

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	1072197
ToLID	ehHolPol1_hapl
Species	<i>Holothuria poli</i>
Class	Holothuroidea
Order	Aspidochirotida

Genome Traits	Expected	Observed
Haploid size (bp)	1,578,169,159	1,825,045,599
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

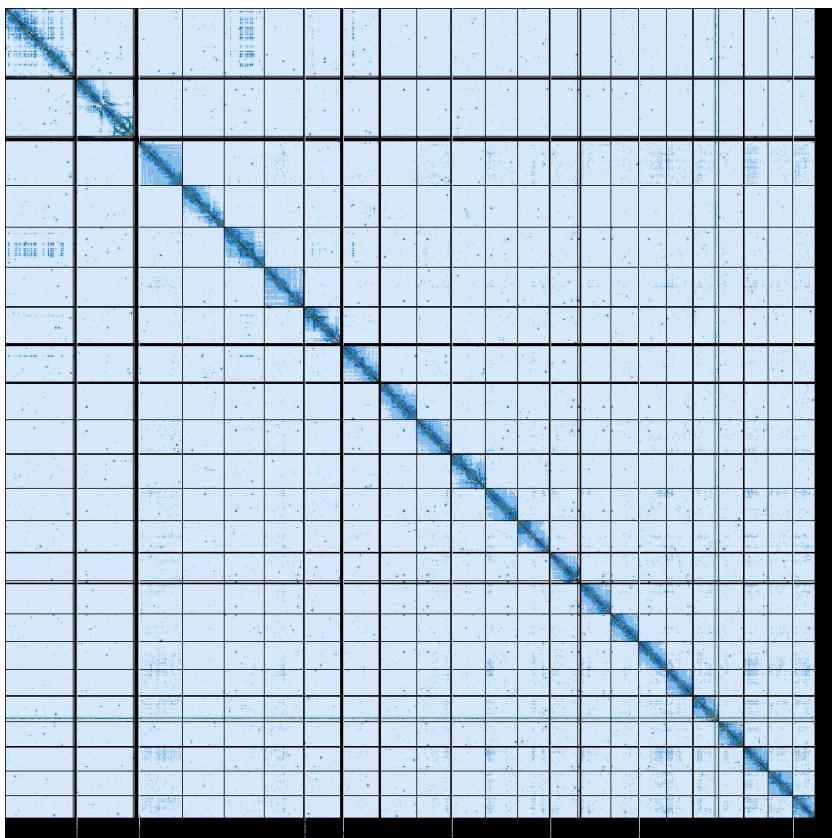
Metrics	Pre-curation collapsed	Curated collapsed
Total bp	1,848,567,075	1,825,045,599
GC %	39.26	39.29
Gaps/Gbp	0	470.67
Total gap bp	0	88,700
Scaffolds	412	833
Scaffold N50	9,961,692	75,092,538
Scaffold L50	57	10
Scaffold L90	192	22
Contigs	412	1,692
Contig N50	9,961,692	3,578,110
Contig L50	57	151
Contig L90	192	536
QV	65.8204	65.0674
Kmer compl.	70.7547	68.236
BUSCO sing.	80.2%	95.1%
BUSCO dupl.	3.6%	2.7%
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)

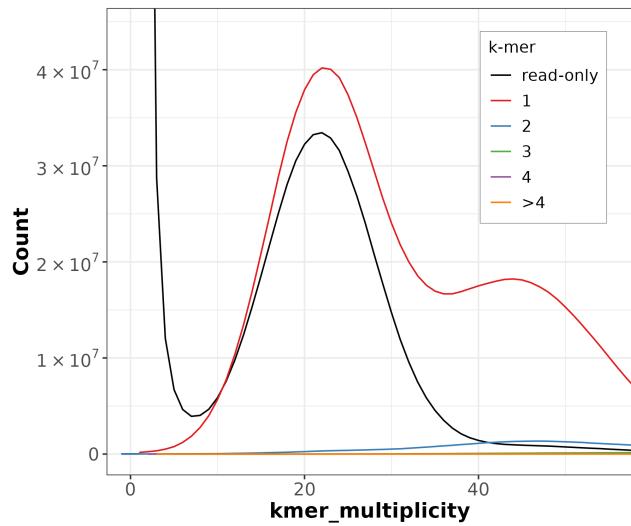
BUSCO: 6.0.0 (euk_genome_min, miniprot) / Lineage: metazoa_odb12 (genomes:206, BUSCOs:672)

HiC contact map of curated assembly

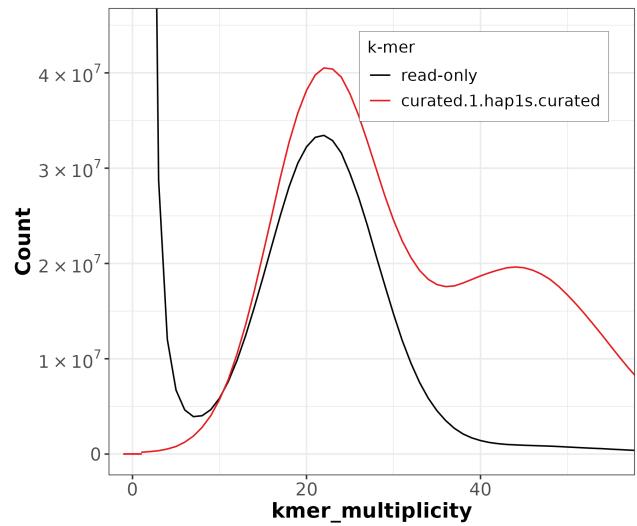


collapsed [\[LINK\]](#)

