

ERGA Assembly Report

v24.04.03_beta

Tags: ERGA-BGE

TxID	420550
ToLID	idCulPerx1
Species	Culex perexiguus
Class	Insecta
Order	Diptera

Genome Traits	Expected	Observed
Haploid size (bp)	353,856,597	436,181,468
Haploid Number	3 (source: ancestor)	3
Ploidy	3 (source: ancestor)	2
Sample Sex	XX	XX

EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 5.8.Q55

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

- . Observed Haploid size (bp) has >20% difference with Expected
- . Observed Ploidy is different from Expected
- . Assembly length loss > 3% for pri
- . More than 1000 gaps/Gbp for pri

Curator notes

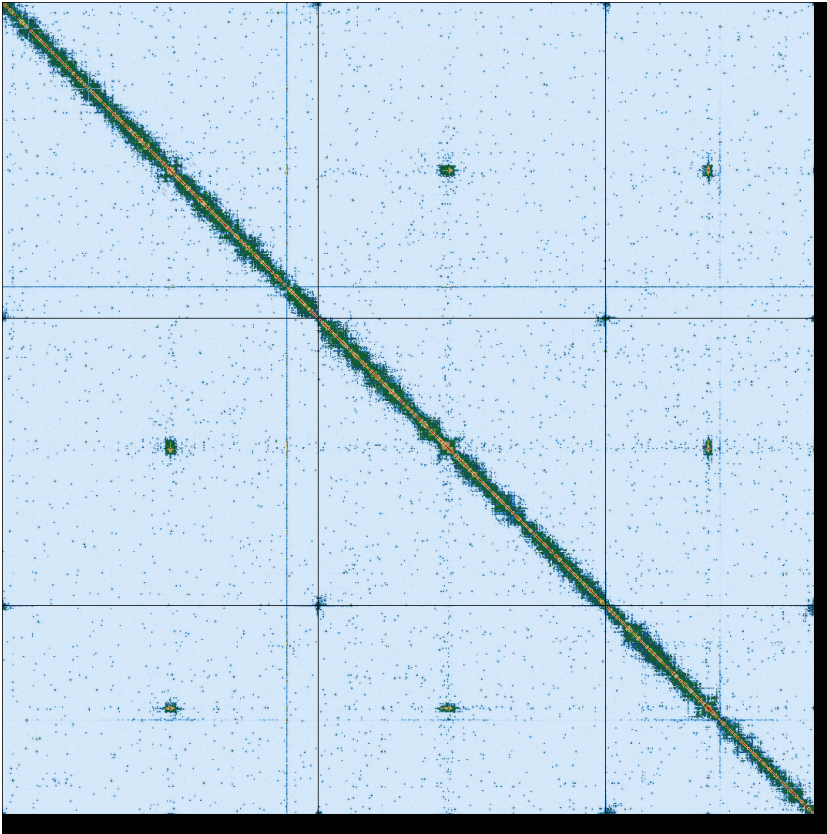
- . Interventions/Gb: 651
- . Contamination notes: "Total length of scaffolds removed: 84,166 (0.0 %); Scaffolds removed: 3 (0.4 %); Largest scaffold removed: (42,305); FCS-GX contaminant species (number of scaffolds; total length of scaffolds): None; Mitochondrion (3; 84,166)"
- . Other observations: "This is the second version of this assembly after feedback from the initial EAR. Chromosomes named by size; PacBio library was ULI hence lower contig N50; Hi-C from a different individual, so assembly is not Hi-C phased"

Quality metrics table

Metrics	Pre-curation pri	Curated pri
Total bp	477,427,365	436,181,468
GC %	38.57	38.62
Gaps/Gbp	3,248.66	3,305.96
Total gap bp	310,200	288,400
Scaffolds	764	474
Scaffold N50	114,754,111	150,416,927
Scaffold L50	2	2
Scaffold L90	4	3
Contigs	2,315	1,916
Contig N50	448,257	473,114
Contig L50	325	289
Contig L90	1,159	931
QV	55.1	55.3
Kmer compl.	99.00	99.16
BUSCO sing.	91.6%	95.7%
BUSCO dupl.	7.7%	3.0%
BUSCO frag.	0.4%	0.4%
BUSCO miss.	0.3%	0.9%

