

# ERGA Assembly Report

v24.10.15

Tags: ATLASea[ INVALID TAG]

TxID	349662
ToLID	<b>fTraRad1</b>
Species	Trachinus radiatus
Class	Actinopteri
Order	Perciformes

Genome Traits	Expected	Observed
Haploid size (bp)	765,073,843	780,274,681
Haploid Number	24 (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.Q49

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

- . Kmer completeness value is less than 90 for collapsed

## Curator notes

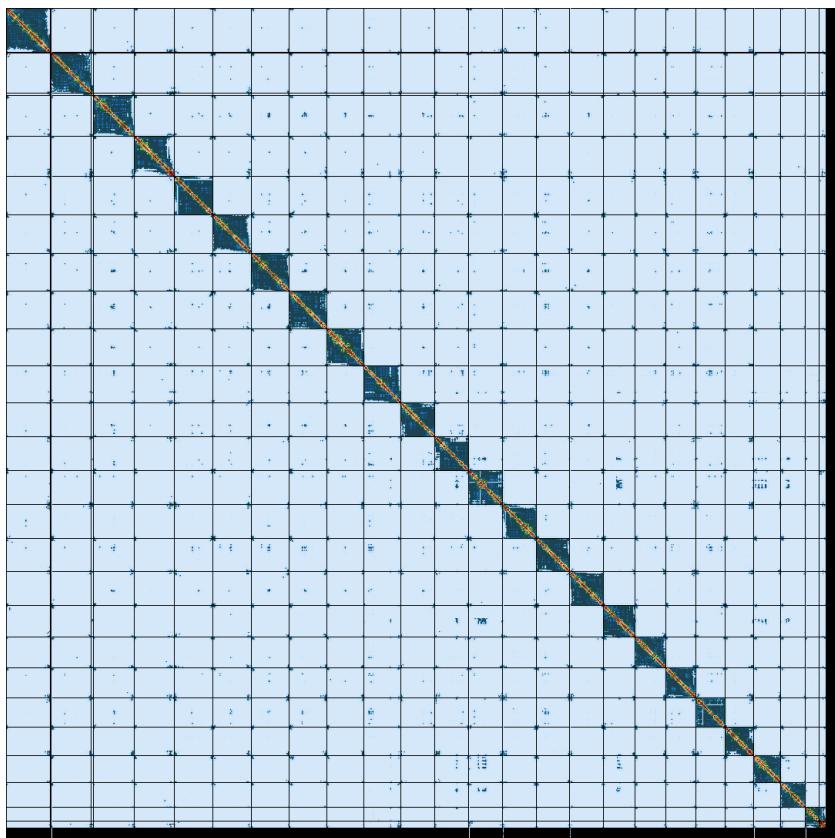
- . Interventions/Gb: 26
- . Contamination notes: ""
- . Other observations: "The assembly of Trachinus radiatus (fTraRad1) is based on 36X PacBio data and 193X Arima Hi-C data generated as part of the ATLASea programme (<https://www.atlasea.fr>). The assembly process included the following steps: initial 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, 1 contigs was identified as contaminants (bacterial, archaeal, or viral), totaling 0.166 Mb (with the largest being 0.166 Mb). Additionally, 90 regions totaling 7.678 Mb (with the largest being 0.27 Mb) were identified as haplotypic duplications and removed. Mitochondrial genome was assembled using OATK. During manual curation, 2 haplotypic regions were removed, totaling 3,155,990 pb (with the largest being 2,558,265 pb). 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	783,450,972	780,274,681
GC %	40.41	40.41
Gaps/Gbp	51.06	52.55
Total gap bp	4,000	4,400
Scaffolds	119	115
Scaffold N50	32,840,703	32,202,939
Scaffold L50	11	11
Scaffold L90	22	22
Contigs	159	156
Contig N50	20,076,630	20,076,630
Contig L50	14	14
Contig L90	38	38
QV	49.2678	49.2765
Kmer compl.	87.786	87.7228
BUSCO sing.	99.0%	99.5%
BUSCO dupl.	0.6%	0.1%
BUSCO frag.	0.1%	0.1%
BUSCO miss.	0.3%	0.3%

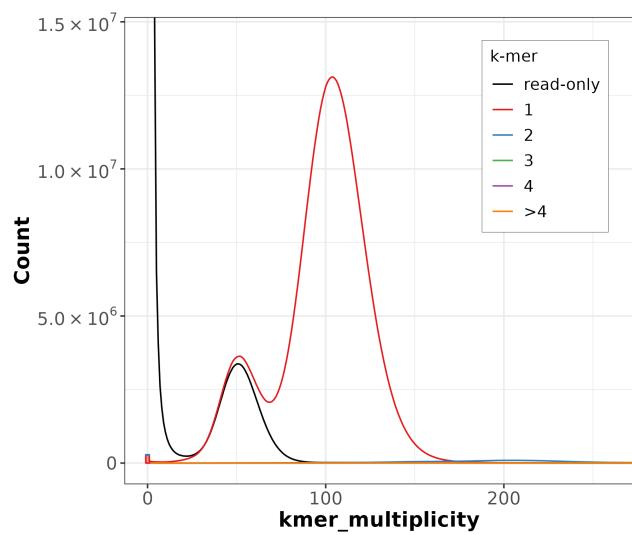
BUSCO: 6.0.0 (euk\_genome\_min, miniprot) / Lineage: actinopterygii\_odb12 (genomes:75, BUSCOs:7207)

