ERGA Assembly Report

v24.09.10

Tags: ATLASea[INVALID TAG]

TxID	6114
ToLID	**jaCalPara1.1**
Species	Calliactis parasitica
Class	Anthozoa
Order	Actiniaria

Genome Traits	Expected	Observed
Haploid size (bp)	303,986,920	293,237,748
Haploid Number	6 (source: ancestor)	8
Ploidy	2 (source: ancestor)	2
Sample Sex	Unknown	Unknown

EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 7.7.Q65

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

. Observed Haploid Number is different from Expected

. Kmer completeness value is less than 90 for collapsed

Curator notes

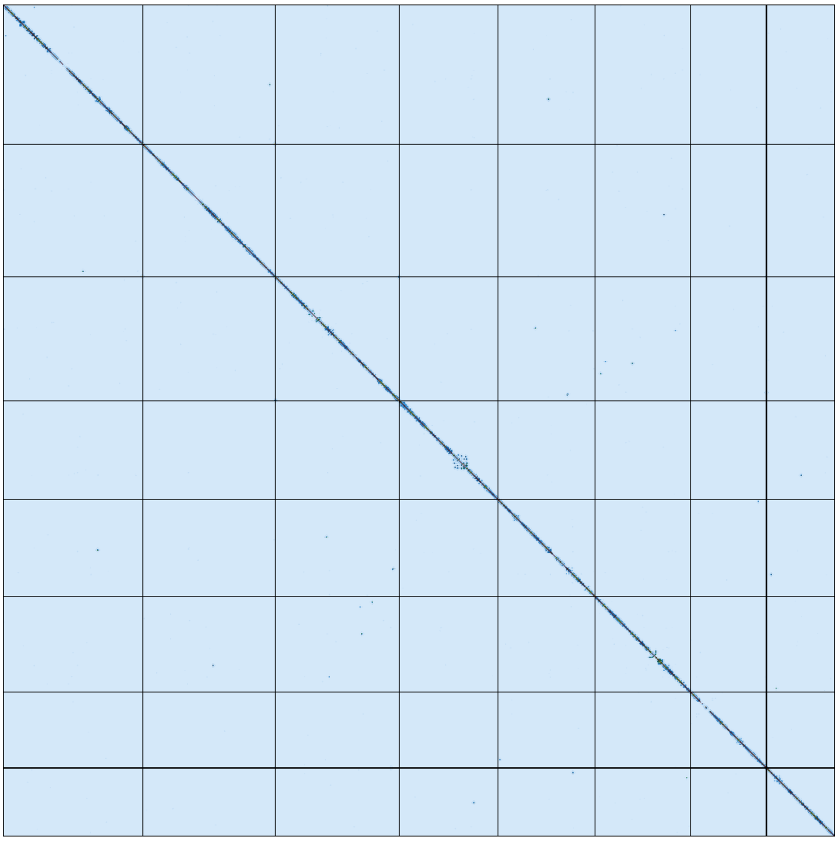
. Interventions/Gb: 57
. Contamination notes: "Only one contig of 24Kb was detected as viral and removed "
. Other observations: "Few modifications, contigs were already mostly chromosome scale. The structure of chromosome 8 is uncertain. Two gaps are located close to the middle, delineating two large regions that could be part of the same chromosome (in which case, the orientation of these two chromosome arms is uncertain) or could represent two different chromosomes. "

Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	294,447,948	293,237,748
GC %	35.82	35.81
Gaps/Gbp	20.38	68.2
Total gap bp	600	3,400
Scaffolds	24	13
Scaffold N50	21,596,100	34,715,374
Scaffold L50	6	4
Scaffold L90	12	7
Contigs	30	33
Contig N50	19,922,692	17,418,000
Contig L50	7	7
Contig L90	15	15
QV	49.8672	65.0817
Kmer compl.	78.4882	78.5996
BUSCO sing.	91.0%	91.1%
BUSCO dupl.	0.4%	0.3%
BUSCO frag.	1.7%	1.7%
BUSCO miss.	6.9%	6.9%

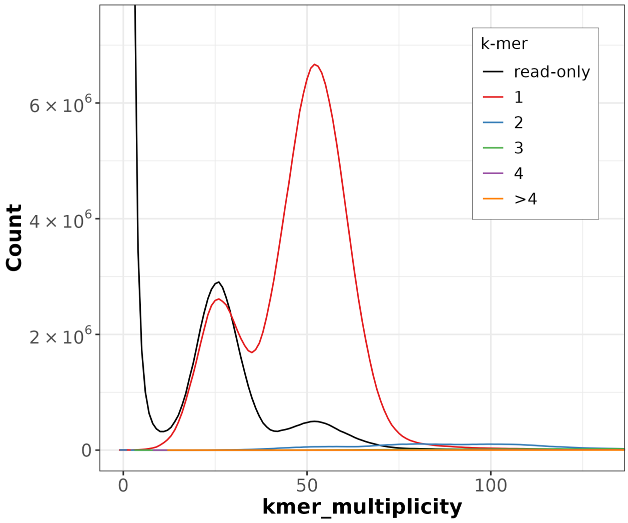
BUSCO 5.4.3 Lineage: metazoa_odb10 (genomes:65, BUSCOs:954)

