# ERGA Assembly Report

v24.10.15

Tags: ATLASea[INVALID TAG]

| | |
|---|---|
| TxID | 8097 |
| ToLID | **fMyoSco2** |
| Species | Myoxocephalus scorpius |
| Class | Actinopteri |
| Order | Perciformes |

| Genome Traits | Expected | Observed |
|---|---|---|
| Haploid size (bp) | 666,059,907 | 708,095,533 |
| Haploid Number | 19 (source: direct) | 18 |
| Ploidy | 2 (source: ancestor) | 2 |
| Sample Sex | Unknown | Unknown |

## EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 7.7.Q46

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

. Observed Haploid Number is different from Expected

### Curator notes

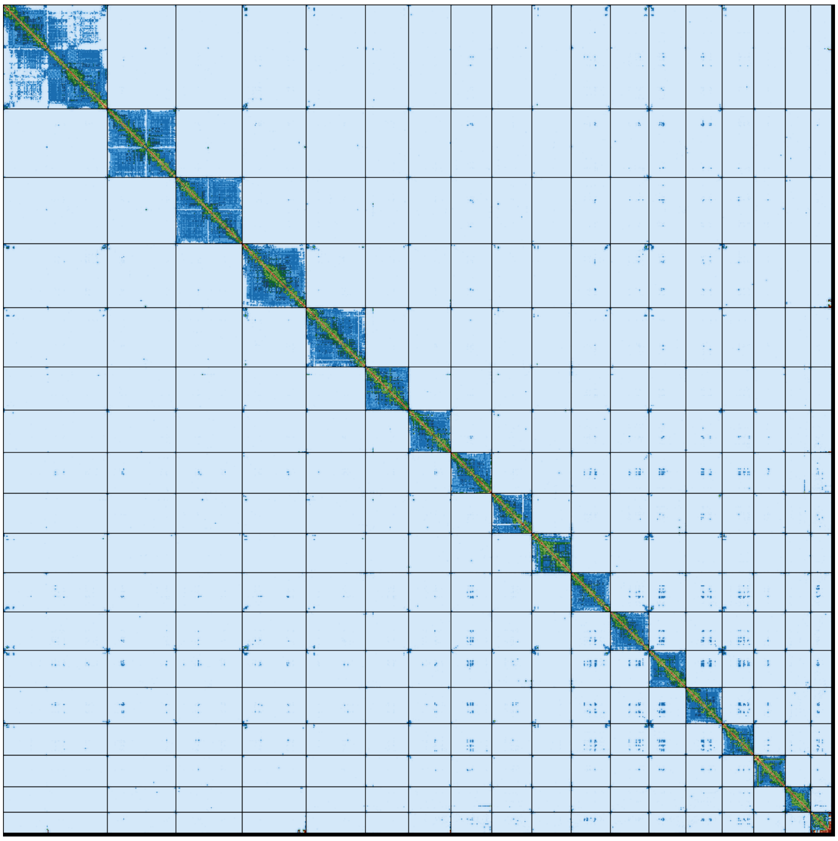
. Interventions/Gb: 25
. Contamination notes: ""
. Other observations: "The assembly of Myoxocephalus scorpius (fMyoSco2) is based on 53X PacBio data and 224X Arima Hi-C data generated as part of the ATLASea programme (https://www.atlasea.fr). The assembly process included the following steps: initial 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, 2 contigs were identified as contaminants (bacterial) , totaling 35 054 pb (with the largest being 20 163 pb) . Additionally, 149 regions totaling 20 895 775 pb (with the largest being 1 910 937 pb) 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, 3 haplotypic regions and 3 contaminant sequences were removed, totaling 1 006 804 bp and 150 867 pb, respectively (with the largest being 450911 pb and 66 000 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 | 709,235,071 | 708,095,533 |
| GC % | 42.55 | 42.55 |
| Gaps/Gbp | 146.64 | 153.93 |
| Total gap bp | 10,400 | 11,800 |
| Scaffolds | 51 | 44 |
| Scaffold N50 | 35,438,856 | 35,438,856 |
| Scaffold L50 | 7 | 7 |
| Scaffold L90 | 15 | 15 |
| Contigs | 155 | 153 |
| Contig N50 | 18,641,818 | 18,641,818 |
| Contig L50 | 15 | 15 |
| Contig L90 | 47 | 47 |
| QV | 46.9023 | 46.9229 |
| Kmer compl. | 91.6564 | 91.6491 |
| BUSCO sing. | 96.9% | 97.0% |
| BUSCO dupl. | 0.5% | 0.4% |
| BUSCO frag. | 0.6% | 0.6% |
| BUSCO miss. | 2.1% | 2.1% |

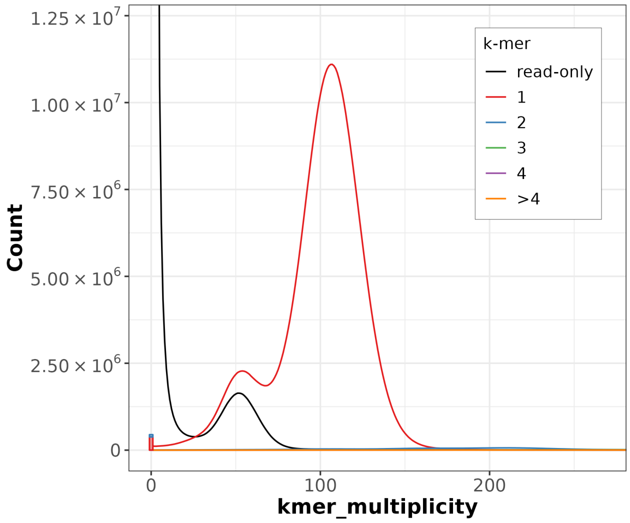
BUSCO: 5.8.2 (euk_genome_met, metaeuk) / Lineage: actinopterygii_odb12 (genomes:75, BUSCOs:7207)

