

# ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

|         |                        |
|---------|------------------------|
| TxID    | 1072197                |
| ToLID   | <b>ehHolPoli1_hap2</b> |
| Species | Holothuria poli        |
| Class   | Holothuroidea          |
| Order   | Aspidochirotida        |

| Genome Traits     | Expected              | Observed      |
|-------------------|-----------------------|---------------|
| Haploid size (bp) | 1,578,169,159         | 1,823,428,318 |
| Haploid Number    | 21 (source: ancestor) | 22            |
| Ploidy            | 2 (source: ancestor)  | 2             |
| Sample Sex        | Unknown               | Unknown       |

## EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 6.7.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: 300
- . Contamination notes: ""
- . Other observations: ""

# Quality metrics table

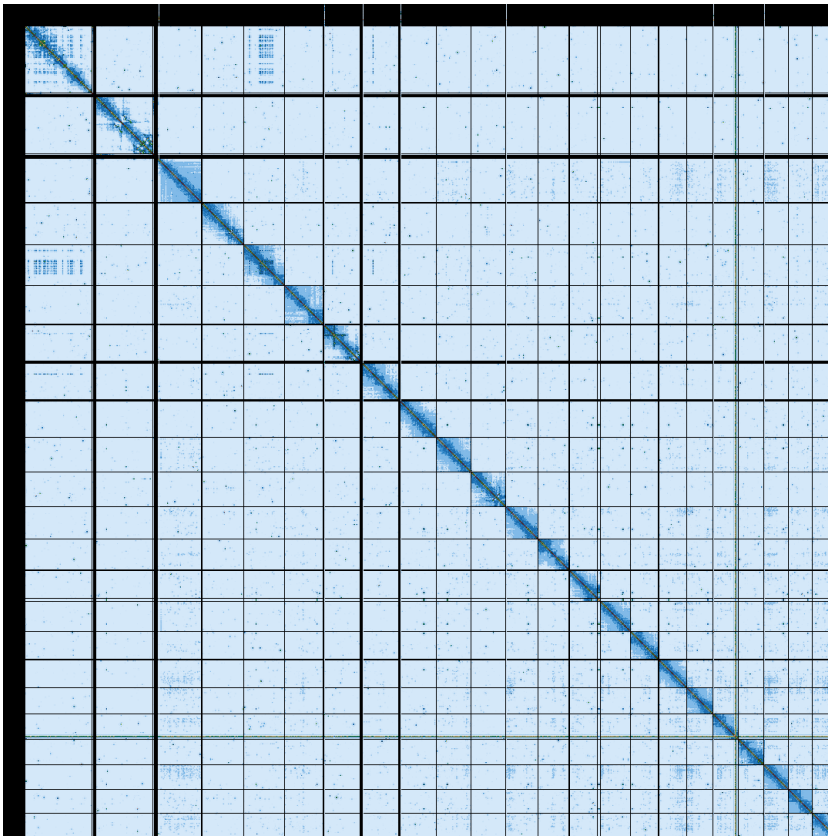
| Metrics      | Pre-curation collapsed | Curated collapsed |
|--------------|------------------------|-------------------|
| Total bp     | 1,848,567,075          | 1,823,428,318     |
| GC %         | 39.26                  | 39.29             |
| Gaps/Gbp     | 0                      | 469.99            |
| Total gap bp | 0                      | 87,700            |
| Scaffolds    | 412                    | 834               |
| Scaffold N50 | 9,961,692              | 75,092,538        |
| Scaffold L50 | 57                     | 10                |
| Scaffold L90 | 192                    | 22                |
| Contigs      | 412                    | 1,691             |
| Contig N50   | 9,961,692              | 3,578,110         |
| Contig L50   | 57                     | 151               |
| Contig L90   | 192                    | 535               |
| QV           | 65.8204                | 65.0772           |
| Kmer compl.  | 70.7547                | 68.1827           |
| BUSCO sing.  | 80.2%                  | 95.2%             |
| BUSCO dupl.  | 3.6%                   | 2.5%              |
| BUSCO frag.  | 14.9%                  | 1.2%              |
| BUSCO miss.  | 1.3%                   | 1.0%              |

Warning! BUSCO versions or lineage datasets are not the same across results:

BUSCO: 5.8.2 (euk\_genome\_met, metaeuk) / Lineage: metazoa\_odb12 (genomes:206, BUSCOs:672)

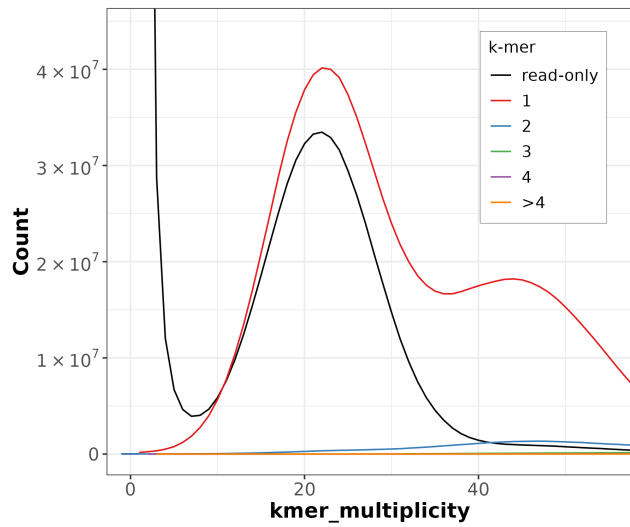
BUSCO: 6.0.0 (euk\_genome\_min, miniprot) / Lineage: metazoa\_odb12 (genomes:206, BUSCOs:672)