HiC contact map of curated assembly

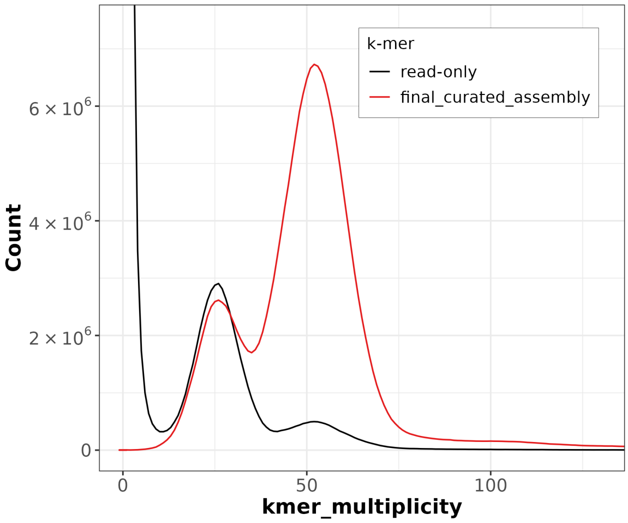


collapsed [LINK]

K-mer spectra of curated assembly

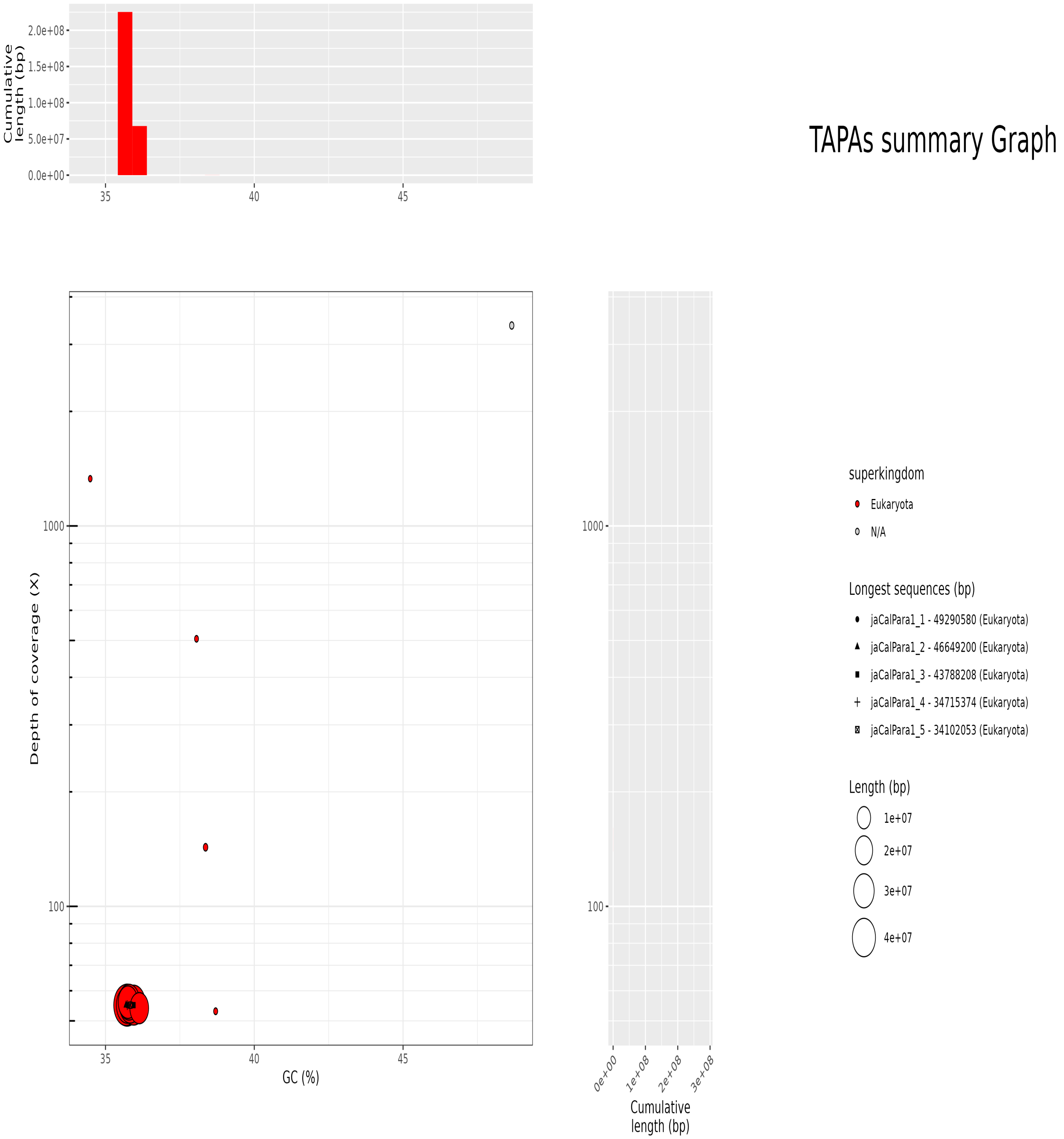


Distribution of k-mer counts per copy numbers found in asm



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

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 (4-enz)
Coverage	52	140

Assembly pipeline

- **Hifiasm**
    - |_ *ver:* 0.19.5-r593
    - |_ *key param:* NA
- **purge_dups**
    - |_ *ver:* 1.2.5
    - |_ *key param:* NA
- **YaHS**
    - |_ *ver:* 1.2
    - |_ *key param:* NA

Curation pipeline

- **PretextMap**
    - |_ *ver:* 0.1.9
    - |_ *key param:* NA
- **PretextView**
    - |_ *ver:* 0.2.5
    - |_ *key param:* NA

Submitter: Jean-Marc Aury
Affiliation: Genoscope

Date and time: 2024-11-07 20:08:35 CET