ERGA Assembly Report
v24.10.15

Tags: ATLASea[INVALID TAG]

TxID	3254613
ToLID	**ehActFlam1**
Species	Actinopyga flammea
Class	Holothuroidea
Order	Aspidochirotida

Genome Traits	Expected	Observed
Haploid size (bp)	1,389,527,578	1,456,933,855
Haploid Number	21 (source: ancestor)	24
Ploidy	2 (source: ancestor)	2
Sample Sex	Unknown	Unknown

EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 7.7.Q51

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

. Observed Haploid Number is different from Expected

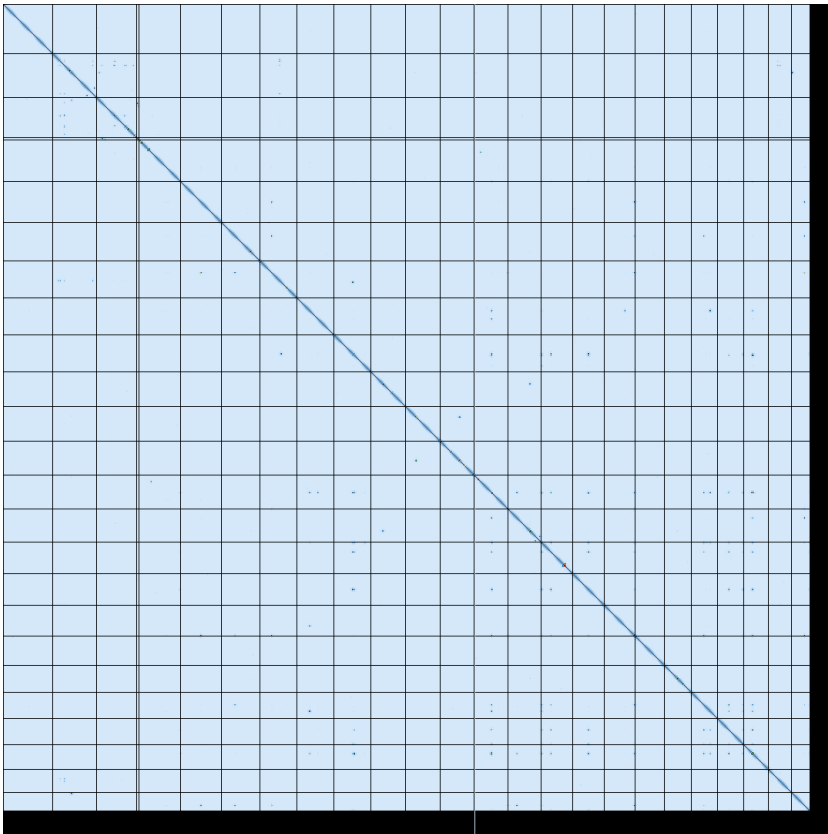. Kmer completeness value is less than 90 for collapsed

Curator notes

. Interventions/Gb: 35
. Contamination notes: ""
. Other observations: "The assembly of Actinopyga flammea (ehActFlam1) is based on 46X PacBio data and 162X Arima Hi-C data generated as part of the ATLASea programme (https://www.atlasea.fr). The assembly process included the following steps: initial PacBio assembly generation with Hifiasm, removal of contaminant sequences using Context, removal of haplotypic duplications using purge_dups, and Hi-C-based scaffolding with YaHS. In total, 12 contigs were identified as contaminants (bacterial, archaeal, or viral), totaling 1.828 Mb (with the largest being 0.912 Mb). Additionally, 273 regions totaling 75.36 Mb (with the largest being 3.052 Mb) were identified as haplotypic duplications and removed. Mitochondrial genome was assembled using OATK. During manual curation, 12 haplotypic regions were removed, totaling 12,96Mb (with the largest being 2.70Mb). Chromosome-scale scaffolds confirmed by Hi-C data were named in order of size. "

