ERGA Assembly Report

v24.10.15

Tags: Other[INVALID TAG]

TxID	8097
ToLID	**fMyoSco1_h1**
Species	Myoxocephalus scorpius
Class	Actinopteri
Order	Perciformes

Genome Traits	Expected	Observed
Haploid size (bp)	611,232,883	726,603,694
Haploid Number	19 (source: direct)	19
Ploidy	2 (source: ancestor)	2
Sample Sex	Unknown	Unknown

EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 6.7.Q53

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

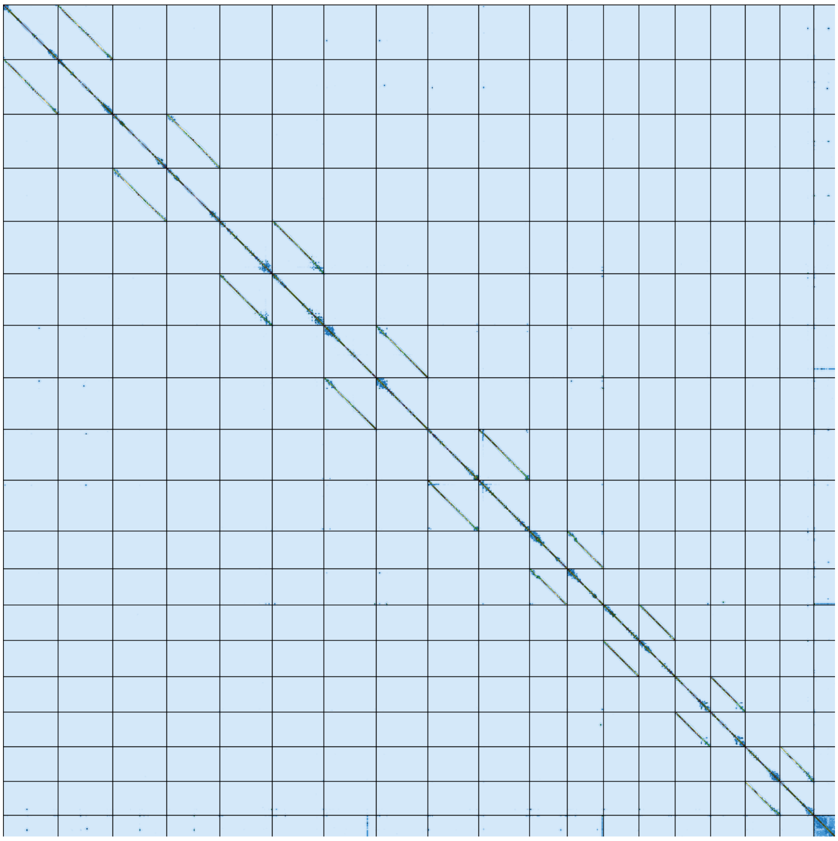
. Interventions/Gb: 120
. Contamination notes: ""
. Other observations: "The assembly of Myoxocephalus scorpius (fMyoSco1.1) was generated as part of the Vertebrate Genomes Project (https://vertebrategenomesproject.org/). Both haplotypes were analyzed and manually improved using Pretext. Chromosome 18 contains a large region (0-8.4 Mb) where the organization of contigs is uncertain. "

Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	715,405,851	726,603,694
GC %	42.51	42.51
Gaps/Gbp	680.73	750.07
Total gap bp	97,400	109,000
Scaffolds	97	60
Scaffold N50	36,375,788	37,154,042
Scaffold L50	8	8
Scaffold L90	17	17
Contigs	584	605
Contig N50	3,080,030	2,948,135
Contig L50	63	73
Contig L90	259	282
QV	53.9733	53.9826
Kmer compl.	89.2493	89.3927
BUSCO sing.	96.1%	96.5%
BUSCO dupl.	0.4%	0.4%
BUSCO frag.	0.8%	0.7%
BUSCO miss.	2.7%	2.4%

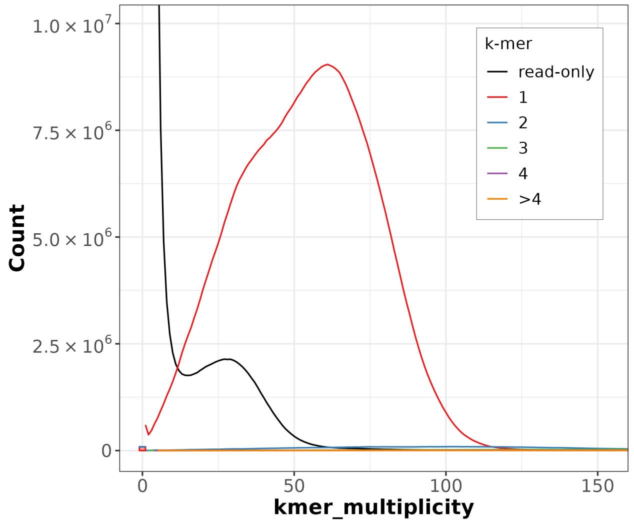
BUSCO: 5.8.2 (euk_genome_met, metaeuk) / Lineage: actinopterygii_odb12 (genomes:75, BUSCOs:7207)

