

ERGA Assembly Report

v24.04.03_beta

Tags: ATLASea [INVALID TAG]

TxID	12959
ToLID	odAxiPoly1.1
Species	Axinella polypoides
Class	Demospongiae
Order	Axinellida

Genome Traits	Expected	Observed
Haploid size (bp)	134,596,807	141,836,590
Haploid Number	5 (source: ancestor)	24
Ploidy	2 (source: ancestor)	2
Sample Sex	Unknown	unknown

EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 5.6.Q55

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
- . Assembly length loss > 3% for collapsed
- . More than 1000 gaps/Gbp for collapsed

Curator notes

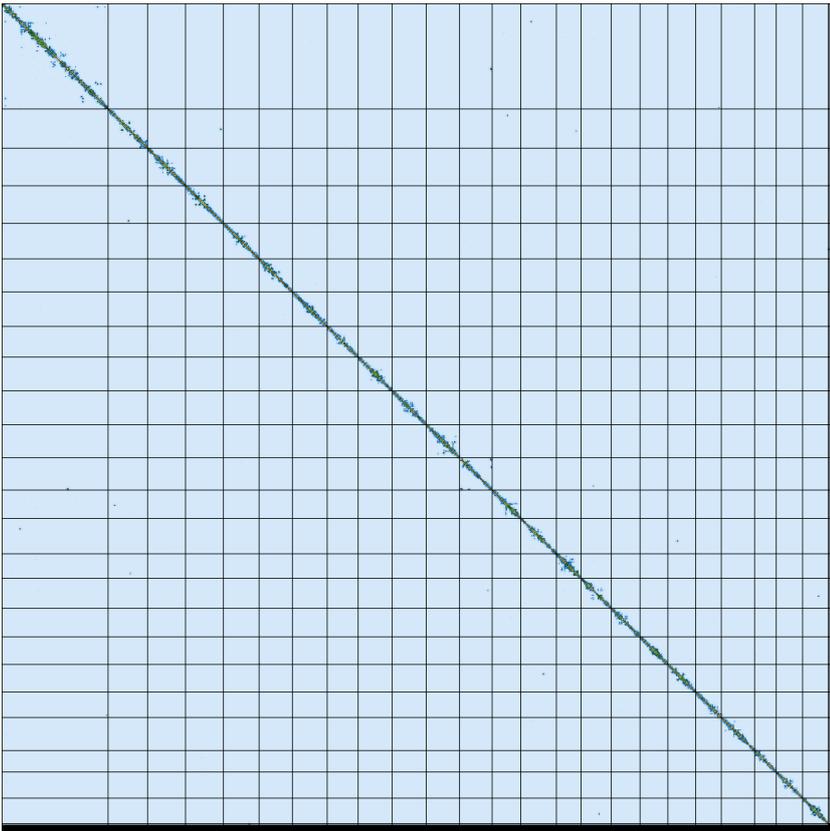
- . Interventions/Gb: 4
- . Contamination notes: "the sample was contaminated by a lot of bacteria and one amphipoda. There were two rounds of decontamination, one after contig assembly and one after scaffolding. "
- . Other observations: "lot of contigs were tagged as haplotigs >"

Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	151,026,055	141,836,590
GC %	44.16	44.19
Gaps/Gbp	2,026.14	2,270.22
Total gap bp	30,600	37,300
Scaffolds	174	94
Scaffold N50	5,723,994	5,695,433
Scaffold L50	11	10
Scaffold L90	23	21
Contigs	480	416
Contig N50	753,704	665,306
Contig L50	46	52
Contig L90	206	205
QV	54.8181	55.6163
Kmer compl.	53.4643	50.7243
BUSCO sing.	89.4%	90.6%
BUSCO dupl.	2.4%	1.2%
BUSCO frag.	3.9%	3.9%
BUSCO miss.	4.3%	4.3%

