

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	3073148
ToLID	icBatTris
Species	Bathyscidius tristictulus
Class	Insecta
Order	Coleoptera

Genome Traits	Expected	Observed
Haploid size (bp)	434,092,953	491,326,132
Haploid Number	11 (source: ancestor)	13
Ploidy	2 (source: ancestor)	2
Sample Sex	NA	X0

EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 6.7.Q66

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
- . Assembly length loss > 3% for pri
- . More than 1000 gaps/Gbp for pri
- . Not 90% of assembly in chromosomes for pri

Curator notes

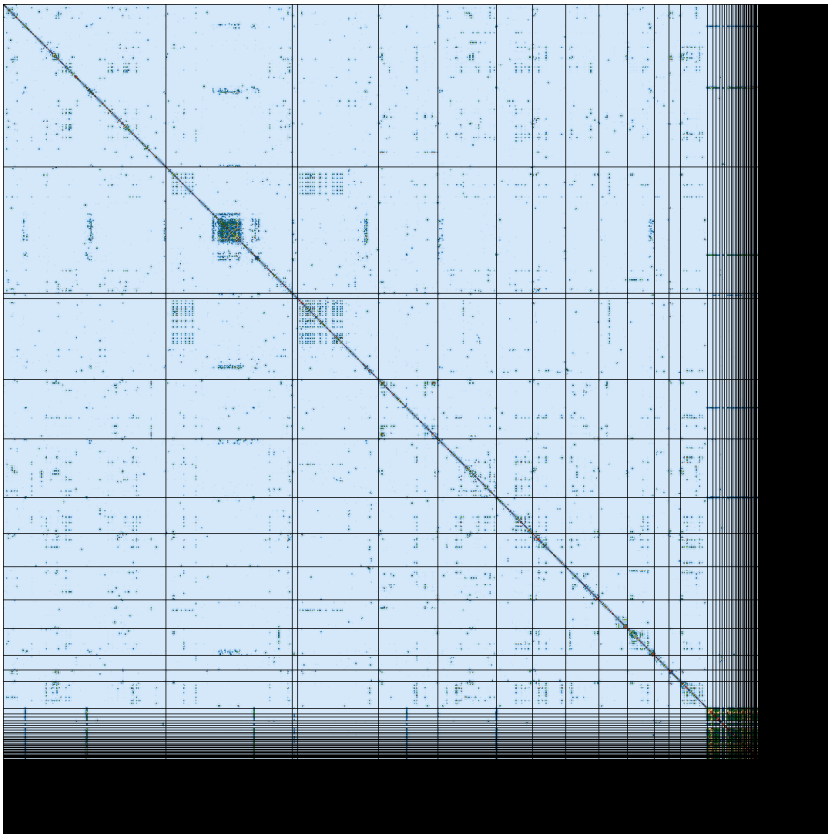
- . Interventions/Gb: None
- . Contamination notes: "No contamination was detected."
- . Other observations: "This genome assembly was produced by assembling PacBio HiFi data from two different individuals with Hifiasm, purging with purge_dups and then scaffolding with Yaws. Curation made 11 cuts in contigs, 22 breaks at gaps and 19 joins. 27 haplotypic sequences, composing a total of 25,475,309 bp were identified and removed during curation. Mitogenome was successfully assembled with FOAM."

Quality metrics table

Metrics	Pre-curation pri	Curated pri
Total bp	516,802,241	491,326,132
GC %	32.89	32.91
Gaps/Gbp	1,079.72	1,127.56
Total gap bp	111,600	110,800
Scaffolds	331	318
Scaffold N50	33,037,159	35,258,742
Scaffold L50	6	4
Scaffold L90	45	38
Contigs	889	872
Contig N50	1,128,672	1,115,878
Contig L50	121	122
Contig L90	468	463
QV	66.3313	66.2905
Kmer compl.	79.3841	78.6821
BUSCO sing.	92.5%	93.8%
BUSCO dupl.	3.3%	1.7%
BUSCO frag.	0.7%	0.7%
BUSCO miss.	3.5%	3.8%

