

# ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	1968893
ToLID	<b>icProCypr1</b>
Species	Propomacrus cypriacus
Class	Insecta
Order	Coleoptera

Genome Traits	Expected	Observed
Haploid size (bp)	471,390,309	512,280,640
Haploid Number	10 (source: ancestor)	10
Ploidy	2 (source: ancestor)	2
Sample Sex	XX	XX

## EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 7.7.Q73

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

### Curator notes

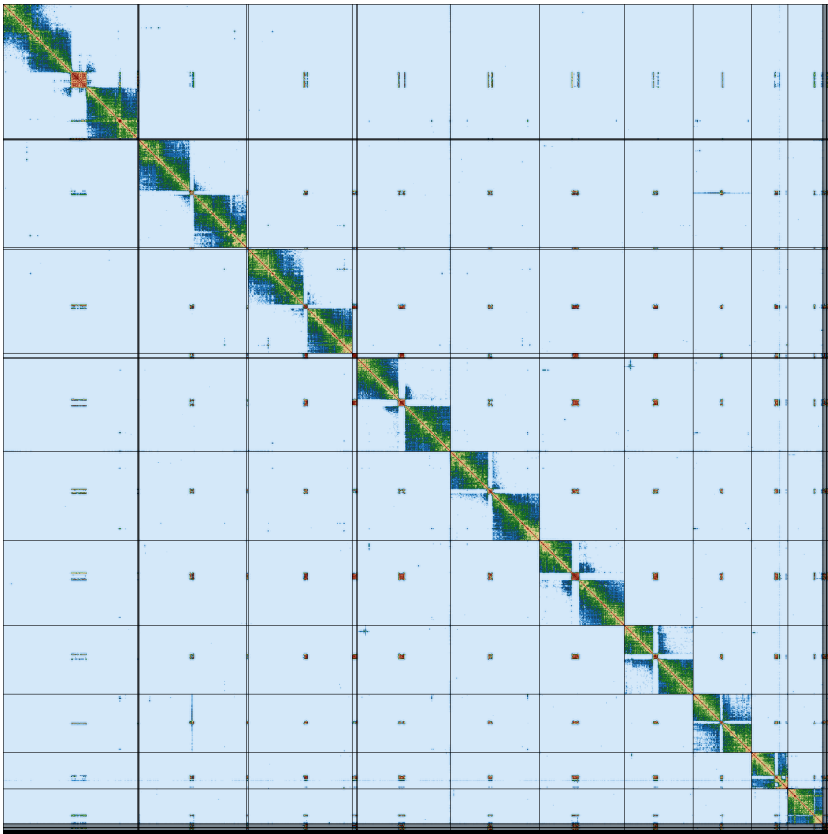
. Interventions/Gb: 0  
. Contamination notes: "No contamination was detected by FCS-GX or blobtoolkit."  
. Other observations: "The assembly was produced with hifiiasm in Hi-C mode. The resulting collapse \*.hic.p\_ctg.gfa was selected, screened for contamination with FCS-GX, and purged of haplotigs with purge\_dups. Scaffolding was performed with YaHS. The X chromosome was assigned based on MCscan analysis of synteny with another Scarabaeoidea beetle, Melinopterus prodromus (GCA\_964023965.1). Mitochondria was assembled with Oatk."

# Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	512,280,640	512,280,640
GC %	33.38	33.38
Gaps/Gbp	17.57	17.57
Total gap bp	1,800	1,800
Scaffolds	41	41
Scaffold N50	57,489,177	57,489,177
Scaffold L50	4	4
Scaffold L90	9	9
Contigs	50	50
Contig N50	29,712,000	29,712,000
Contig L50	8	8
Contig L90	17	17
QV	73.1572	73.1572
Kmer compl.	91.4389	91.4389
BUSCO sing.	98.6%	98.6%
BUSCO dupl.	1.2%	1.2%
BUSCO frag.	0.1%	0.1%
BUSCO miss.	0.1%	0.1%

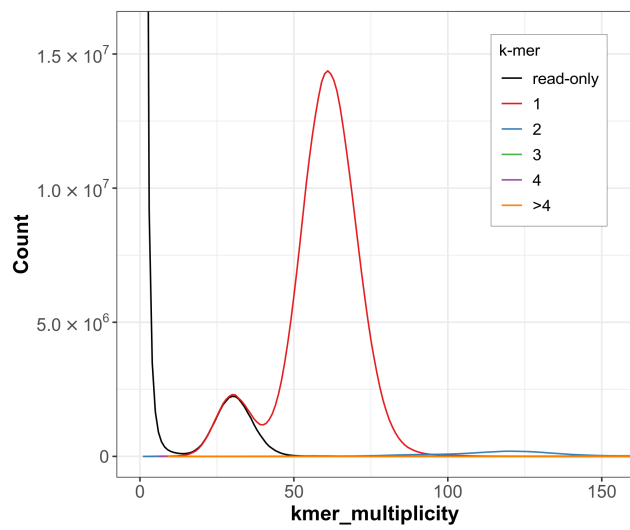
BUSCO: 6.0.0 (euk\_genome\_min, miniprot) / Lineage: endopterygota\_odb10 (genomes:56, BUSCOs:2124)

