ERGA Assembly Report

v24.10.15

Tags: Other[INVALID TAG]

TxID	8097
ToLID	**fMyoSco1_h2**
Species	Myoxocephalus scorpius
Class	Actinopteri
Order	Perciformes

Genome Traits	Expected	Observed
Haploid size (bp)	611,232,883	710,080,943
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

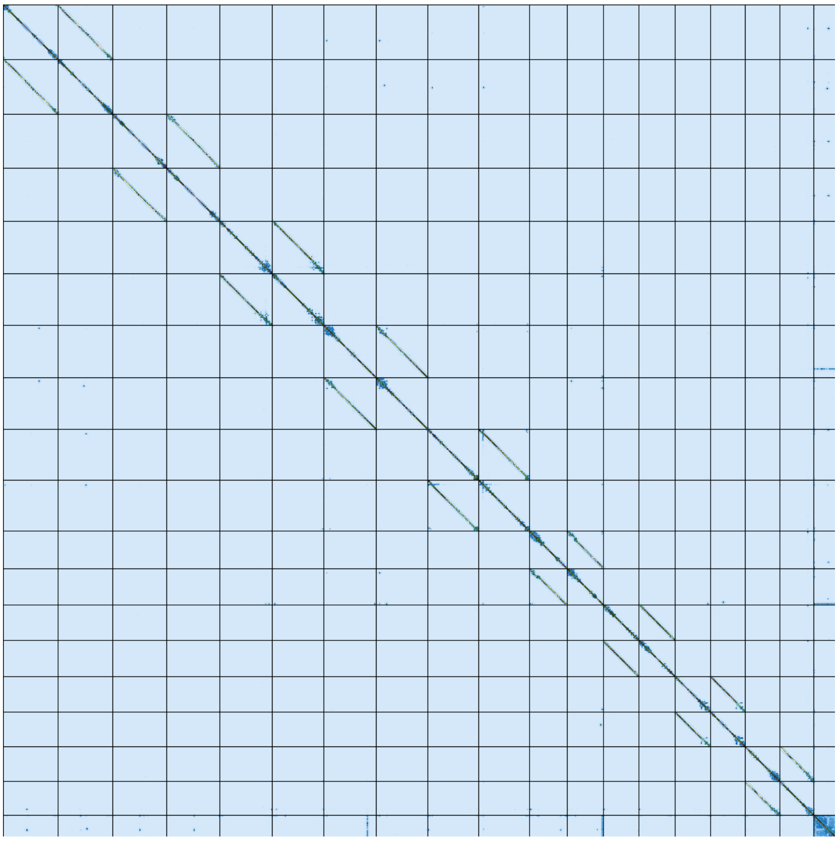
. Interventions/Gb: 120
. Contamination notes: ""
. Other observations: "The assembly of Myoxocephalus scorpius (fMyoSco1.1) was generated as part of the Vertebrate Genomes Project (https://vertebrategenomesproject.org/). Both haplotypes were analyzed and manually improved using Pretext. Chromosome 18 contains a large region (0-3.6 Mb) where the organization of contigs is uncertain. "

Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	721,243,703	710,080,943
GC %	42.52	42.52
Gaps/Gbp	671.06	729.49
Total gap bp	96,800	103,600
Scaffolds	106	54
Scaffold N50	36,611,539	36,375,788
Scaffold L50	8	8
Scaffold L90	17	16
Contigs	590	572
Contig N50	3,025,679	3,381,805
Contig L50	71	61
Contig L90	274	253
QV	53.9182	53.908
Kmer compl.	89.3389	89.1271
BUSCO sing.	96.5%	96.1%
BUSCO dupl.	0.4%	0.5%
BUSCO frag.	0.8%	0.8%
BUSCO miss.	2.4%	2.7%

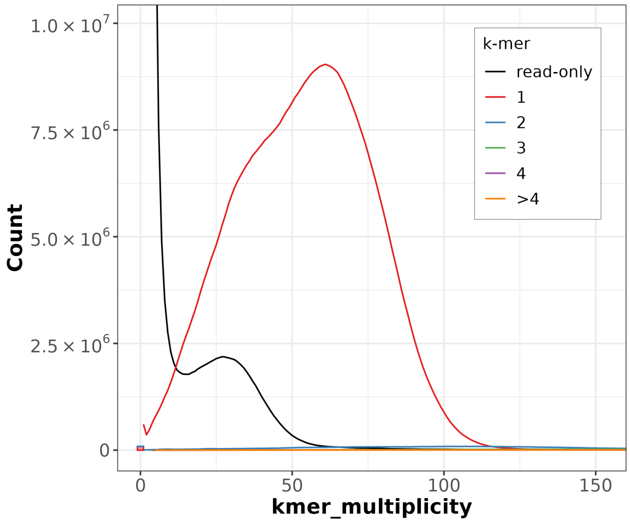
BUSCO: 5.8.2 (euk_genome_met, metaeuk) / Lineage: actinopterygii_odb12 (genomes:75, BUSCOs:7207)