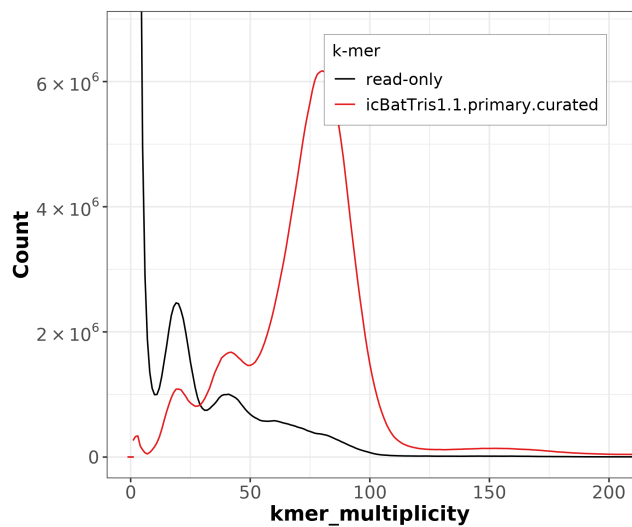
BUSCO: 6.0.0 (euk_genome_min, miniprot) / Lineage: insecta_odb12 (genomes:79, BUSCOs:3114)

HiC contact map of curated assembly

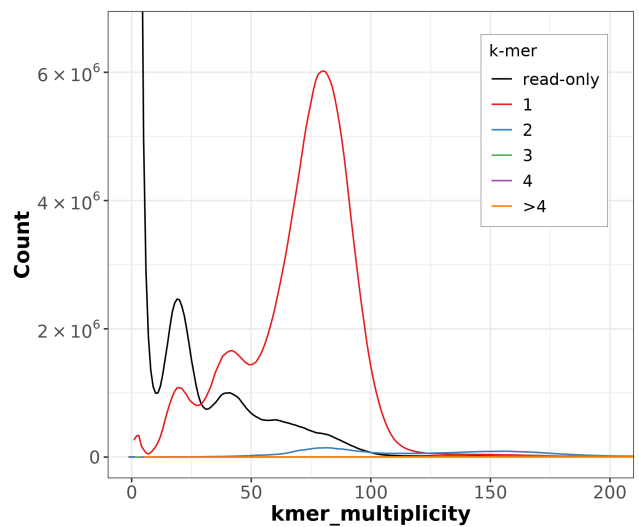


pri [\[LINK\]](#)