Quality metrics table

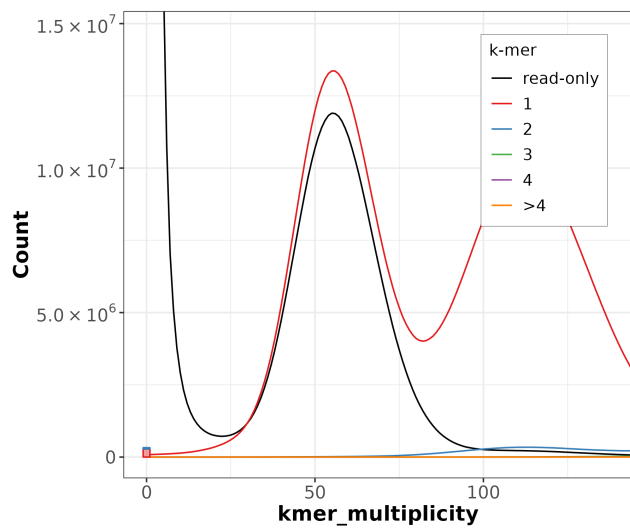| Metrics	Pre-curation collapsed	Curated collapsed
Total bp	1,470,030,140	1,456,933,855
GC %	40.27	40.27
Gaps/Gbp	185.03	194.24
Total gap bp	27,200	31,200
Scaffolds	556	516
Scaffold N50	59,097,810	60,457,396
Scaffold L50	11	11
Scaffold L90	23	22
Contigs	828	799
Contig N50	12,950,000	12,950,000
Contig L50	34	33
Contig L90	111	109
QV	51.4232	51.4409
Kmer compl.	72.6483	72.2119
BUSCO sing.	95.1%	96.7%
BUSCO dupl.	2.4%	0.7%
BUSCO frag.	1.5%	1.5%
BUSCO miss.	1.0%	1.0%

BUSCO: 6.0.0 (euk_genome_min, miniprot) / Lineage: metazoa_odb12 (genomes:206, BUSCOs:672)
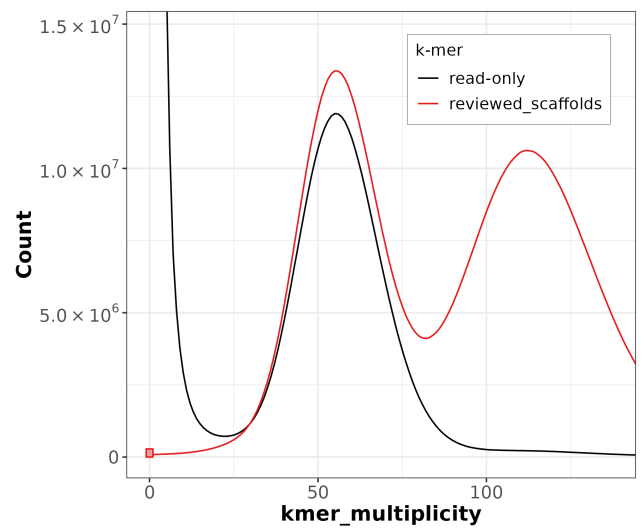
HiC contact map of curated assembly

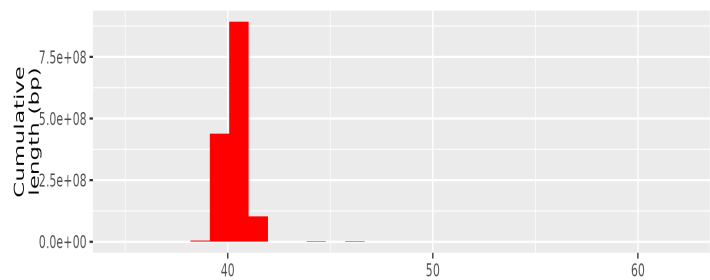**collapsed** [LINK]