HiC contact map of curated assembly

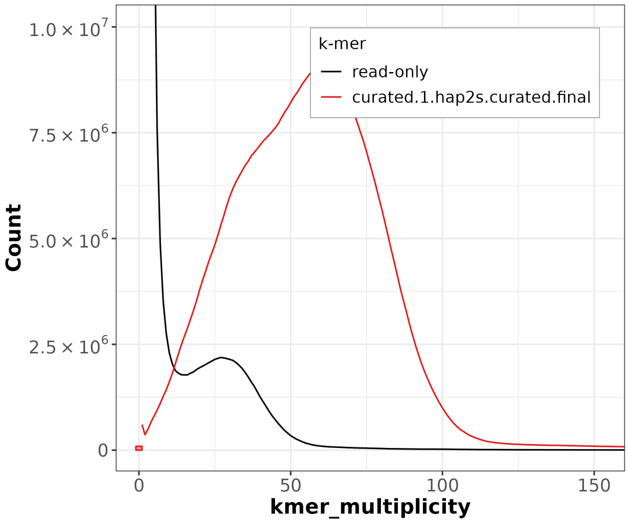


collapsed [LINK]

K-mer spectra of curated assembly

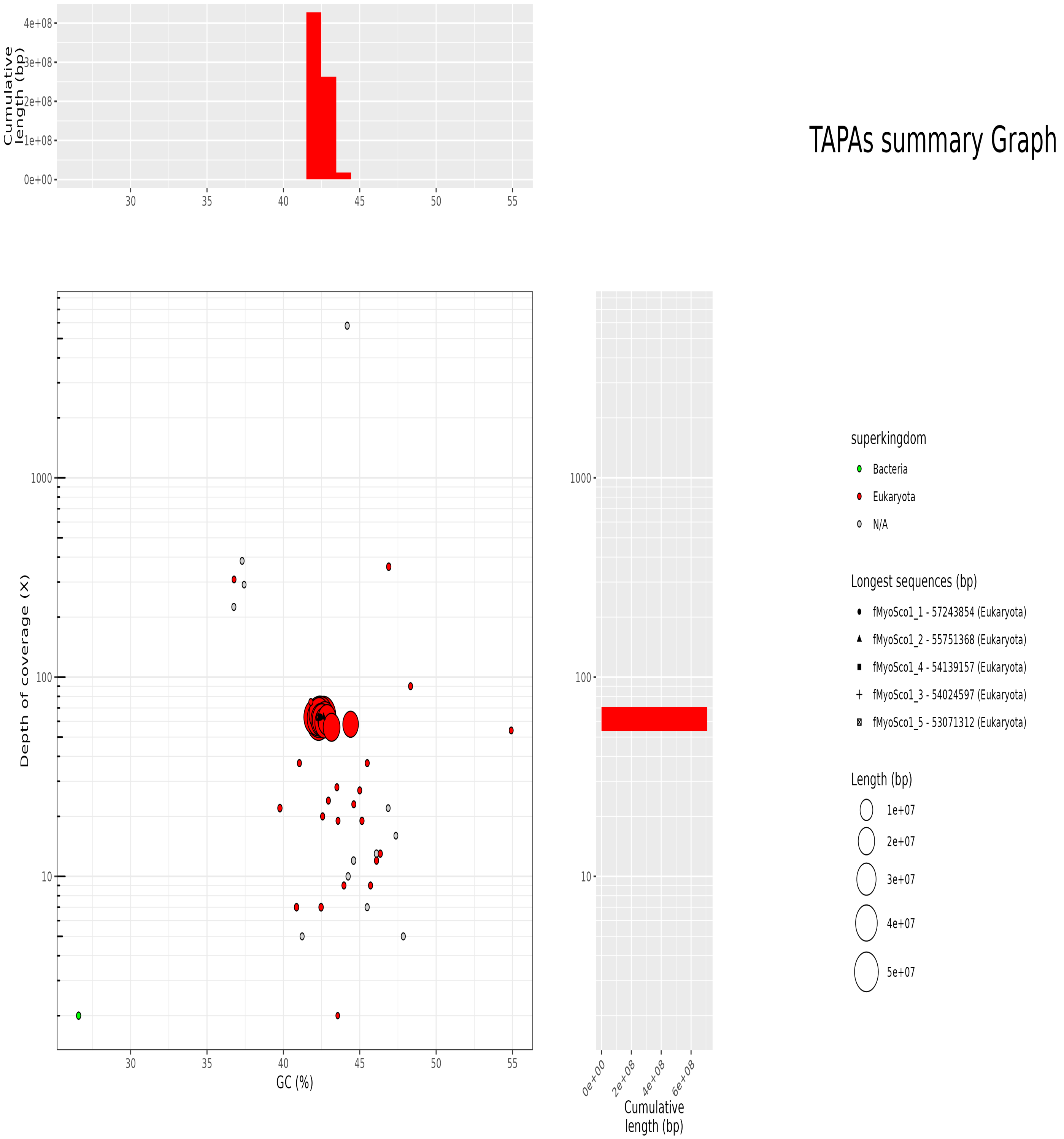


Distribution of k-mer counts per copy numbers found in asm



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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