# ERGA Assembly Report

v24.10.15

Tags: ATLASea[INVALID TAG]

| | |
|---|---|
| TxID | 50593 |
| ToLID | **fPagEry1** |
| Species | Pagellus erythrinus |
| Class | Actinopteri |
| Order | Spariformes |

| Genome Traits | Expected | Observed |
|---|---|---|
| Haploid size (bp) | 741,282,998 | 765,667,122 |
| 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.Q48

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

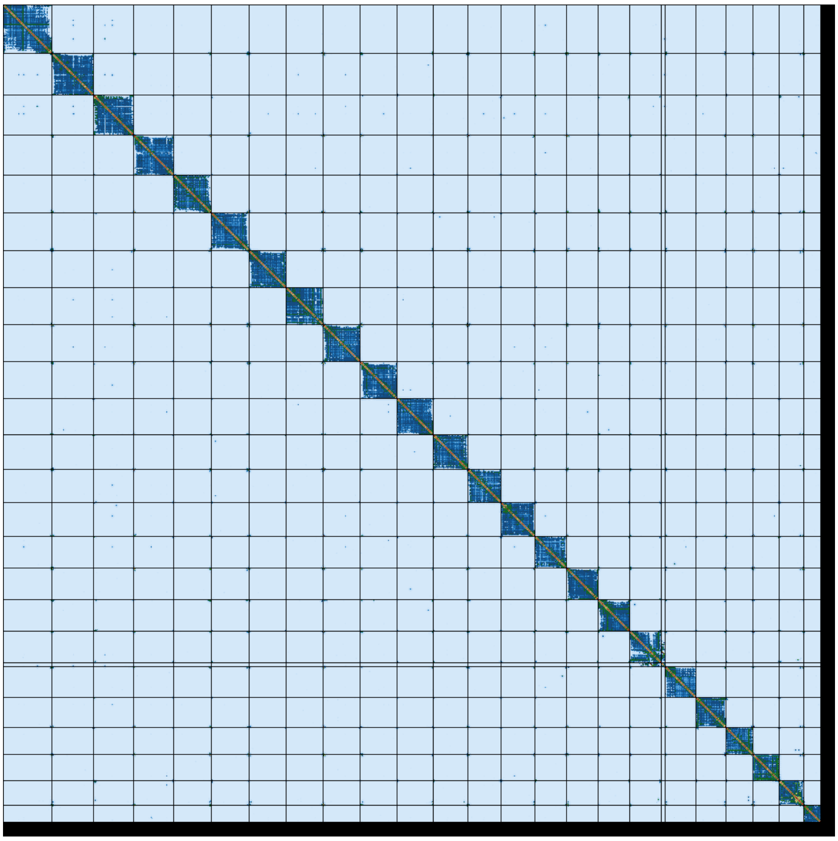
. Interventions/Gb: 3
. Contamination notes: ""
. Other observations: "The assembly of Pagellus erythrinus (fPagEry1) is based on 78X PacBio data and 181X Arima Hi-C data generated as part of the ATLASea programme (https://www.atlasea.fr). The assembly process included the following steps: initial PacBio 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 contig was identified as contaminants (bacterial) , totaling 0.18 Mb. Additionally, 75 regions totaling 7.5 Mb (with the largest being 3.3 Mb) were identified as haplotypic duplications and removed. The mitochondrial genome was assembled using OATK. Finally, the primary assembly was analyzed and manually improved using Pretext. During manual curation, no regions were tagged as allelic duplications or contaminants.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 | 765,694,102 | 765,667,122 |
| GC % | 41.84 | 41.84 |
| Gaps/Gbp | 23.51 | 24.81 |
| Total gap bp | 1,800 | 2,100 |
| Scaffolds | 96 | 94 |
| Scaffold N50 | 33,590,000 | 33,590,000 |
| Scaffold L50 | 11 | 11 |
| Scaffold L90 | 22 | 22 |
| Contigs | 114 | 113 |
| Contig N50 | 28,986,652 | 28,986,652 |
| Contig L50 | 12 | 12 |
| Contig L90 | 27 | 27 |
| QV | 48.9186 | 48.9234 |
| Kmer compl. | 79.3514 | 79.3514 |
| BUSCO sing. | 96.8% | 96.8% |
| BUSCO dupl. | 0.9% | 0.9% |
| BUSCO frag. | 0.6% | 0.6% |
| BUSCO miss. | 1.6% | 1.6% |

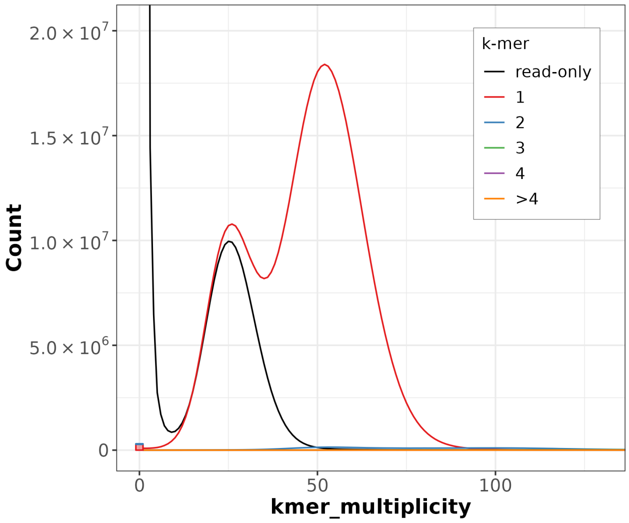
BUSCO: 5.8.2 (euk_genome_met, metaeuk) / Lineage: actinopterygii_odb12 (genomes:75, BUSCOs:7207)