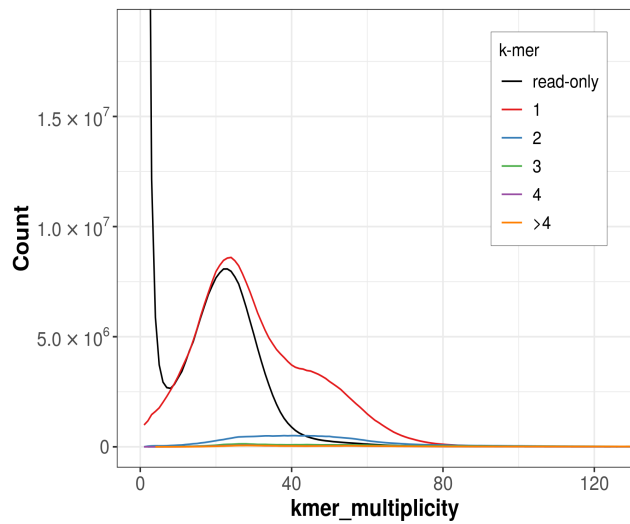
BUSCO 5.3.0 Lineage: insecta_odb10 (genomes:75, BUSCOs:1367)

HiC contact map of curated assembly

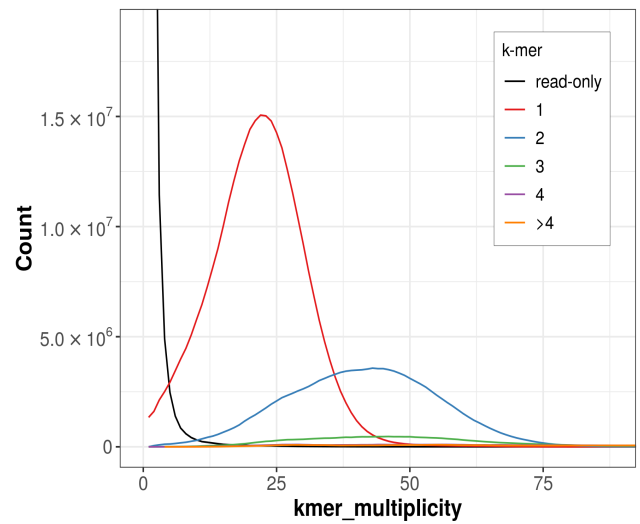


pri [\[LINK\]](#)

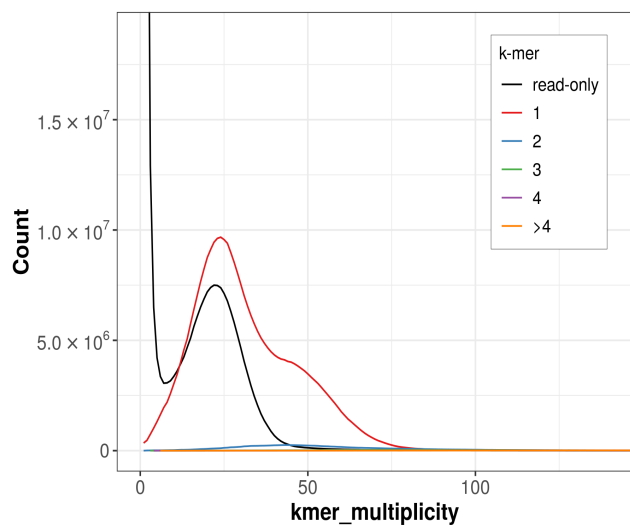
K-mer spectra of curated assembly



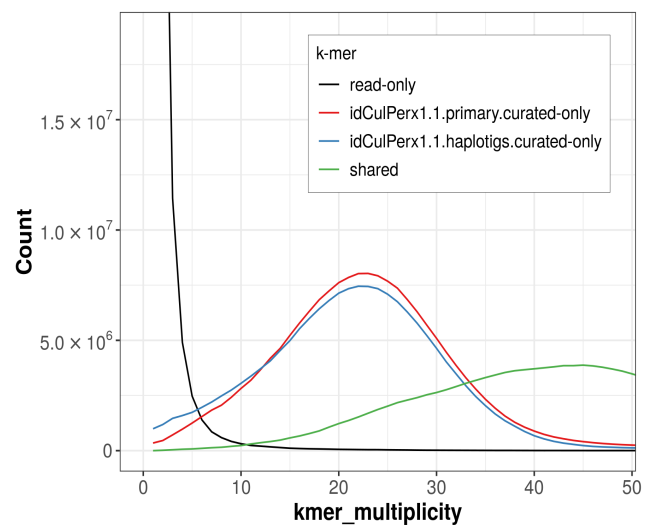
Distribution of k-mer counts per copy numbers found in **haplotigs** (hapl.)



Distribution of k-mer counts per copy numbers found in **asm** (dipl.)