# HiC contact map of curated assembly

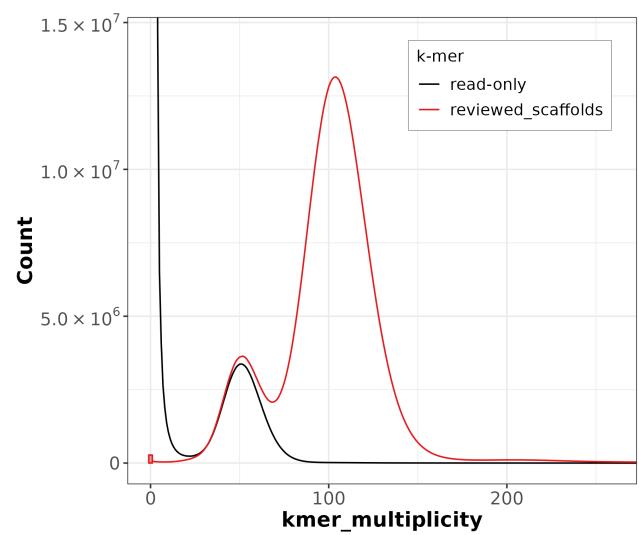


collapsed [\[LINK\]](#)

# K-mer spectra of curated assembly

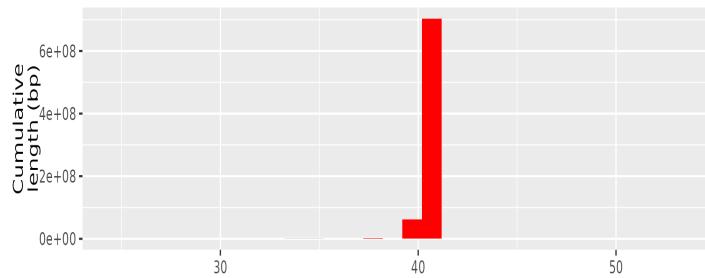


Distribution of k-mer counts per copy numbers found in asm

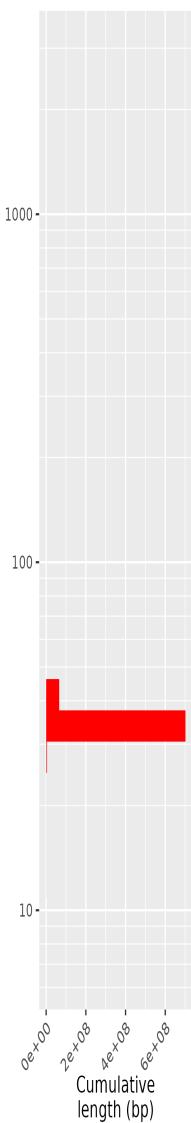
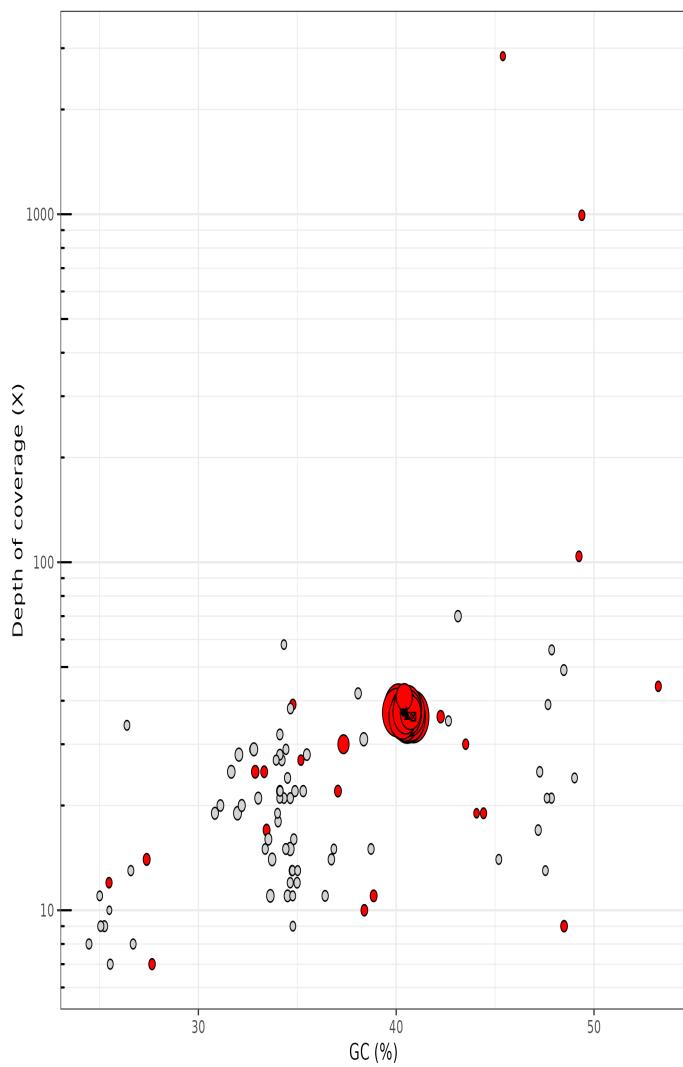


Distribution of k-mer counts coloured by their presence in reads/assemblies

# Post-curation contamination screening



TAPAs summary Graph



Longest sequences (bp)

- fTraRad1\_1 - 41721904 (Eukaryota)
- ▲ fTraRad1\_2 - 38069093 (Eukaryota)
- fTraRad1\_3 - 37995520 (Eukaryota)
- + fTraRad1\_4 - 37480113 (Eukaryota)
- ▣ fTraRad1\_5 - 36470062 (Eukaryota)

Length (bp)

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

superkingdom

- Eukaryota
- N/A

**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	36	193

## 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

Date and time: 2026-01-10 13:03:15 CET