# HiC contact map of curated assembly



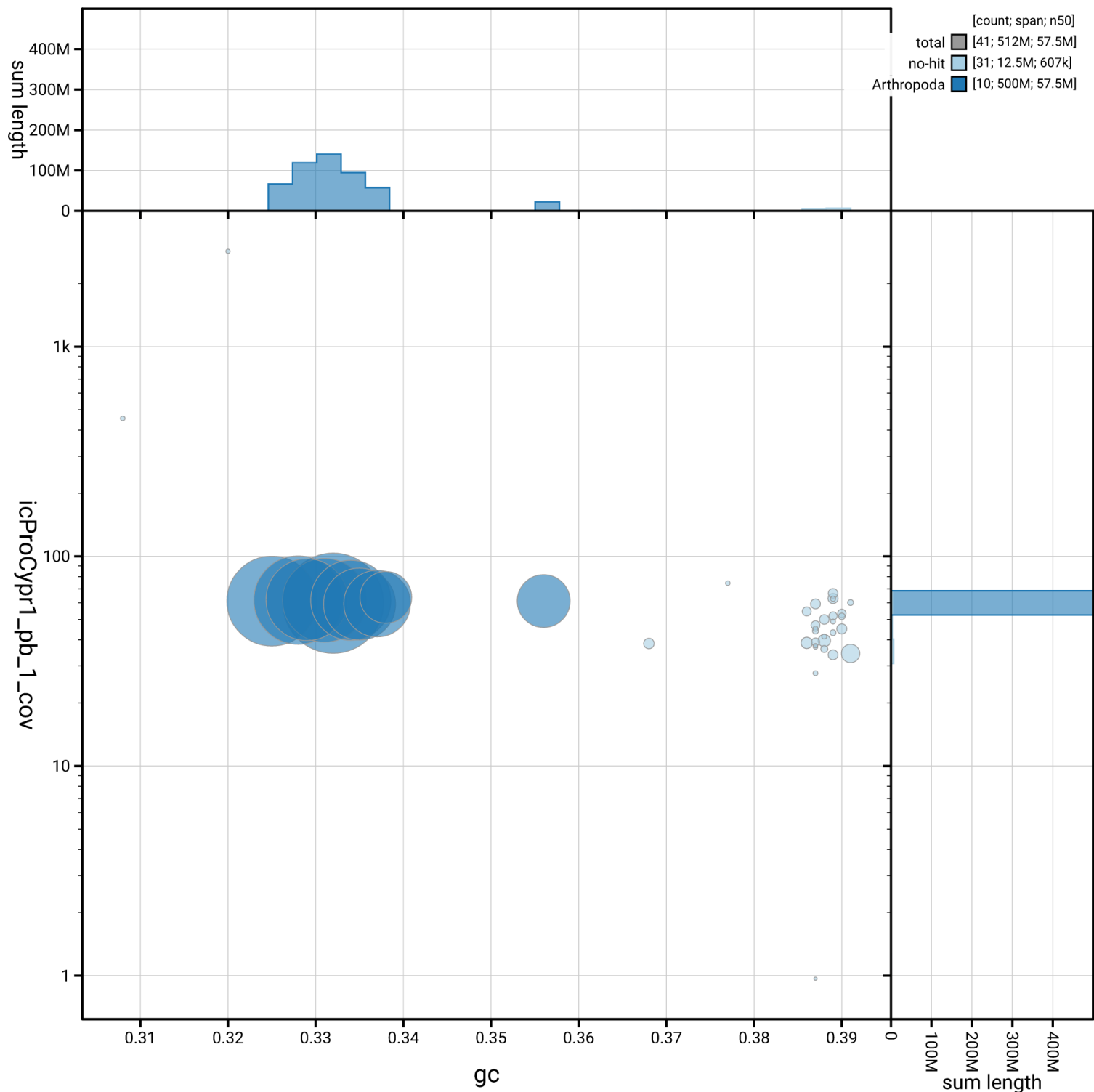
collapsed [\[LINK\]](#)

# K-mer spectra of curated assembly



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

# Post-curation contamination screening



**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	PacBio HiFi	Arima HiC v2
Coverage	61x	27x

# Assembly pipeline

- **hifiasm-hic**
  - |\_ *ver*: 0.25.0-r726
  - |\_ *key param*: --h1
  - |\_ *key param*: --h2
- **purge\_dups**
  - |\_ *ver*: 1.2.5
  - |\_ *key param*: NA
- **YaHS**
  - |\_ *ver*: 1.2a.2
  - |\_ *key param*: NA
- **NBIS/Earth-Biogenome-Project-pilot**
  - |\_ *ver*: 99c8937
  - |\_ *key param*: NA
- **sanger-tol/blobtoolkit**
  - |\_ *ver*: 0.8.0
  - |\_ *key param*: NA
- **Oatk**
  - |\_ *ver*: 1.0
  - |\_ *key param*: -m insecta.fam
  - |\_ *key param*: -c 100

# Curation pipeline

- **sanger-tol/curationpretext**
  - |\_ *ver*: 1.4.1
  - |\_ *key param*: NA
- **sanger-tol/agp-tpf-utils**
  - |\_ *ver*: 1.2.3
  - |\_ *key param*: NA

Submitter: Guilherme B. Dias  
Affiliation: SciLifeLab

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