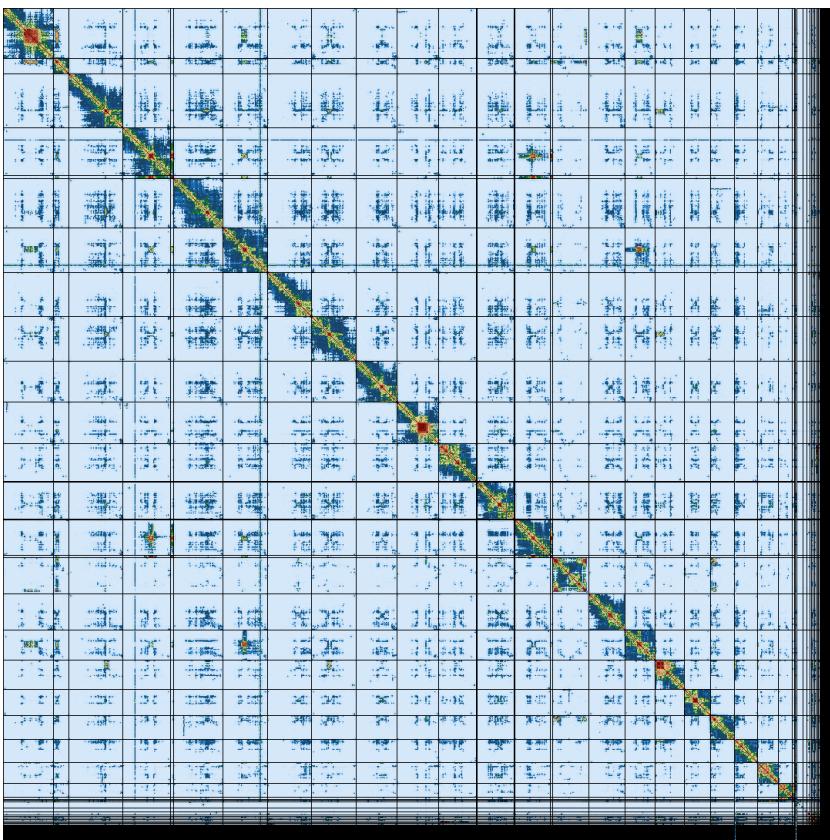
- . Interventions/Gb: None
- . Contamination notes: "Blobtoolkit detected no contamination."
- . Other observations: "This assembly was obtained with Hifiasm from ONT data. Mitogenome was successfully assembled with FOAM. Curation made 10 cuts in contigs, 3 breaks at gaps and 15 joins. Four haplotig sequences, adding up a total of 25.2 Mb of sequence, were removed during curatton."

Quality metrics table

Metrics	Pre-curation Pri	Curated Pri
Total bp	1,778,658,397	1,753,491,222
GC %	35.31	35.32
Gaps/Gbp	20.8	27.94
Total gap bp	7,400	9,800
Scaffolds	179	173
Scaffold N50	86,794,555	86,231,057
Scaffold L50	9	9
Scaffold L90	22	20
Contigs	216	222
Contig N50	48,742,161	45,976,650
Contig L50	14	15
Contig L90	42	45
QV	62.4669	62.4982
Kmer compl.	79.8695	79.6503
BUSCO sing.	98.5%	98.7%
BUSCO dupl.	1.5%	1.3%
BUSCO frag.	0.0%	0.0%
BUSCO miss.	0.0%	0.0%

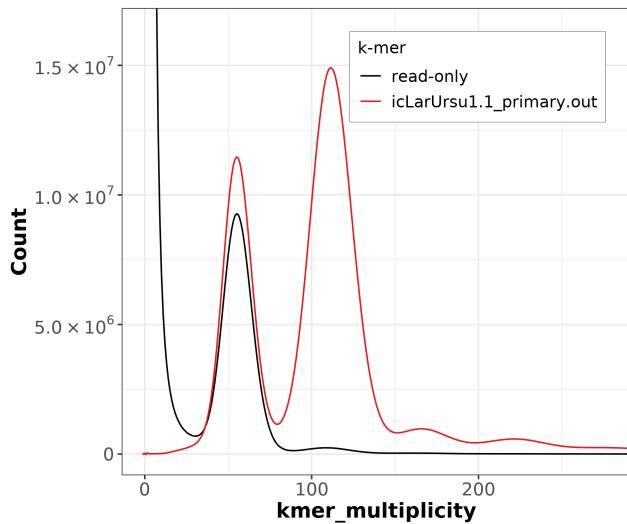
BUSCO: 6.0.0 (euk_genome_min, miniprot) / Lineage: insecta_odb10 (genomes:75, BUSCOs:1367)

HiC contact map of curated assembly

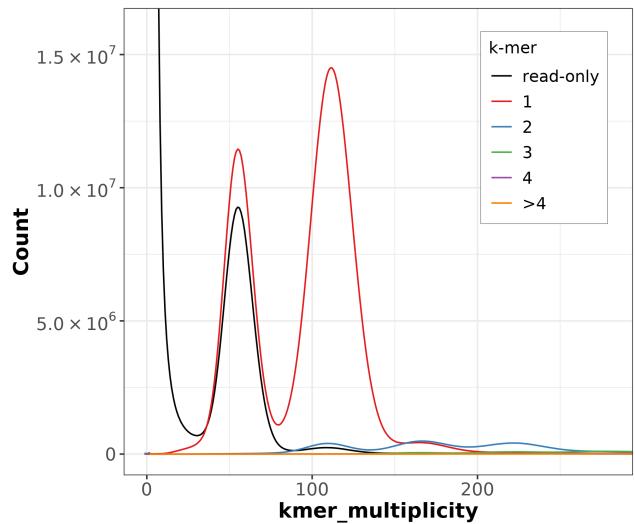


Pri [LINK]

