

# ERGA Assembly Report

v24.04.03\_beta

Tags: ERGA-BGE

TxID	561267
ToLID	<b>idCulThei1</b>
Species	Culex theileri
Class	Insecta
Order	Diptera

Genome Traits	Expected	Observed
Haploid size (bp)	735,857,783	832,043,836
Haploid Number	3 (source: ancestor)	3
Ploidy	3 (source: ancestor)	2
Sample Sex	F	unknown

## EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 5.8.Q56

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

- . Observed Ploidy is different from Expected
- . Observed sex is different from Sample sex
- . Assembly length loss > 3% for pri
- . More than 1000 gaps/Gbp for pri

### Curator notes

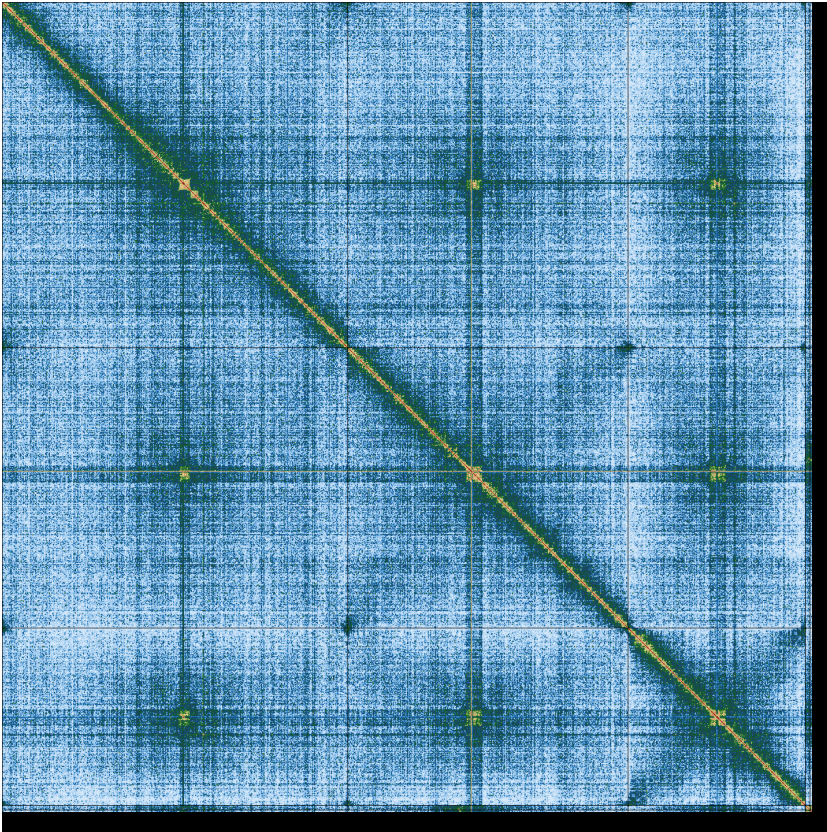
. Interventions/Gb: 440  
. Contamination notes: "Total length of scaffolds removed: 434,537 (0.1 %);Scaffolds removed: 16 (2.0 %);Largest scaffold removed: (64,299);FCS-GX contaminant species (number of scaffolds; total length of scaffolds):Acinetobacter guillouiae, g-proteobacteria (15; 419,725);Mitochondrion (1; 14,812)"  
. Other observations: "Hi-C mapping + YaHS scaffolding was run twice. PacBio is from a ULI library and Hi-C is from a different individual (idCulThei2). We did not identify the sex chromosome(s) as sequence data from the heterogametic sex was not available and homology is unreliable for sex chromosome identification in Diptera due to frequent sex chromosome turnover (<https://doi.org/10.1371/journal.pbio.1002078>)."