HiC contact map of curated assembly

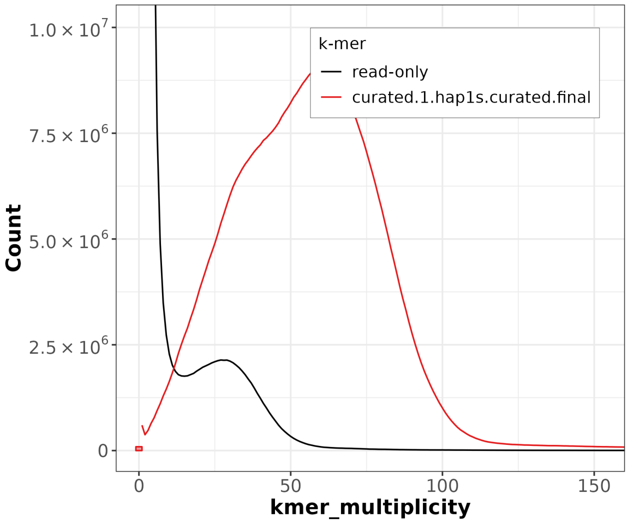


collapsed [LINK]

K-mer spectra of curated assembly

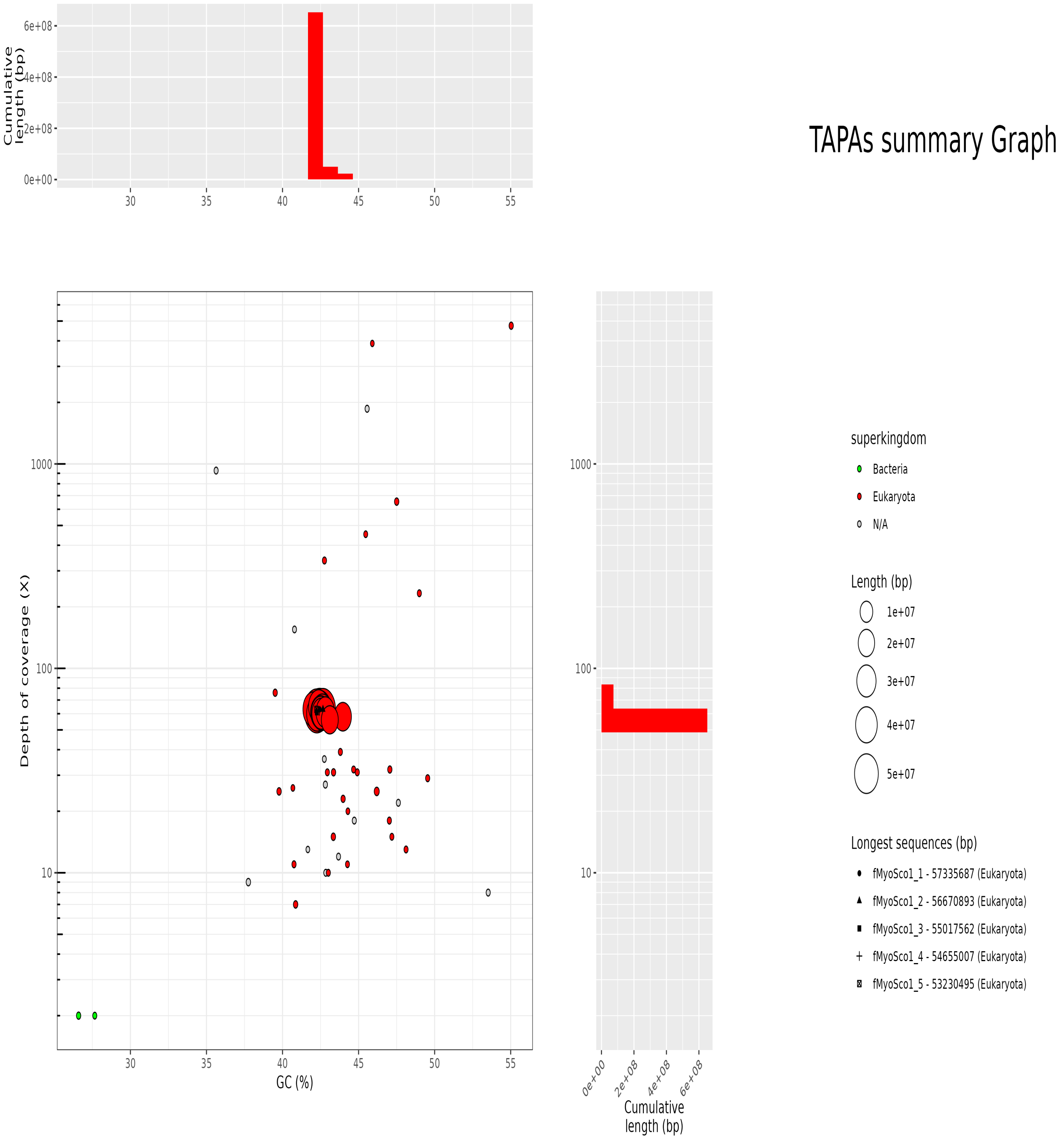


Distribution of k-mer counts per copy numbers found in asm



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	NA	NA

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
```

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