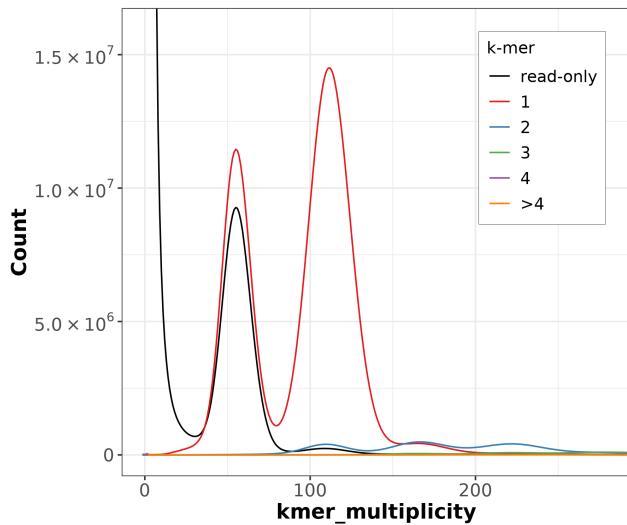
K-mer spectra of curated assembly



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

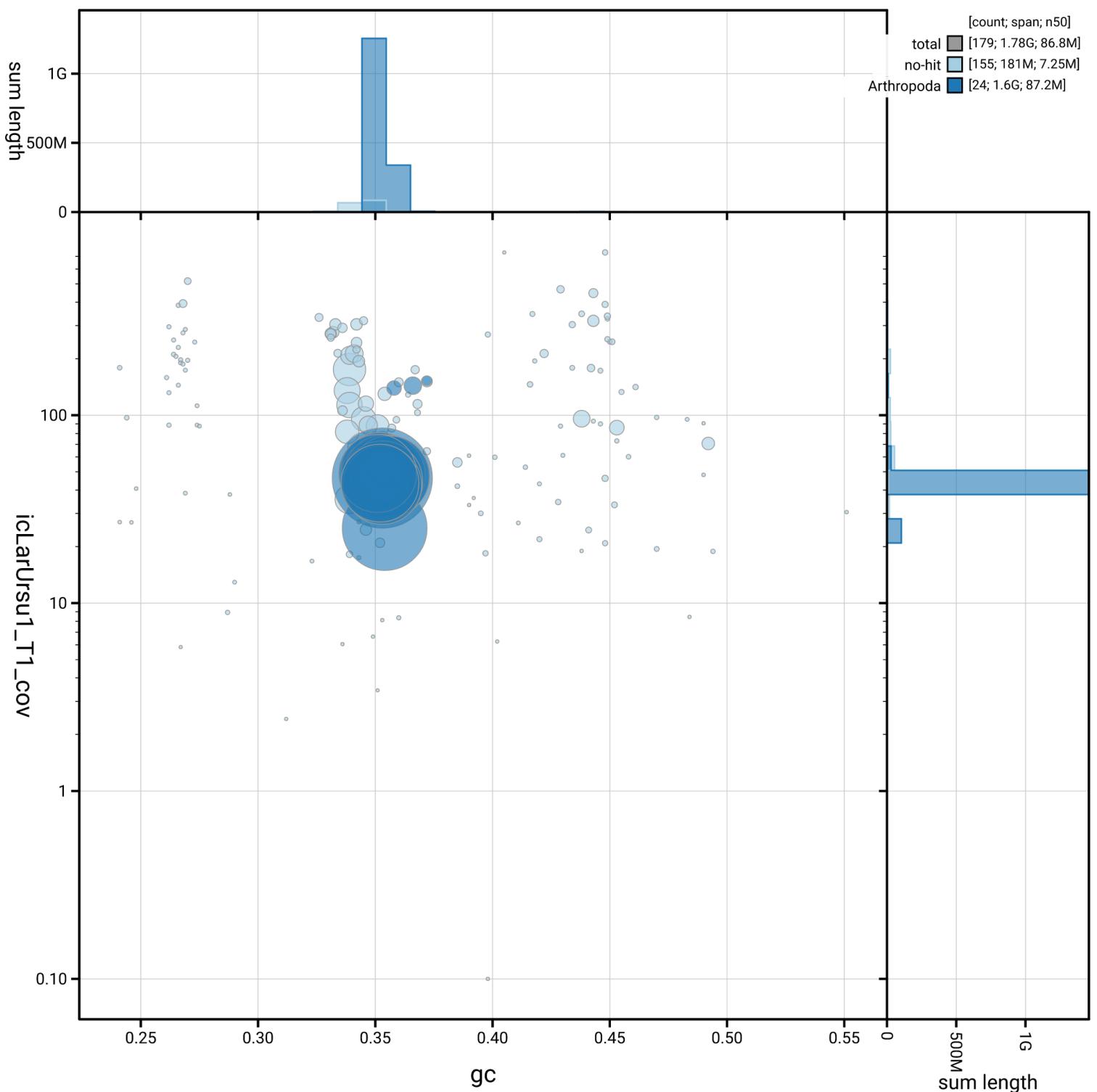


Distribution of k-mer counts per copy numbers found in asm



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

Post-curation contamination screening



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 AAACTAACCC
- Yahs
  |_ ver: 1.2a
  |_ key param: -mq 10
  |_ key param: --no-contig-ec
- FOAM
  |_ ver: 0.5
  |_ key param: NA
```

Curation pipeline

```
- Blob toolkit Nextflow pipeline
  |_ ver: 0.6
  |_ key param: NA
- PretextViewAI
  |_ ver: 1.0.5
  |_ key param: NA
```

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