# Quality metrics table

Metrics	Pre-curation pri	Curated pri
Total bp	865,191,608	832,043,836
GC %	39.12	39.13
Gaps/Gbp	2,115.14	2,397.71
Total gap bp	366,000	399,200
Scaffolds	816	708
Scaffold N50	54,461,784	280,593,608
Scaffold L50	7	2
Scaffold L90	20	3
Contigs	2,646	2,703
Contig N50	788,000	770,000
Contig L50	329	317
Contig L90	1,145	1,115
QV	56.4	56.3
Kmer compl.	99.24	99.38
BUSCO sing.	95.0%	95.8%
BUSCO dupl.	4.0%	2.3%
BUSCO frag.	0.4%	0.6%
BUSCO miss.	0.6%	1.3%

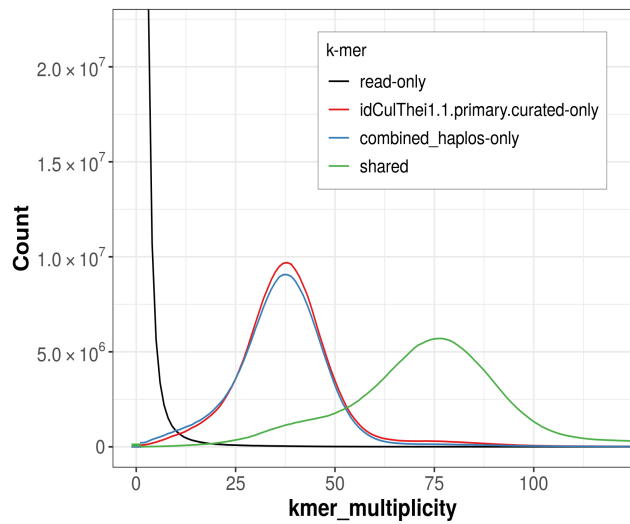
BUSCO 5.3.0 Lineage: insecta\_odb10 (genomes:75, BUSCOs:1367)

# HiC contact map of curated assembly

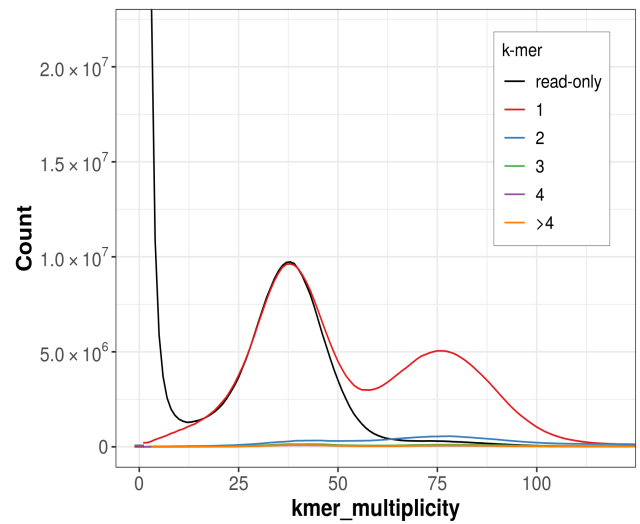


pri [\[LINK\]](#)

