ERGA Assembly Report
v24.10.15

Tags: ERGA-BGE

TxID	1968893
ToLID	**icProCypr1**
Species	Propomacrus cypriacus
Class	Insecta
Order	Coleoptera

Genome Traits	Expected	Observed
Haploid size (bp)	471,390,309	511,276,245
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 hifiasm in Hi-C mode. The resulting collapsetd *.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	511,276,245
GC %	33.38	33.37
Gaps/Gbp	17.57	17.6
Total gap bp	1,800	1,800
Scaffolds	41	40
Scaffold N50	57,489,177	57,489,177
Scaffold L50	4	4
Scaffold L90	9	9
Contigs	50	49
Contig N50	29,712,000	29,712,000
Contig L50	8	8
Contig L90	17	16
QV	73.1572	73.3452
Kmer compl.	91.4389	91.4387
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)
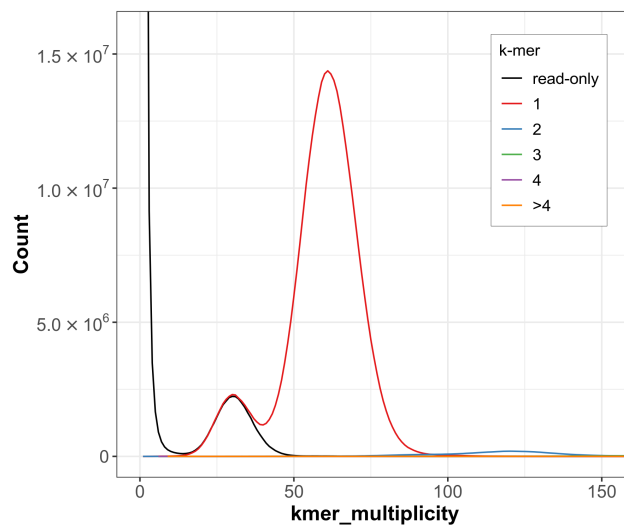
HiC contact map of curated assembly
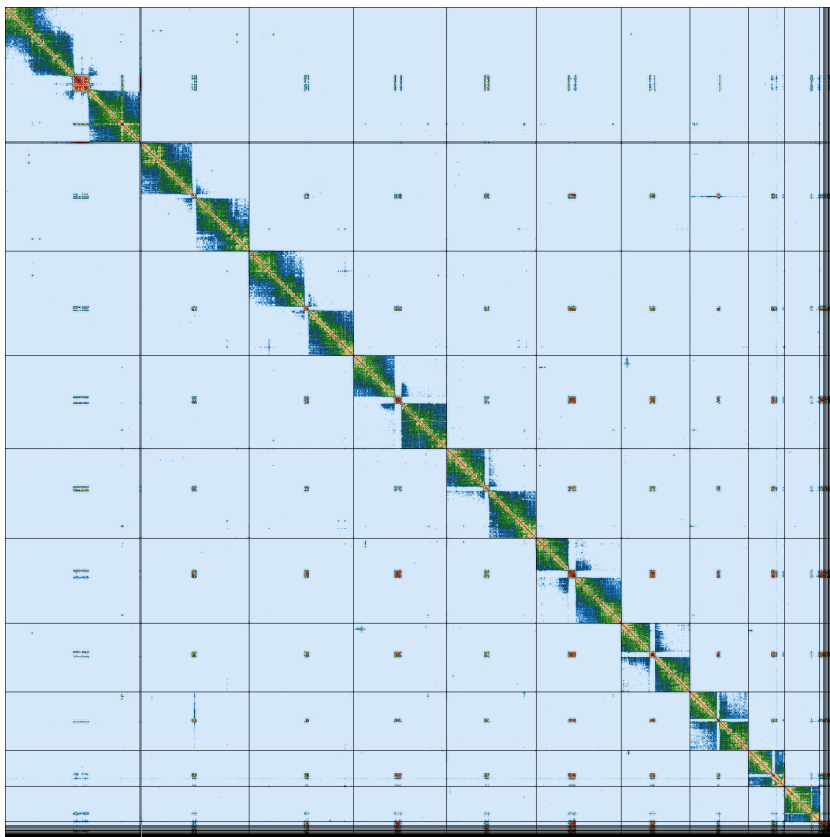
collapsed [LINK]
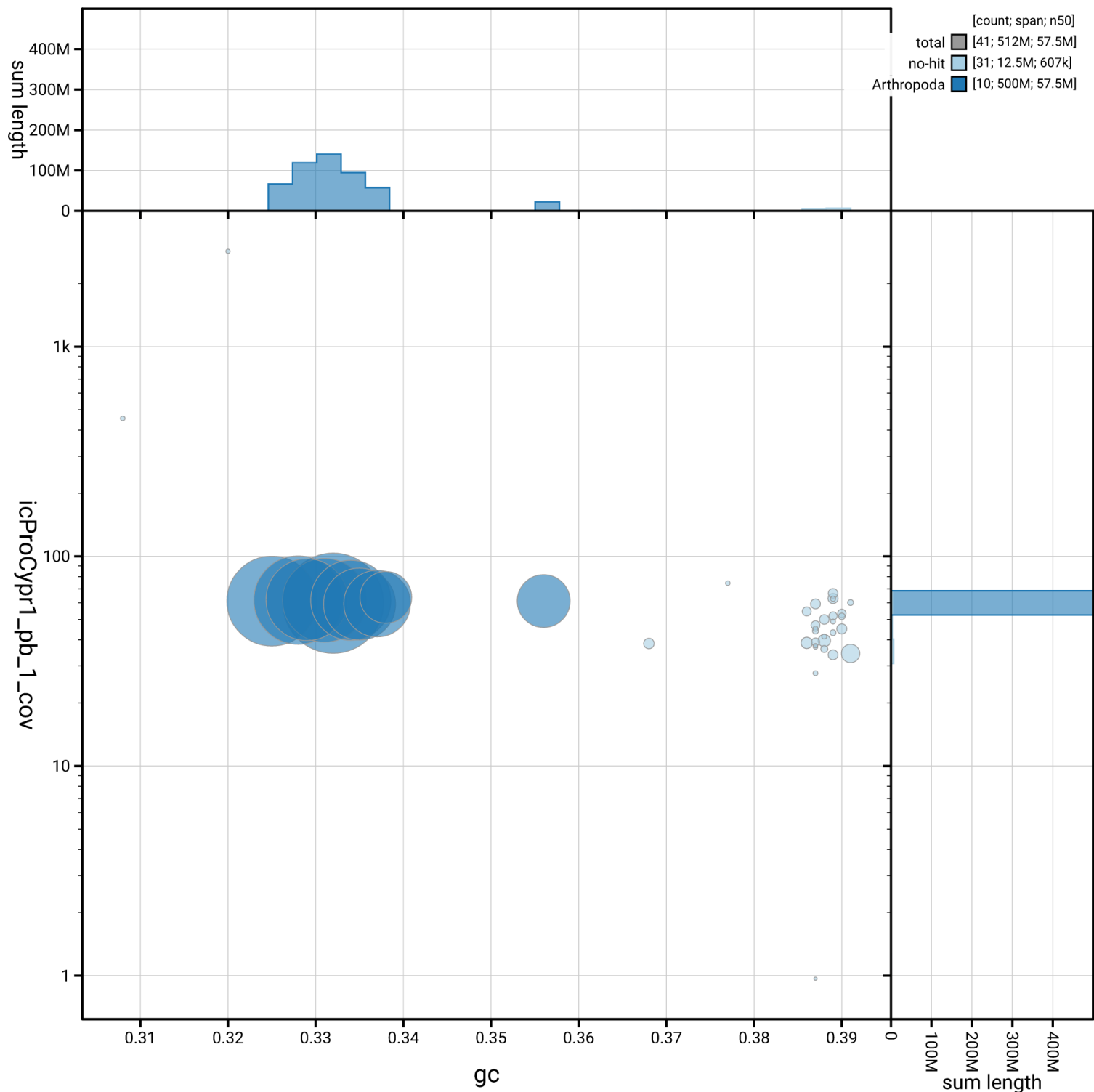
K-mer spectra of curated assembly
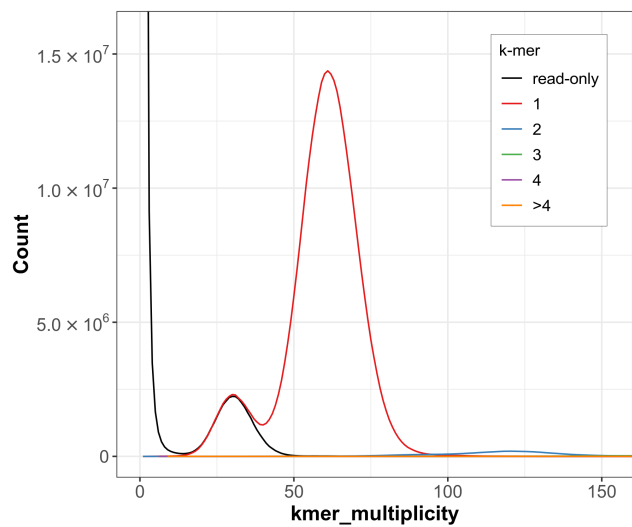
Distribution of k-mer counts per copy
numbers found in asm

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

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