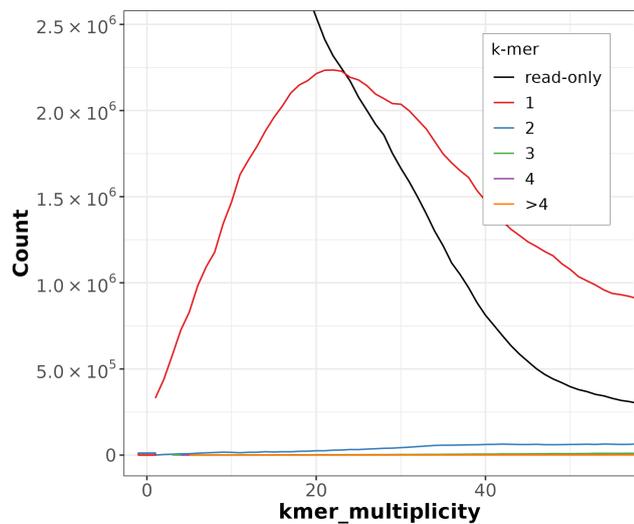
BUSCO 5.4.3 Lineage: eukaryota_odb10 (genomes:70, BUSCOs:255)

HiC contact map of curated assembly

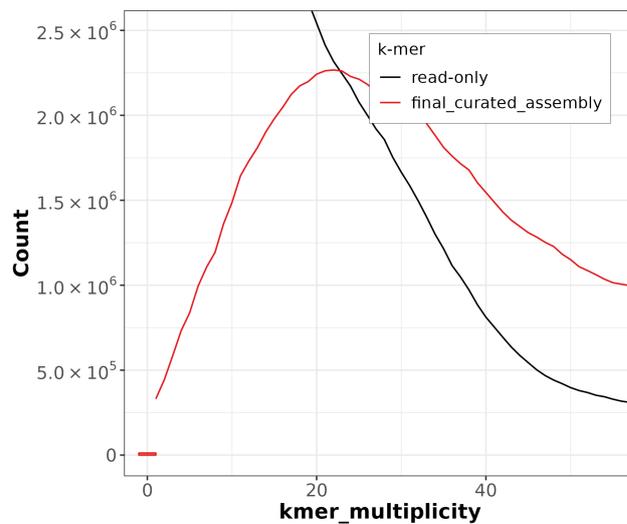


collapsed [\[LINK\]](#)