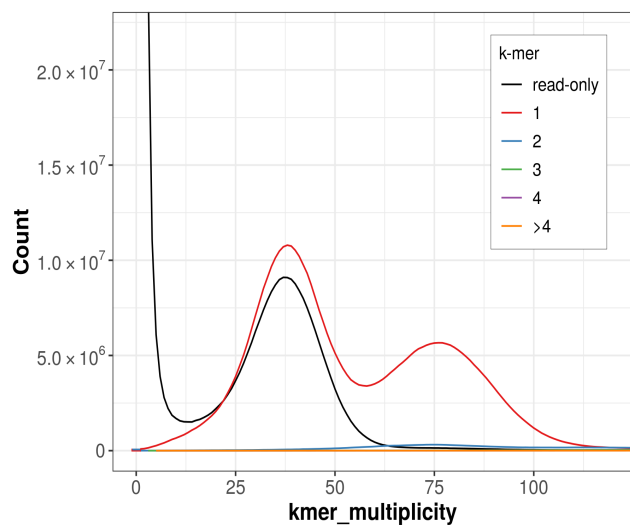
# K-mer spectra of curated assembly



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

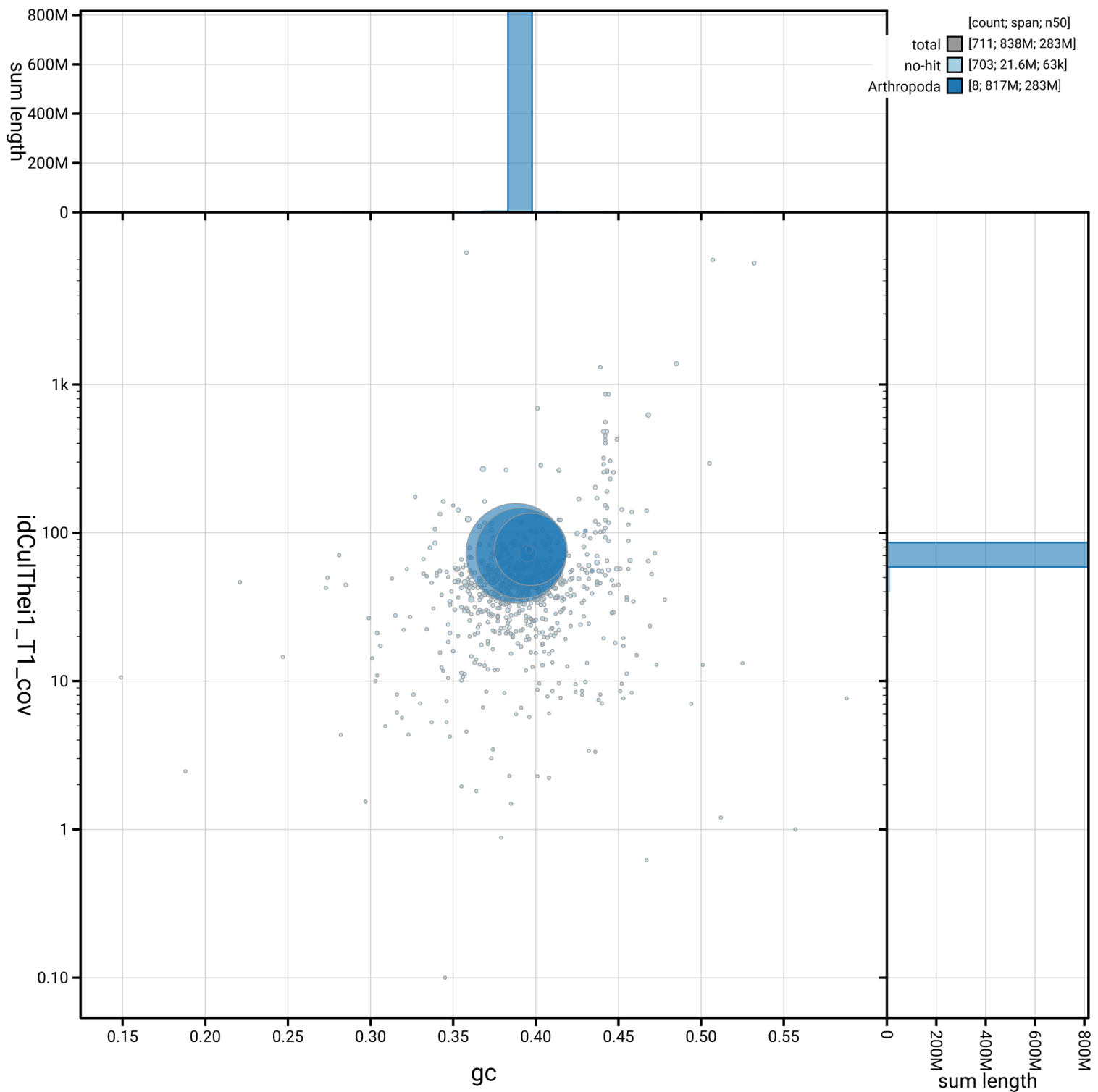


Distribution of k-mer counts per copy numbers found in asm



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 v2
Coverage	78x	140x

# 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*: 1.1.1
  - |\_ *key param*: NA

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