

# ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	446453
ToLID	<b>inOsmFulv5</b>
Species	Osmylus fulvicephalus
Class	Insecta
Order	Neuroptera

Genome Traits	Expected	Observed
Haploid size (bp)	625,527,197	674,762,019
Haploid Number	8 (source: ancestor)	11
Ploidy	2 (source: ancestor)	2
Sample Sex	unknown	unknown

## EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 7.7.Q68

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

- . Observed Haploid Number is different from Expected

### Curator notes

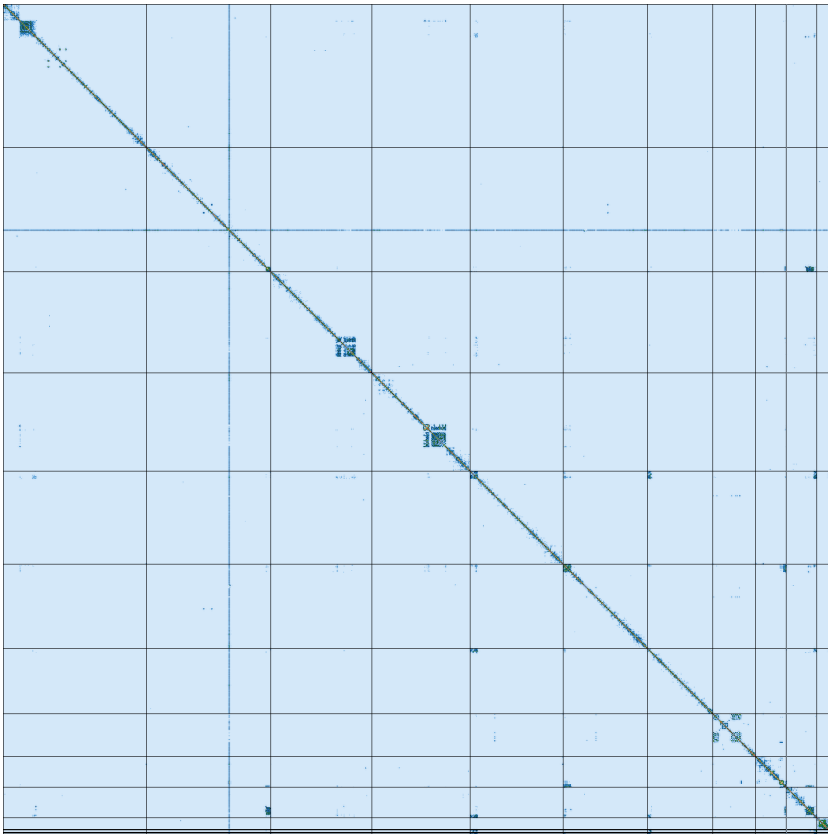
- . Interventions/Gb: 5
- . Contamination notes: "No contaminations were detected with FCS-GX."
- . Other observations: "PacBio reads were subsampled to 60X. Reads were assembled with hifiiasm (yield: 488M, N50: 49.1Mb, 176 contigs). FCS-GX detected no contaminations. Purge\_dups was run on the contigs but only the the dups.bed file was used in the manual curation step, as it removed too much sequence and telomere motifs. Due to the low HiC quality (2.8M cis-read pairs >40Kb) the scaffolding was manually done in the first manual curation round. In this step the information from tiara, mitohifi, blobtools and purge\_dups was used and 110 contigs (15M) were removed. SUPER\_9 and SUPER\_11 have a very low coverage profile - roughly half coverage. A synteny analysis with GCA\_958496175 and GCA\_958496155 suggests that SUPER\_9 could be the X chromosome."

## Quality metrics table

Metrics	Pre-curation pri	Curated pri
Total bp	666,151,682	674,762,019
GC %	36.31	36.29
Gaps/Gbp	90.07	48.91
Total gap bp	12,000	6,600
Scaffolds	123	27
Scaffold N50	104,575,600	79,514,024
Scaffold L50	3	4
Scaffold L90	16	8
Contigs	183	60
Contig N50	22,977,000	51,542,635
Contig L50	8	5
Contig L90	43	16
QV	70.6914	68.5933
Kmer compl.	90.8782	90.828
BUSCO sing.	93.3%	94.4%
BUSCO dupl.	1.6%	0.4%
BUSCO frag.	1.4%	1.4%
BUSCO miss.	3.7%	3.8%

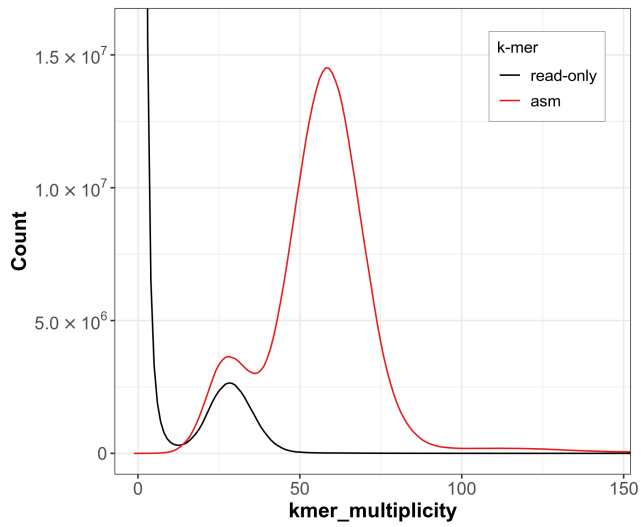
BUSCO: 5.8.3 (euk\_genome\_min, miniprot) / Lineage: endopterygota\_odb12 (genomes:76, BUSCOs:3754)