# HiC contact map of curated assembly

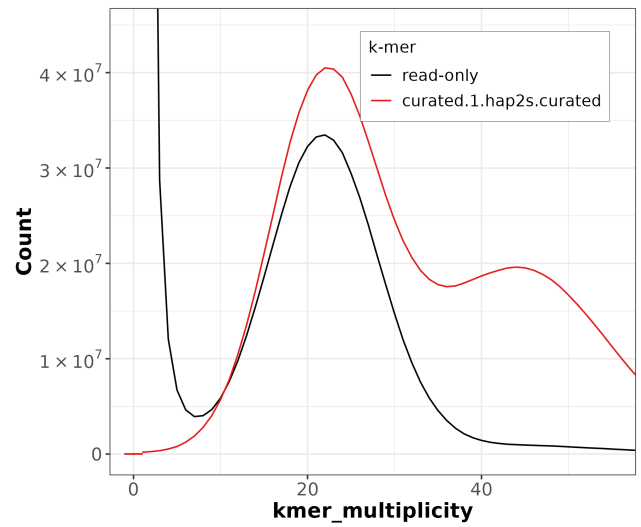


collapsed [\[LINK\]](#)

# K-mer spectra of curated assembly

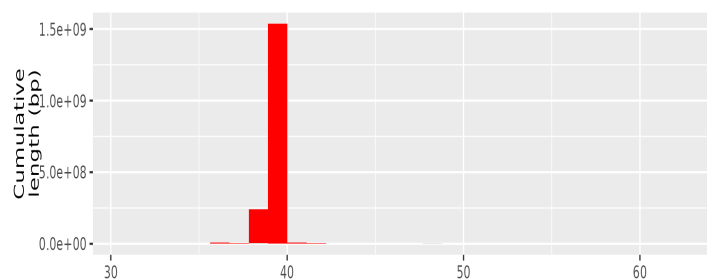


Distribution of k-mer counts per copy numbers found in asm

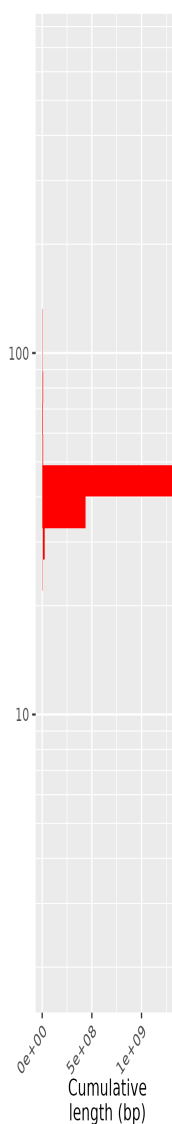
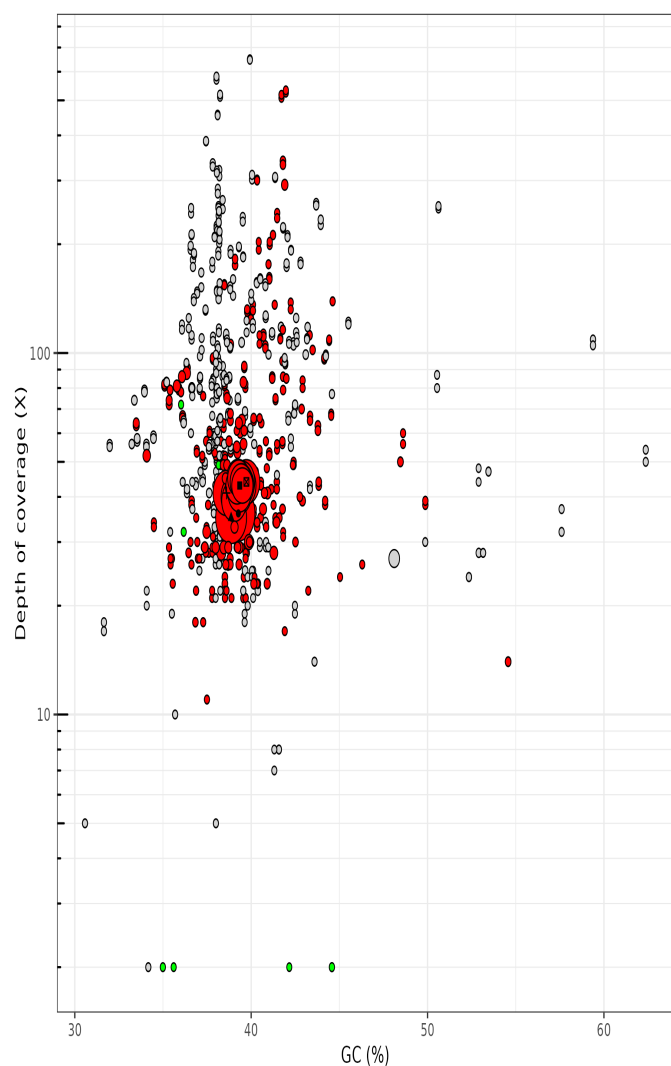


Distribution of k-mer counts coloured by their presence in reads/assemblies

# Post-curation contamination screening



## TAPAs summary Graph



### superkingdom

- Bacteria
- Eukaryota
- N/A

### Longest sequences (bp)

- ehHolPoli1\_1 - 148282284 (Eukaryota)
- ▲ ehHolPoli1\_2 - 125562457 (Eukaryota)
- ehHolPoli1\_3 - 95916429 (Eukaryota)
- + ehHolPoli1\_4 - 91637517 (Eukaryota)
- ⊠ ehHolPoli1\_5 - 88573848 (Eukaryota)

### Length (bp)

- 5.0e+07
- 1.0e+08

**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 | 48         | 662   |

## 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: 2025-11-28 07:05:21 CET