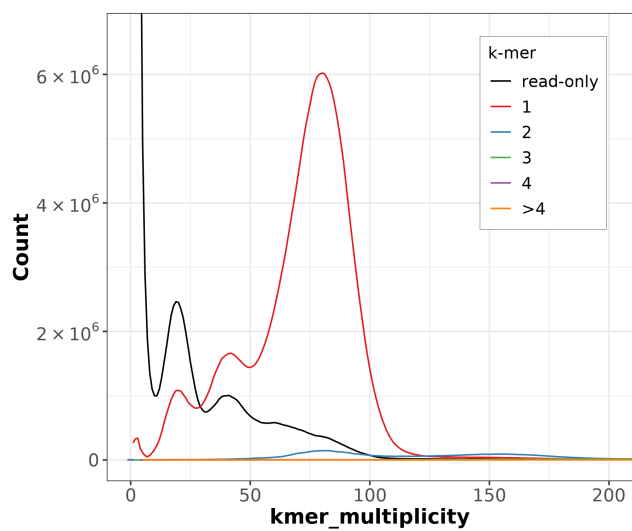
K-mer spectra of curated assembly



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

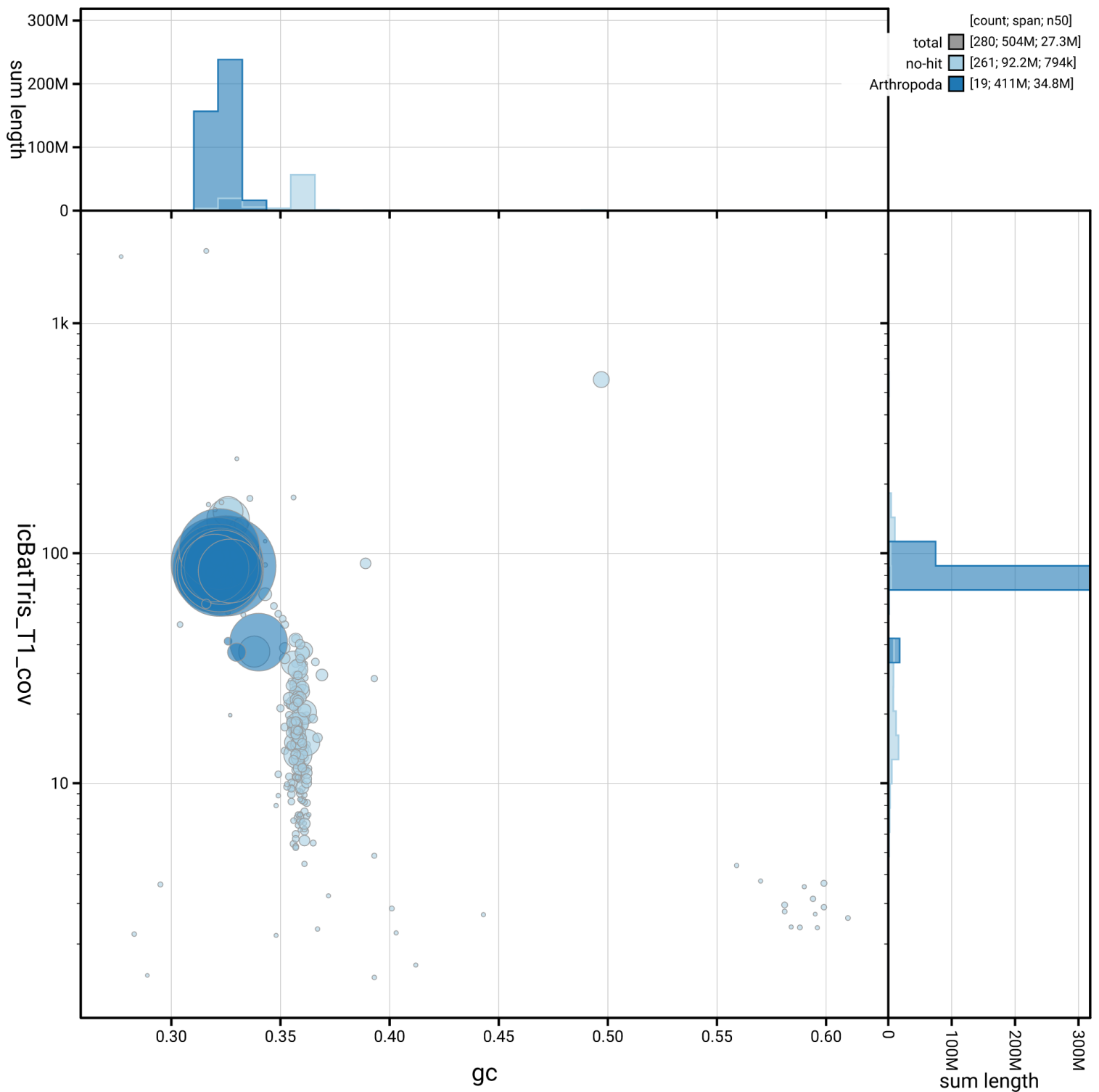


Distribution of k-mer counts per copy numbers found in asm



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	PacBio HiFi	Arima Hi-C
Coverage	74	171

Assembly pipeline

- **CLAWS**
 - |_ *ver*: v3.0
 - |_ *key param*: NA
- **Hifiasm**
 - |_ *ver*: 0.24.0
 - |_ *key param*: --telo-m ACACAC
 - |_ *key param*: --n-perturb 30000
 - |_ *key param*: --f-perturb 0.3
 - |_ *key param*: --min-hist-cnt 5
 - |_ *key param*: -N 150
- **Purge_dups**
 - |_ *ver*: 1.2.6
 - |_ *key param*: NA
- **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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