K-mer spectra of curated assembly

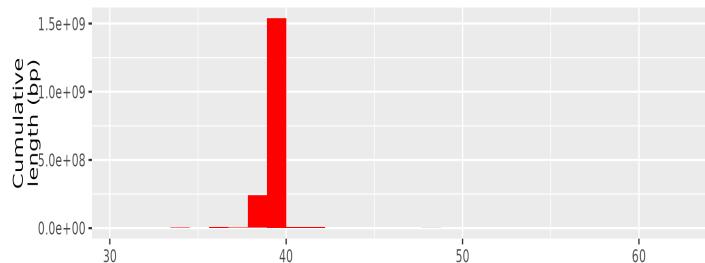


Distribution of k-mer counts per copy numbers found in asm

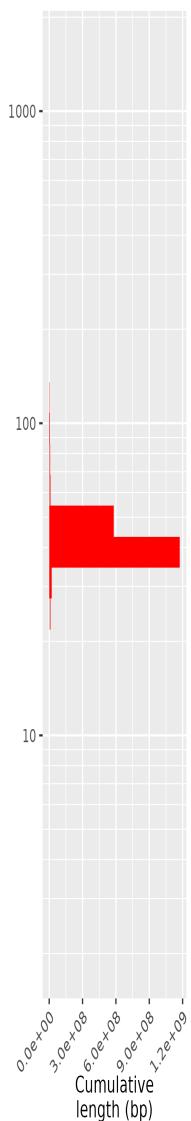
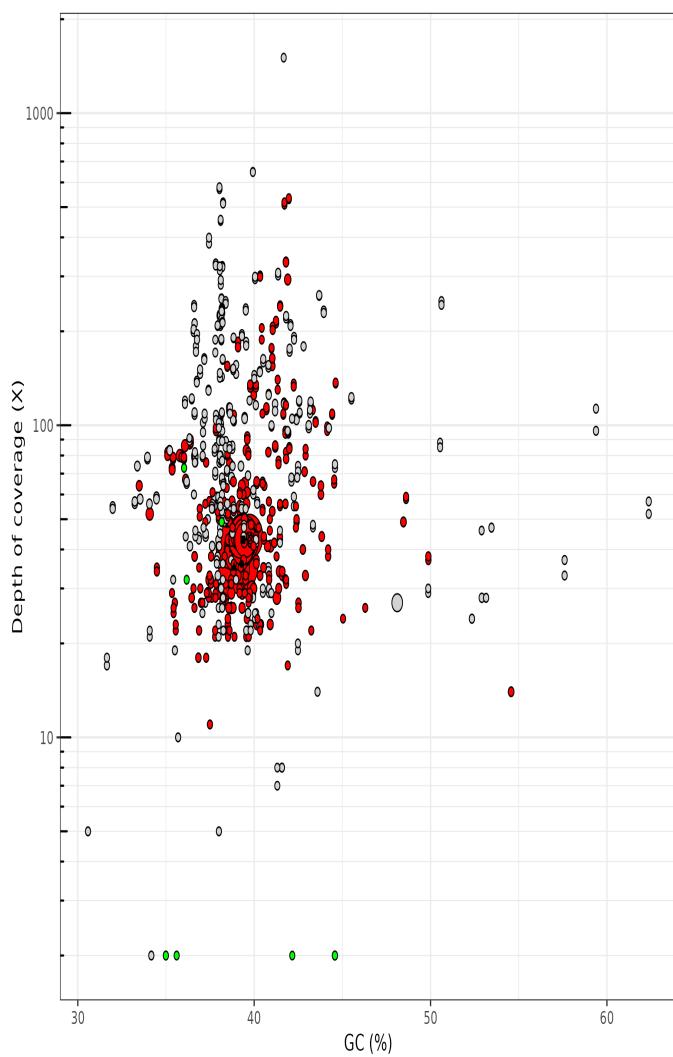


Distribution of k-mer counts coloured by their presence in reads/assemblies

Post-curation contamination screening



TAPAs summary Graph



superkingdom

● Bacteria

● Eukaryota

○ N/A

Longest sequences (bp)

● ehHolPoli1_1 - 149470392 (Eukaryota)

▲ ehHolPoli1_2 - 125562657 (Eukaryota)

■ ehHolPoli1_3 - 96759529 (Eukaryota)

+ ehHolPoli1_4 - 91822892 (Eukaryota)

✖ ehHolPoli1_5 - 88573848 (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	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
```

Submitter: Lola Demirdjian
Affiliation: Genoscope

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