

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	544679
ToLID	tzSchErrt1
Species	Schizoporella errata
Class	Gymnolaemata
Order	Cheilostomatida

Genome Traits	Expected	Observed
Haploid size (bp)	343,009,412	386,019,586
Haploid Number	11 (source: ancestor)	11
Ploidy	2 (source: ancestor)	2
Sample Sex	Unknown	Unknown

EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 6.7.Q59

The following metrics were automatically flagged as below EBP recommended standards or 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

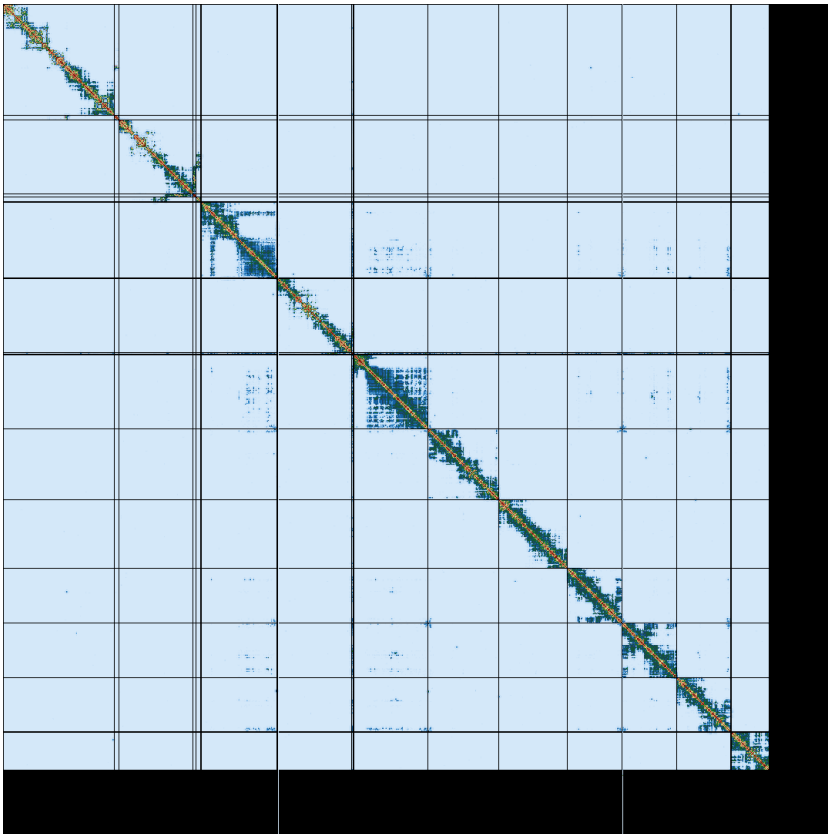
- . Interventions/Gb: 320
- . Contamination notes: ""
- . Other observations: "The assembly of Schizoporella errata (tzSchErrt1) is based on 63,48X PacBio data and 282,50X Arima Hi-C data generated as part of the European Reference Genome Atlas (ERGA, <https://www.erga-biodiversity.eu/>) via the Biodiversity Genomics Europe project (BGE, <https://biodiversitygenomics.eu/>). The assembly process included the following steps: initial PacBio assembly generation with Hifiiasm, removal of contaminant sequences using Context, removal of haplotypic duplications using purge_dups, and Hi-C-based scaffolding with YaHS. In total, 2501 contigs were identified as contaminants (bacterial, archaeal, or viral), totaling 203.001 Mb (with the largest being 11.897 Mb). Additionally, 633 regions totaling 18.648 Mb (with the largest being 0.641 Mb) were identified as haplotypic duplications and removed. During manual curation, 33 haplotypic regions were removed, totaling 13.007135Mb (with the largest being 1.870936Mb).. 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	399,442,775	386,019,586
GC %	41.78	41.8
Gaps/Gbp	1,011.41	1,121.7
Total gap bp	40,400	49,300
Scaffolds	925	744
Scaffold N50	25,342,757	32,950,285
Scaffold L50	6	6
Scaffold L90	22	11
Contigs	1,329	1,177
Contig N50	3,538,013	3,242,362
Contig L50	31	36
Contig L90	151	156
QV	59.2567	59.2757
Kmer compl.	70.2415	68.8968
BUSCO sing.	91.4%	92.2%
BUSCO dupl.	3.4%	2.6%
BUSCO frag.	2.2%	2.2%
BUSCO miss.	3.0%	3.0%

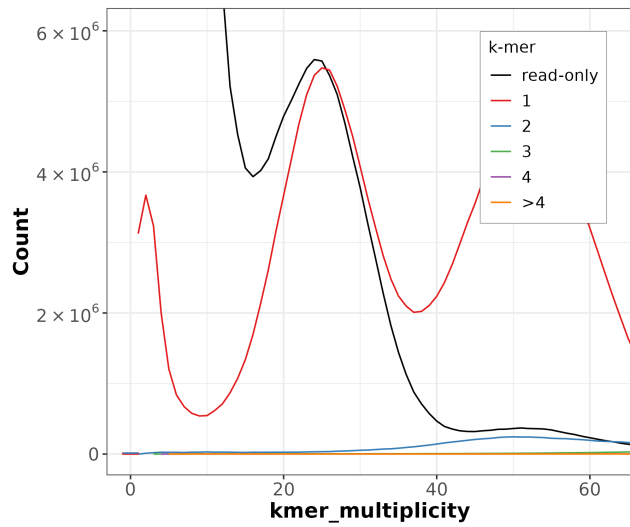
BUSCO: 6.0.0 (euk_genome_min, miniprot) / Lineage: lophotrochozoa_odb12 (genomes:75, BUSCOs:1252)