# HiC contact map of curated assembly

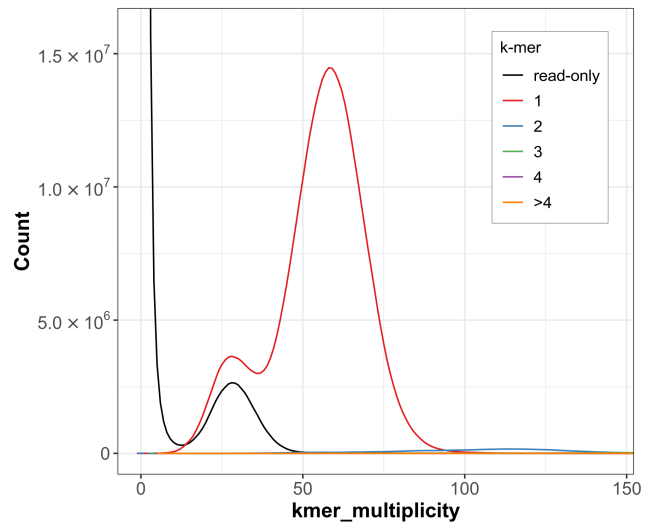


pri [\[LINK\]](#)

# K-mer spectra of curated assembly

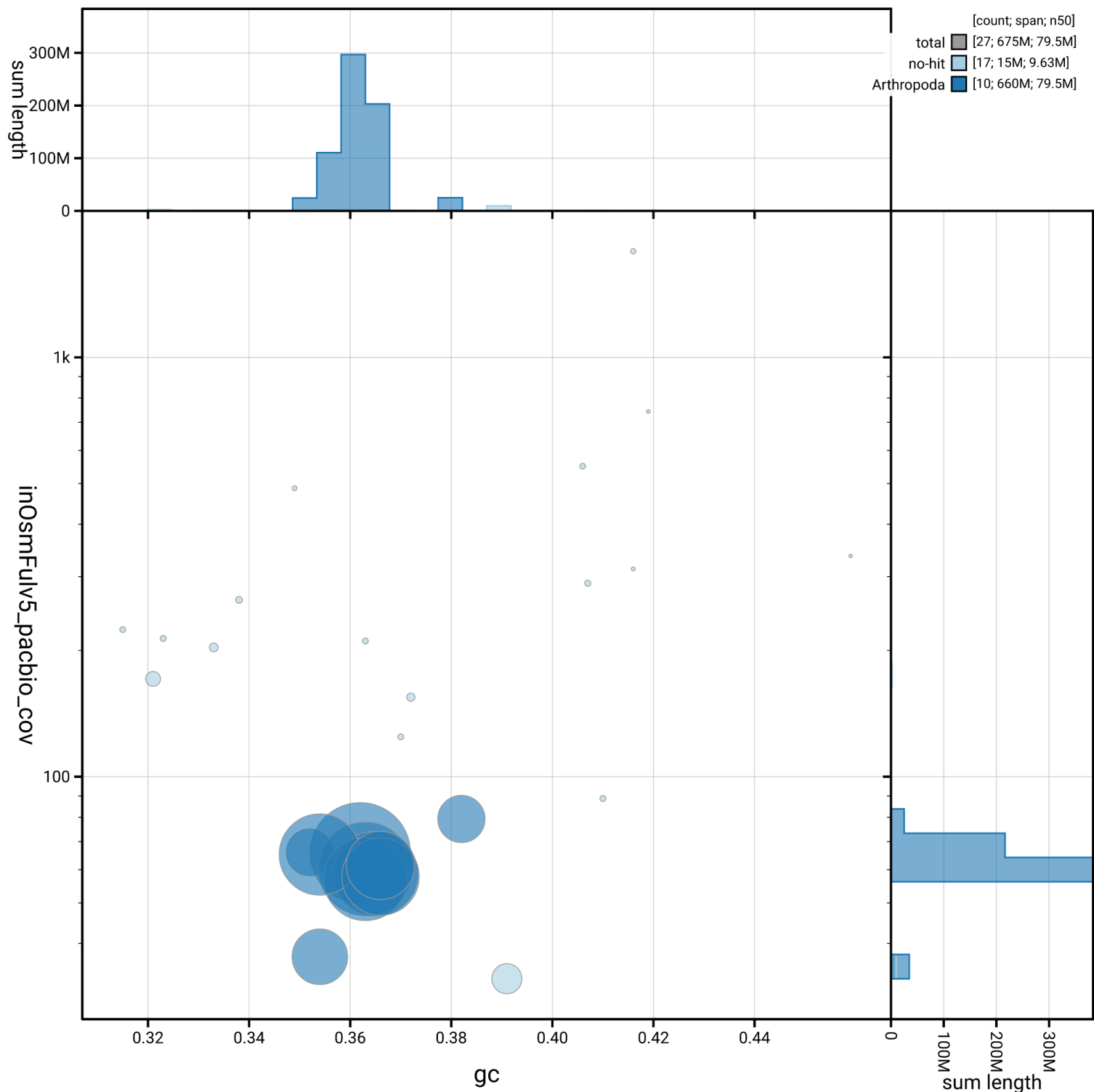


Distribution of k-mer counts coloured by their presence in reads/assemblies



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

# 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	HiFi	HiC
Coverage	164x	49x

# Assembly pipeline

- **Hifiasm**
  - |\_ *ver*: 0.25.0-r726
  - |\_ *key param*: 13
- **purge\_dups**
  - |\_ *ver*: 1.2.6
  - |\_ *key param*: NA

# Curation pipeline

- **GRIT\_Rapid**
  - |\_ *ver*: 1a3d79a8
  - |\_ *key param*: NA
- **HiGlass**
  - |\_ *ver*: 0.10.4
  - |\_ *key param*: NA

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