

# ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	491806
ToLID	<b>ehHolsanc2</b>
Species	<i>Holothuria sancta</i>
Class	Holothuroidea
Order	Aspidochirotida

Genome Traits	Expected	Observed
Haploid size (bp)	1,028,481,939	1,171,681,863
Haploid Number	21 (source: ancestor)	23
Ploidy	2 (source: ancestor)	2
Sample Sex	Unknown	Unknown

## EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 7.7.Q61

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

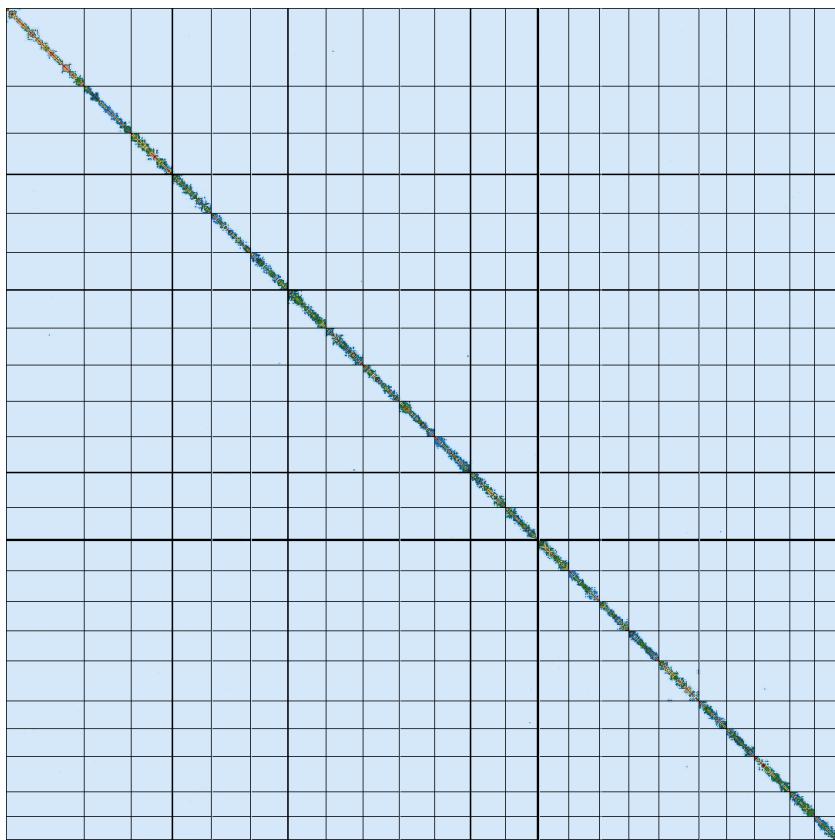
- Interventions/Gb: 35
- Contamination notes: ""
- Other observations: "A large number of duplications have been removed and many sequences at the end of the scaffold have been replaced in the chromosomes. "

## Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	1,194,060,647	1,171,681,863
GC %	39.37	39.37
Gaps/Gbp	35.17	75.96
Total gap bp	4,200	15,000
Scaffolds	59	47
Scaffold N50	49,855,781	50,699,391
Scaffold L50	10	10
Scaffold L90	21	20
Contigs	101	136
Contig N50	31,981,105	19,932,592
Contig L50	16	21
Contig L90	42	63
QV	61.1747	61.1746
Kmer compl.	70.1165	69.3222
BUSCO sing.	95.0%	94.4%
BUSCO dupl.	0.5%	0.3%
BUSCO frag.	2.7%	2.7%
BUSCO miss.	1.8%	2.6%

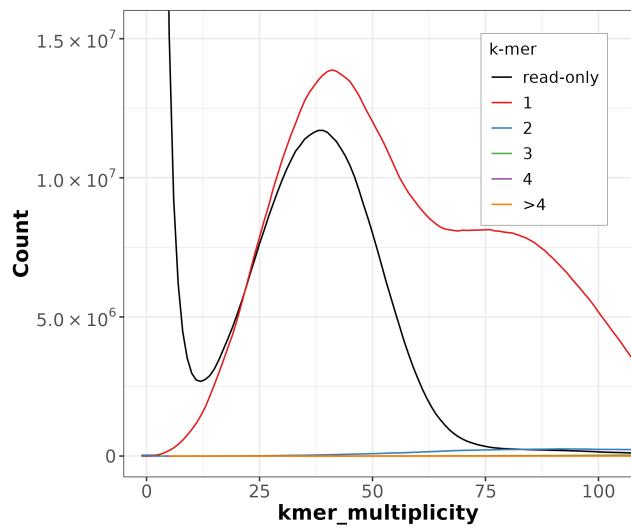
BUSCO: 5.4.3 (euk\_genome\_met, metaeuk) / Lineage: metazoa\_odb10 (genomes:65, BUSCOs:954)