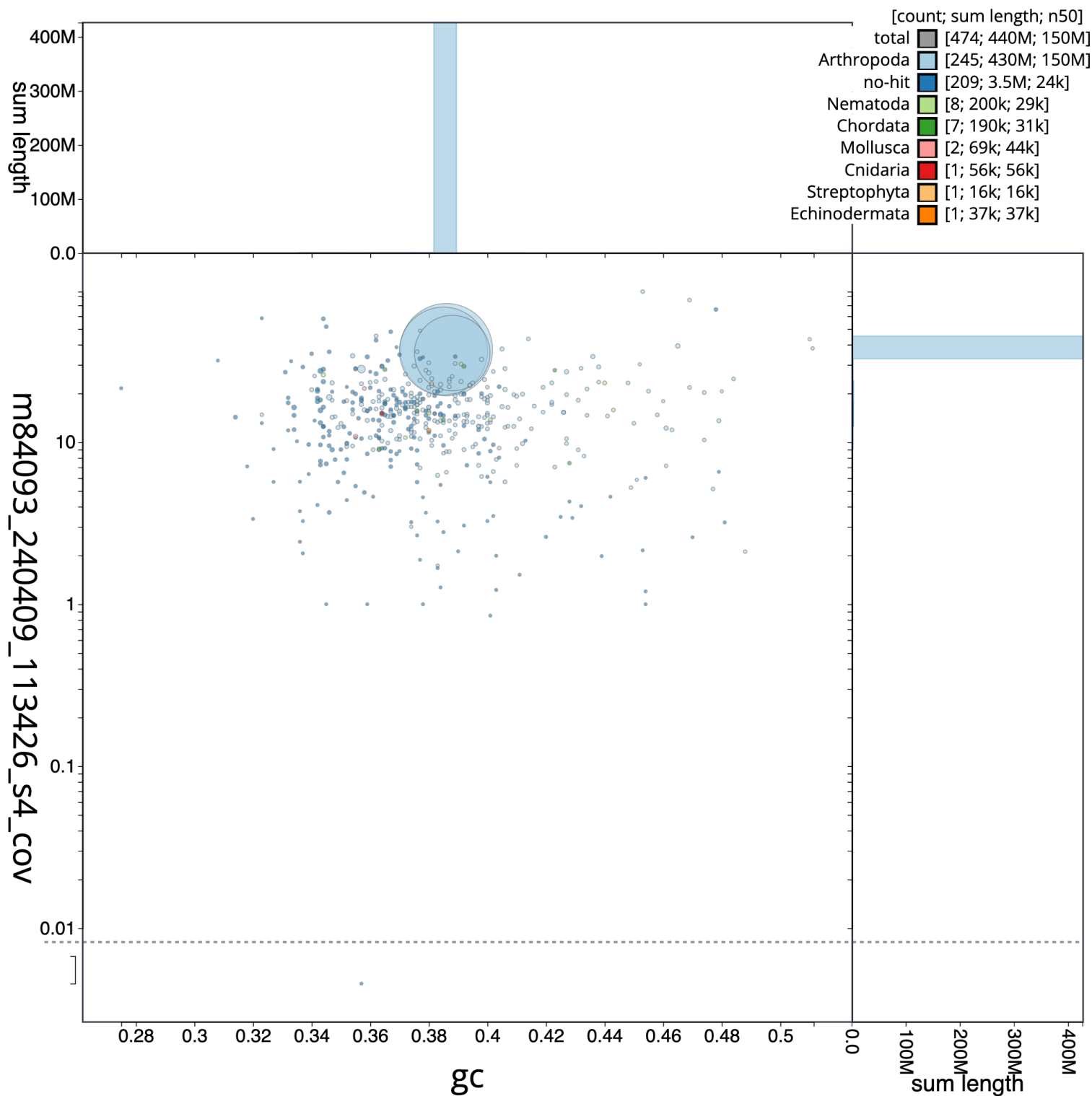


Distribution of k-mer counts per copy numbers found in (hapl.)



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

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 v2
Coverage	49x	187x

Assembly pipeline

- **hifiasm**
 - |_ *ver*: 0.19.8-r603
 - |_ *key param*: --primary
- **purge_dups**
 - |_ *ver*: 1.2.5
 - |_ *key param*: -e
- **yahs**
 - |_ *ver*: 1.2a.2
 - |_ *key param*: NA

Curation pipeline

- **hifiasm**
 - |_ *ver*: 0.19.8-r603
 - |_ *key param*: --primary
- **purge_dups**
 - |_ *ver*: 1.2.5
 - |_ *key param*: -e
- **yahs**
 - |_ *ver*: 1.2a.2
 - |_ *key param*: NA
- **TreeVal**
 - |_ *ver*: 1.1
 - |_ *key param*: NA

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Date and time: 2024-08-16 17:44:05 CEST