K-mer spectra of curated assembly

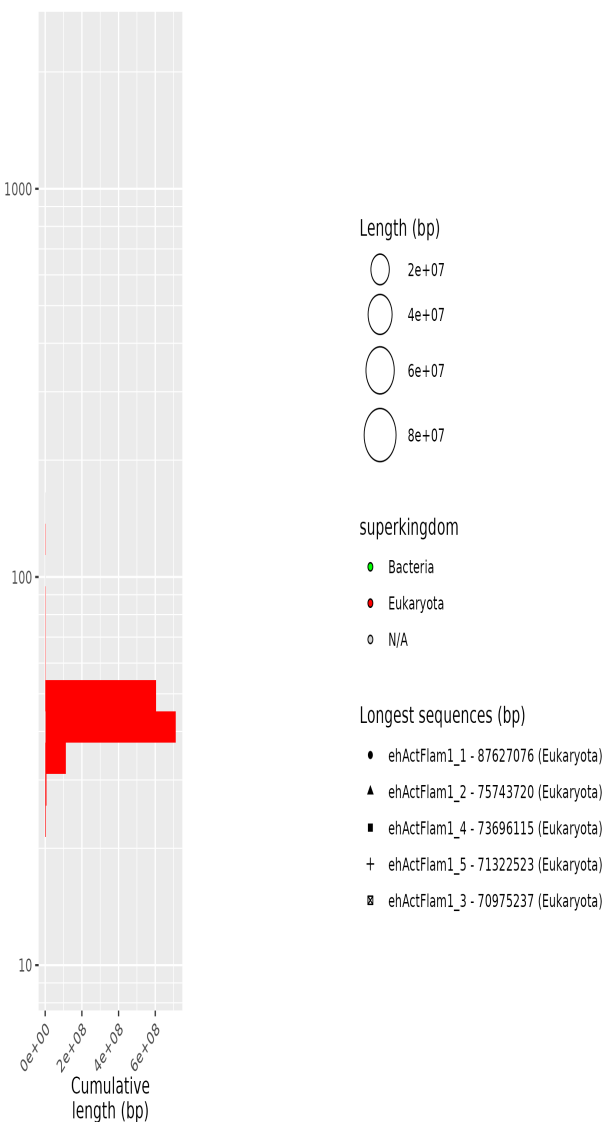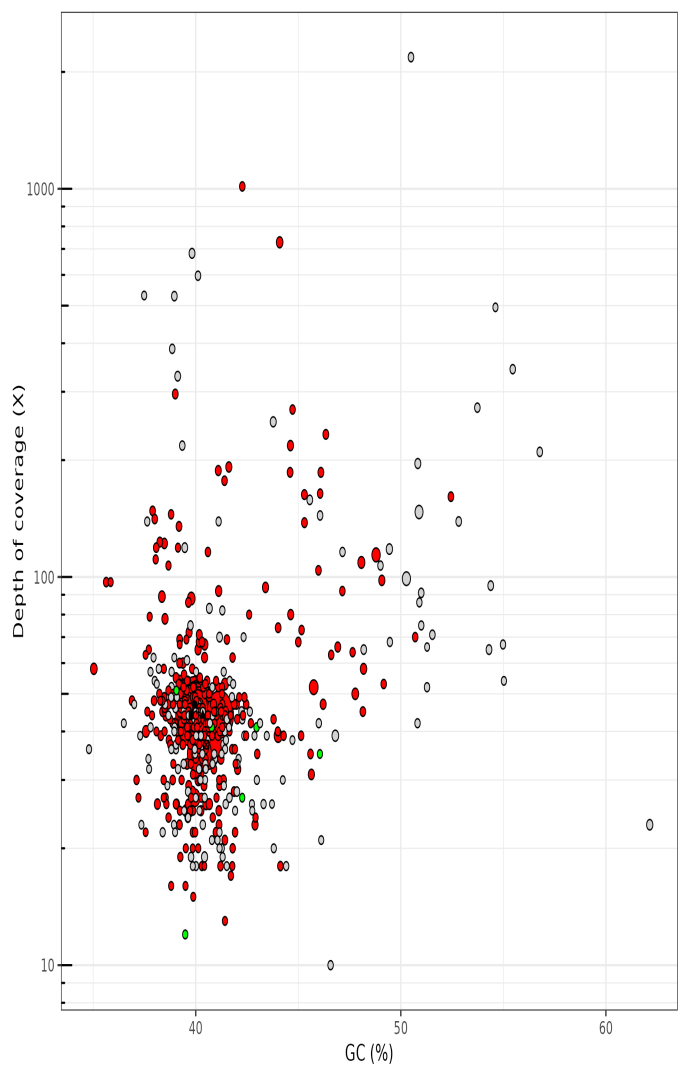
Distribution of k-mer counts per copy
numbers found in asm

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	Long reads	Arima
Coverage	46	162

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: Arnaud Couloux
Affiliation: Genoscope

Date and time: 2025-12-01 02:45:33 CET