HiC contact map of curated assembly

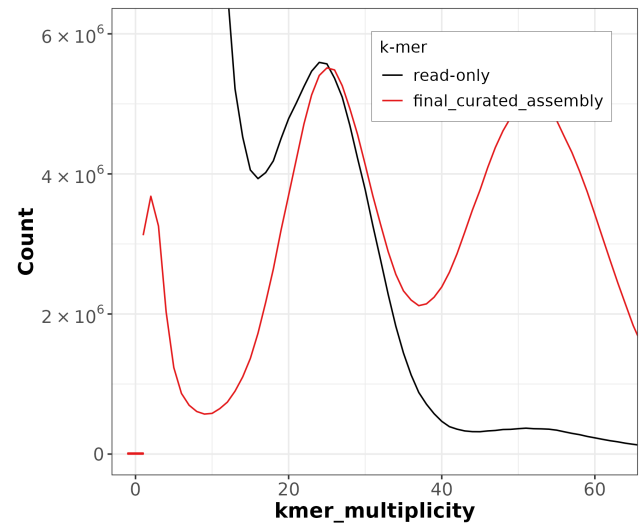


collapsed [\[LINK\]](#)

K-mer spectra of curated assembly

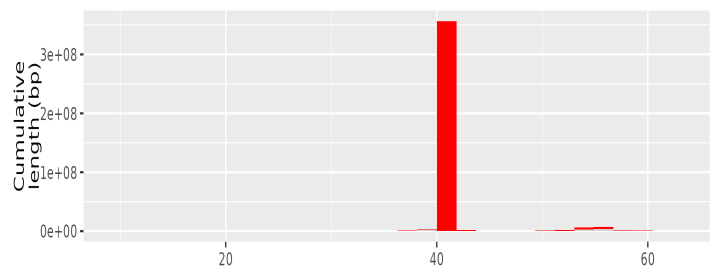


Distribution of k-mer counts per copy numbers found in asm

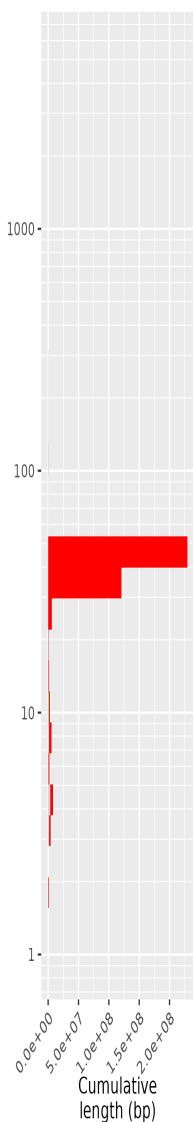
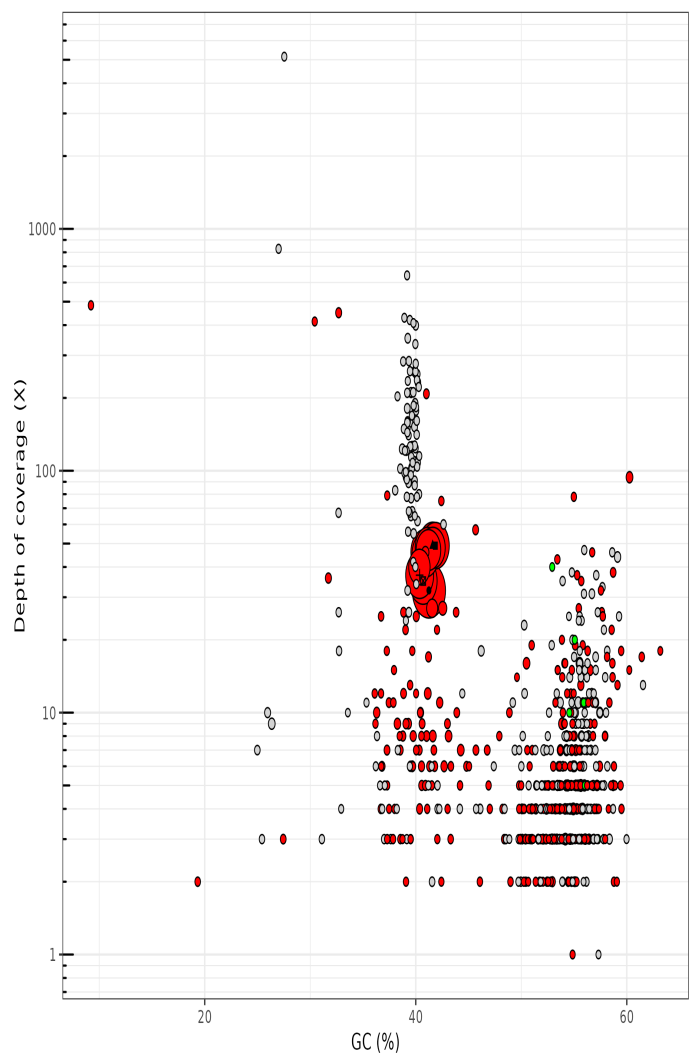


Distribution of k-mer counts coloured by their presence in reads/assemblies

Post-curation contamination screening



TAPAs summary Graph



superkingdom

- Bacteria
- Eukaryota
- N/A

Longest sequences (bp)

- tzSchErrt1_1 - 51619566 (Eukaryota)
- ▲ tzSchErrt1_3 - 35189465 (Eukaryota)
- tzSchErrt1_5 - 34391491 (Eukaryota)
- + tzSchErrt1_4 - 34323971 (Eukaryota)
- ▣ tzSchErrt1_2 - 34259804 (Eukaryota)

Length (bp)

- 1e+07
- 2e+07
- 3e+07
- 4e+07
- 5e+07

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	63	282

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: Phuong Doan

Affiliation: Genoscope

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