# HiC contact map of curated assembly

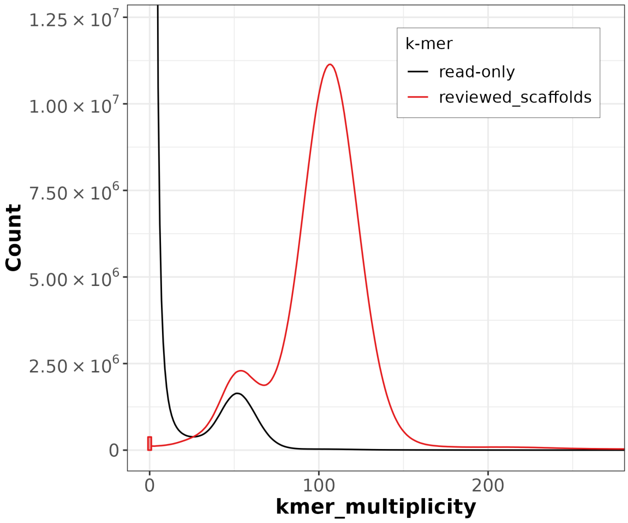


**collapsed** [LINK]

# K-mer spectra of curated assembly

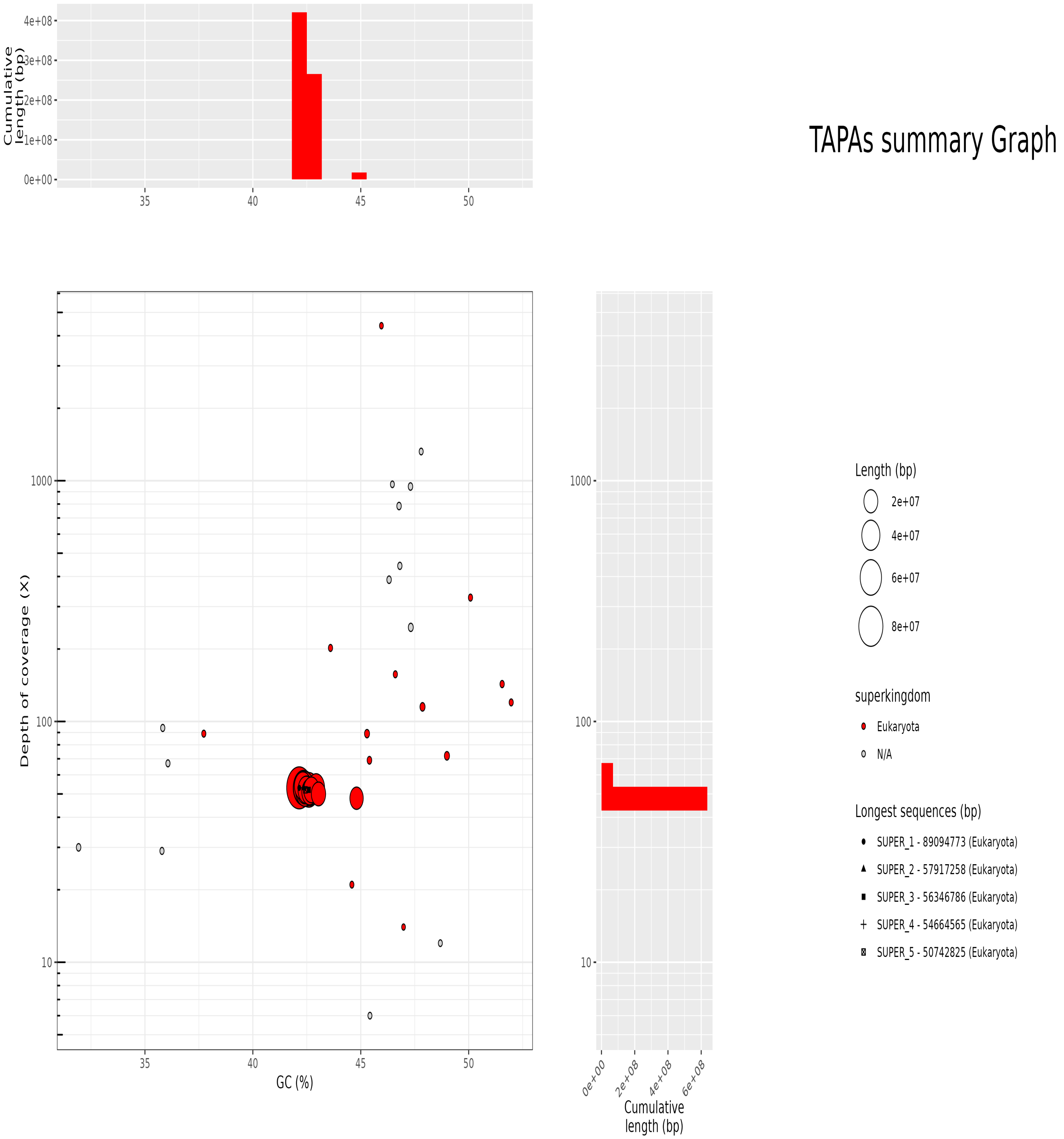


Distribution of k-mer counts per copy numbers found in asm



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 | 53 | 224 |

# 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: Arnaud Couloux
Affiliation: Genoscope

Date and time: 2025-09-03 13:27:17 CEST