# HiC contact map of curated assembly

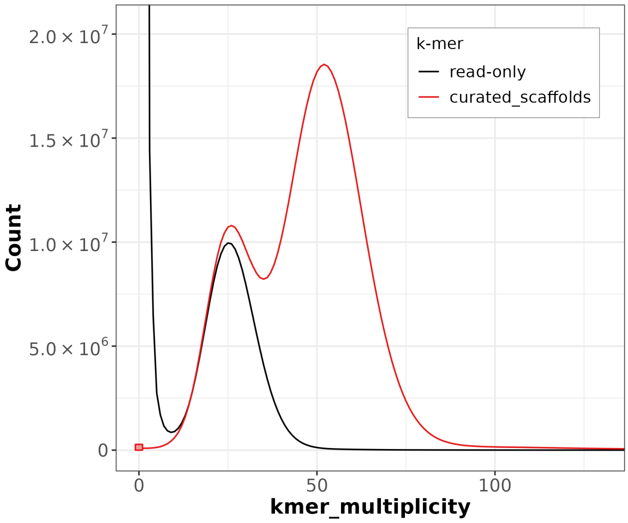


**collapsed** [LINK]

# K-mer spectra of curated assembly

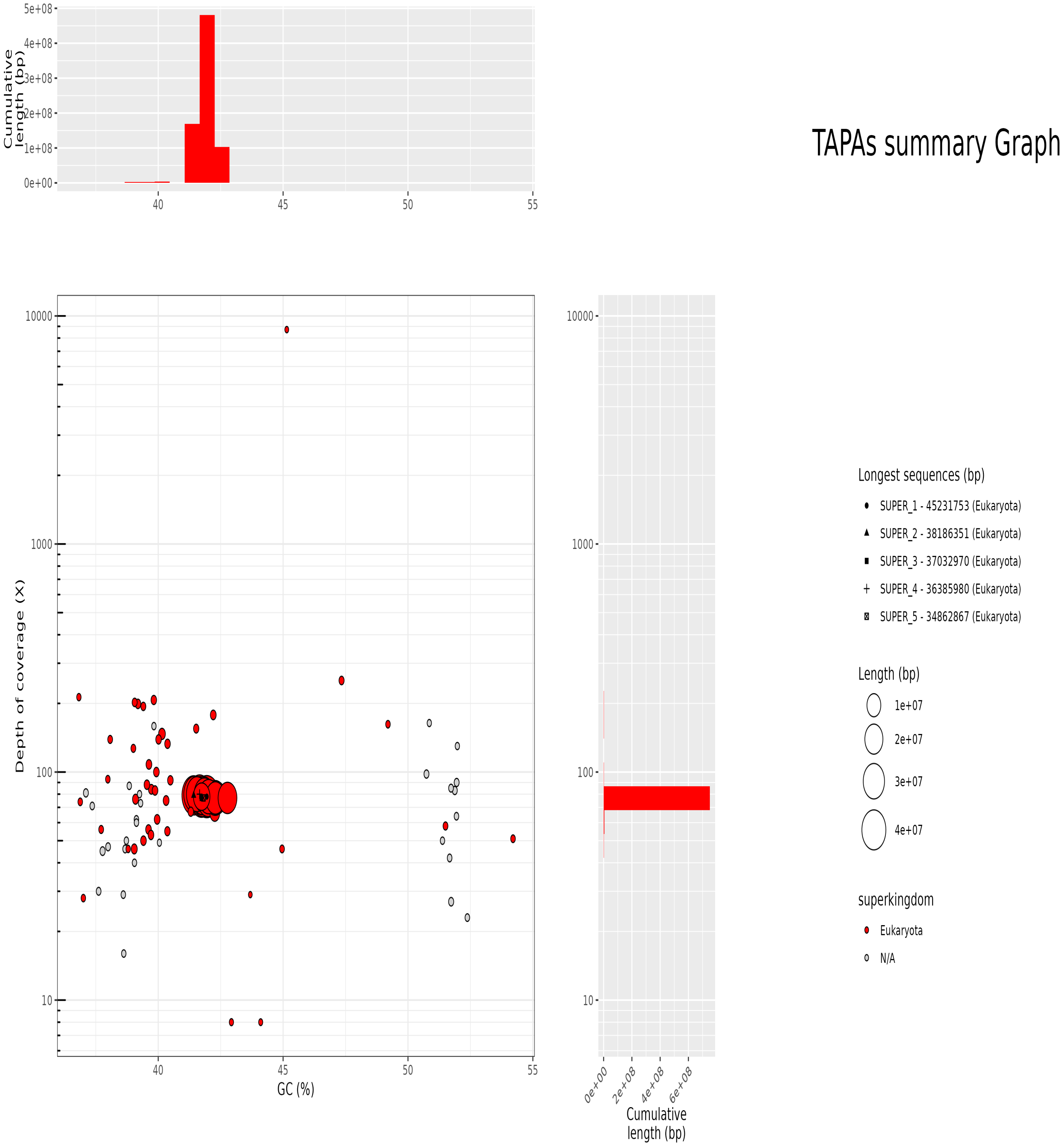


Distribution of k-mer counts per copy numbers found in asm



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

# Post-curation contamination screening



**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 | 78 | 181 |

# 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: Sophie Layac
Affiliation: Genoscope

Date and time: 2025-06-18 09:23:38 CEST