# HiC contact map of curated assembly

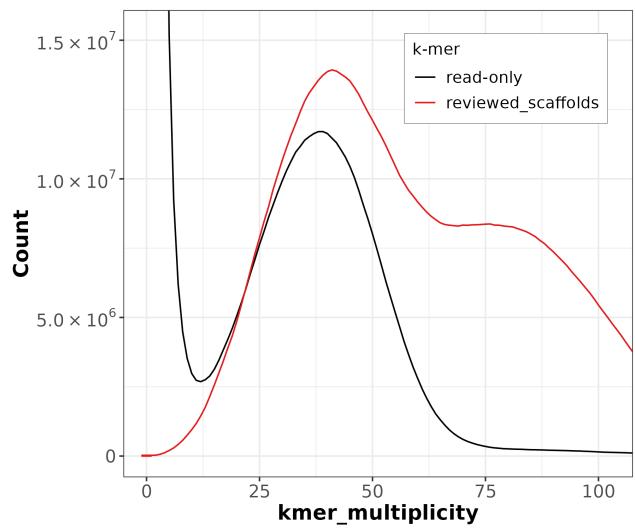


collapsed [\[LINK\]](#)

# K-mer spectra of curated assembly

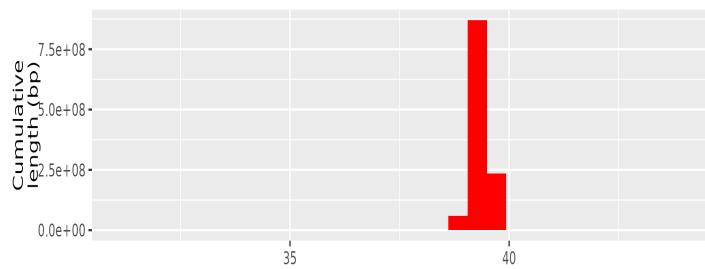


Distribution of k-mer counts per copy numbers found in asm

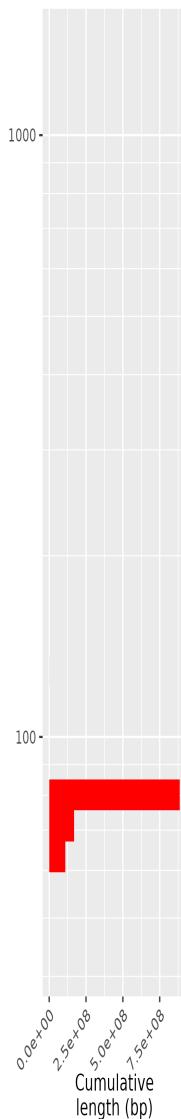
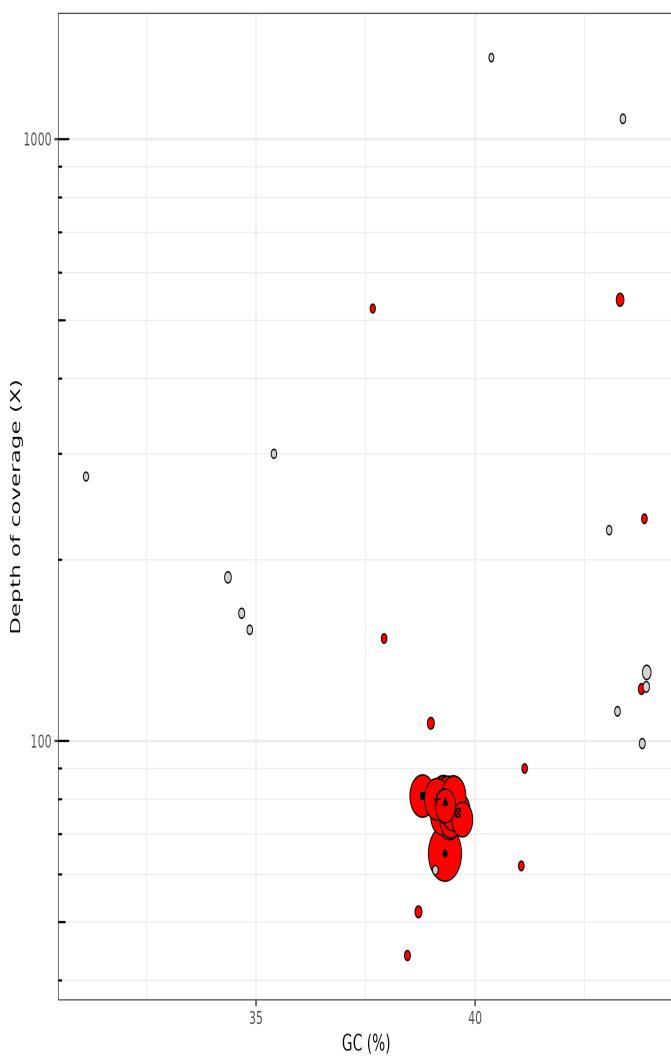


Distribution of k-mer counts coloured by their presence in reads/assemblies

# Post-curation contamination screening



TAPAs summary Graph



Length (bp)

- 2.5e+07
- 5.0e+07
- 7.5e+07
- 1.0e+08

superkingdom

- Eukaryota
- N/A

Longest sequences (bp)

- SUPER\_1 - 110078028 (Eukaryota)
- ▲ SUPER\_2 - 66213667 (Eukaryota)
- SUPER\_3 - 57996851 (Eukaryota)
- + SUPER\_18 - 56096604 (Eukaryota)
- ▣ SUPER\_4 - 55061395 (Eukaryota)

**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
Coverage	90	50

## 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

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Date and time: 2025-02-04 15:38:42 CET