K-mer spectra of curated assembly

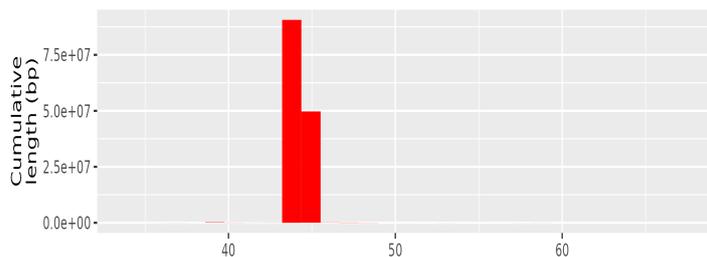


Distribution of k-mer counts per copy numbers found in asm

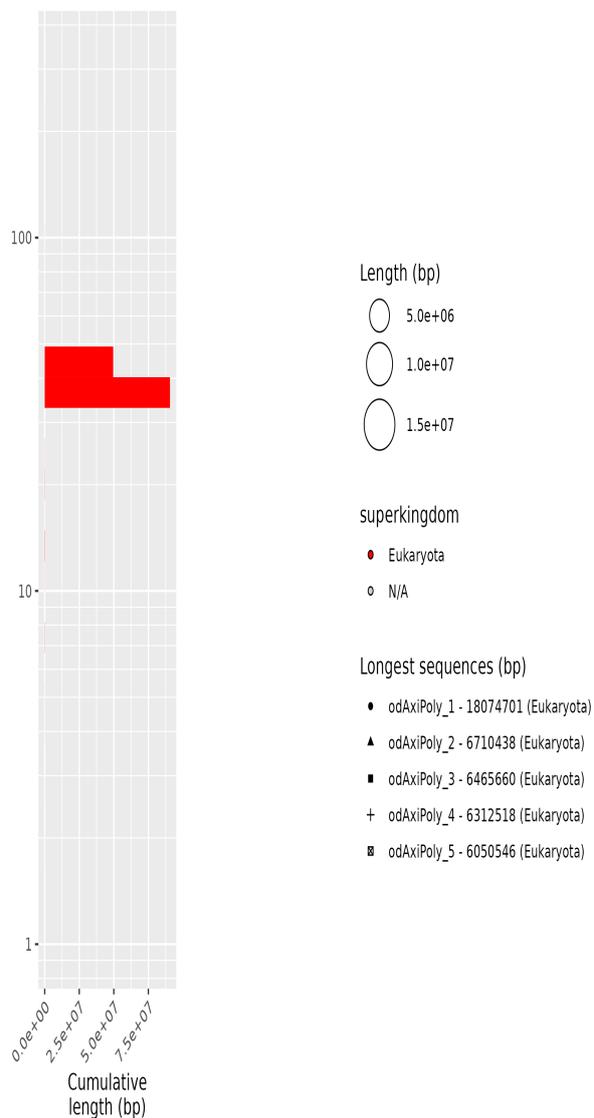
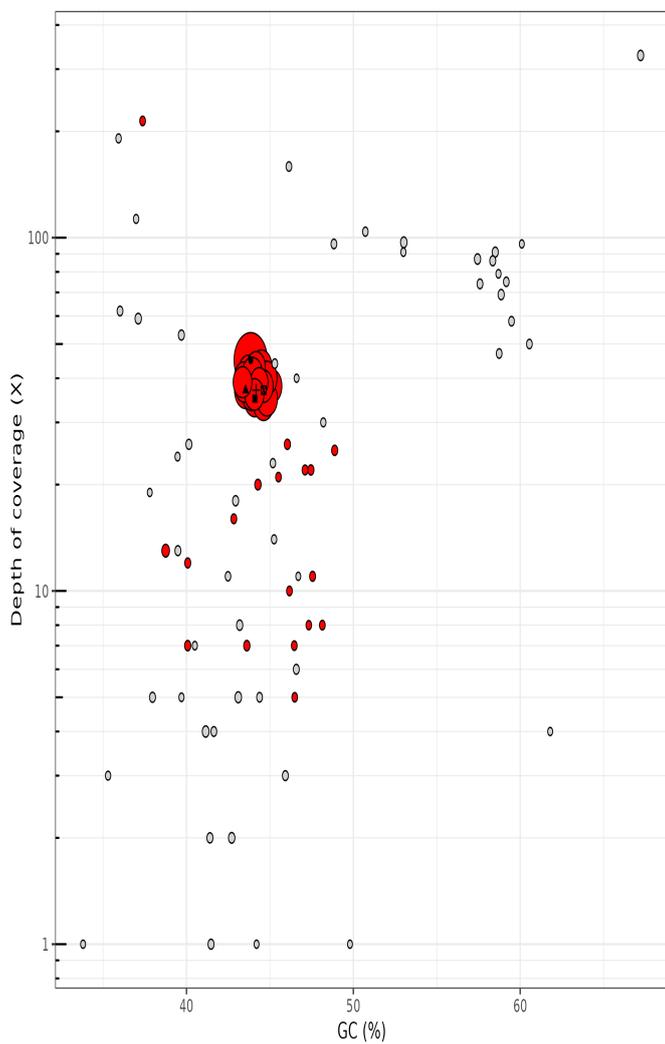


Distribution of k-mer counts coloured by their presence in reads/assemblies

Post-curation contamination screening



TAPAs summary Graph



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	95	390

Assembly pipeline

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

Curation 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

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