ERGA Assembly Report

v24.10.15

Tags: ATLASea[INVALID TAG]

TxID	56737
ToLID	**fTraDra6**
Species	Trachinus draco
Class	Actinopteri
Order	Perciformes

Genome Traits	Expected	Observed
Haploid size (bp)	798,748,962	817,383,733
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

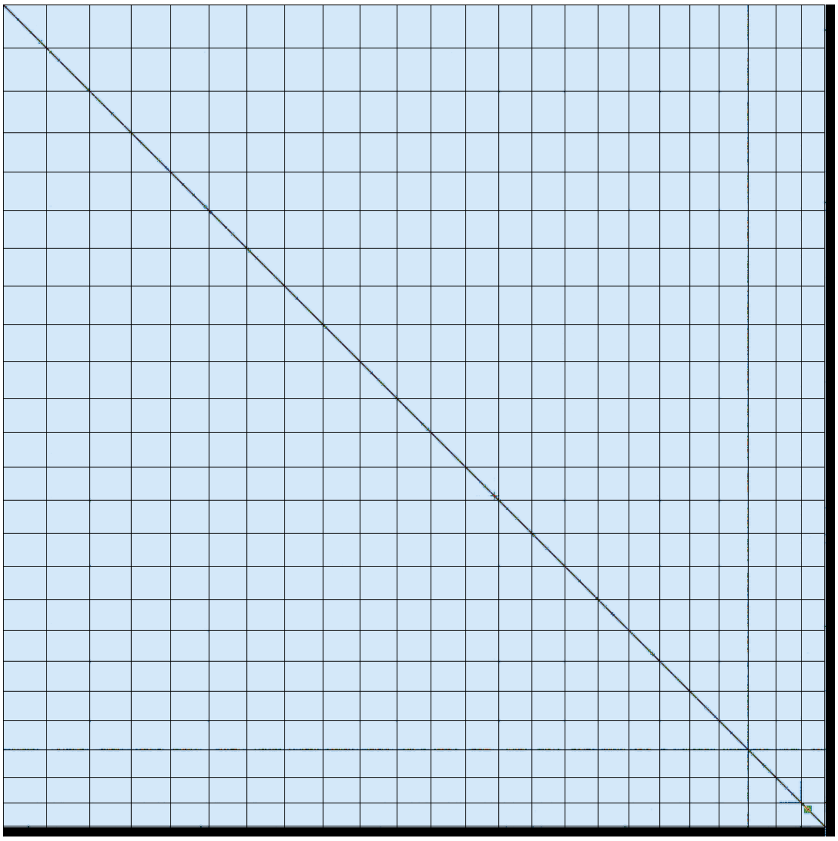
. Interventions/Gb: 9
. Contamination notes: ""
. Other observations: "The assembly of Trachinus draco (fTraDra6) is based on 44X PacBio data and 279X OmniC Hi-C data generated as part of the ATLASea programme (https://www.atlasea.fr). The assembly process included the following steps: initial PacBio assembly generation with Hifiasm, removal of contaminant sequences using Context, removal of haplotypic duplications using purge_dups, and Hi-C-based scaffolding with YaHS. No contigs were found to be contaminants (bacterial, archaeal, or viral). Additionally, 172 regions totaling 30.625 Mb (with the largest being 8.654 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. 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	817,413,905	817,383,733
GC %	40.7	40.7
Gaps/Gbp	94.2	94.2
Total gap bp	8,500	9,100
Scaffolds	81	77
Scaffold N50	33,434,452	33,434,452
Scaffold L50	10	11
Scaffold L90	21	22
Contigs	154	154
Contig N50	28,153,903	28,153,903
Contig L50	13	13
Contig L90	30	30
QV	49.3314	49.3394
Kmer compl.	75.4663	75.4663
BUSCO sing.	97.3%	99.3%
BUSCO dupl.	0.2%	0.2%
BUSCO frag.	0.6%	0.0%
BUSCO miss.	1.9%	0.4%

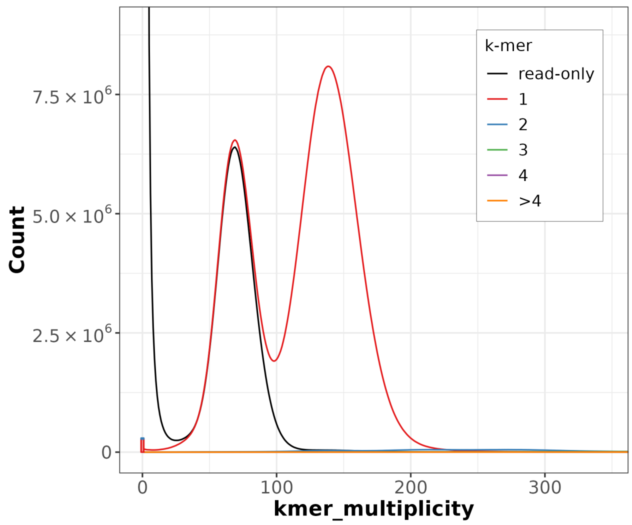
Warning! BUSCO versions or lineage datasets are not the same across results:
BUSCO: 5.8.2 (euk_genome_met, metaeuk) / Lineage: actinopterygii_odb12 (genomes:75, BUSCOs:7207)
BUSCO: 6.0.0 (euk_genome_min, miniprot) / Lineage: actinopterygii_odb12 (genomes:75, BUSCOs:7207)

HiC contact map of curated assembly

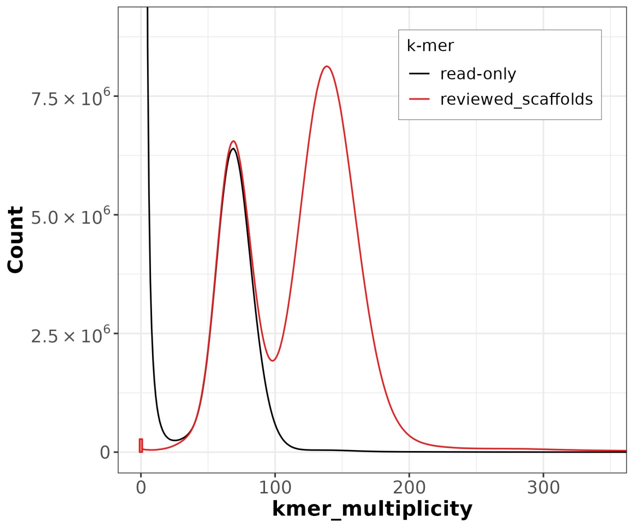


collapsed [LINK]

K-mer spectra of curated assembly

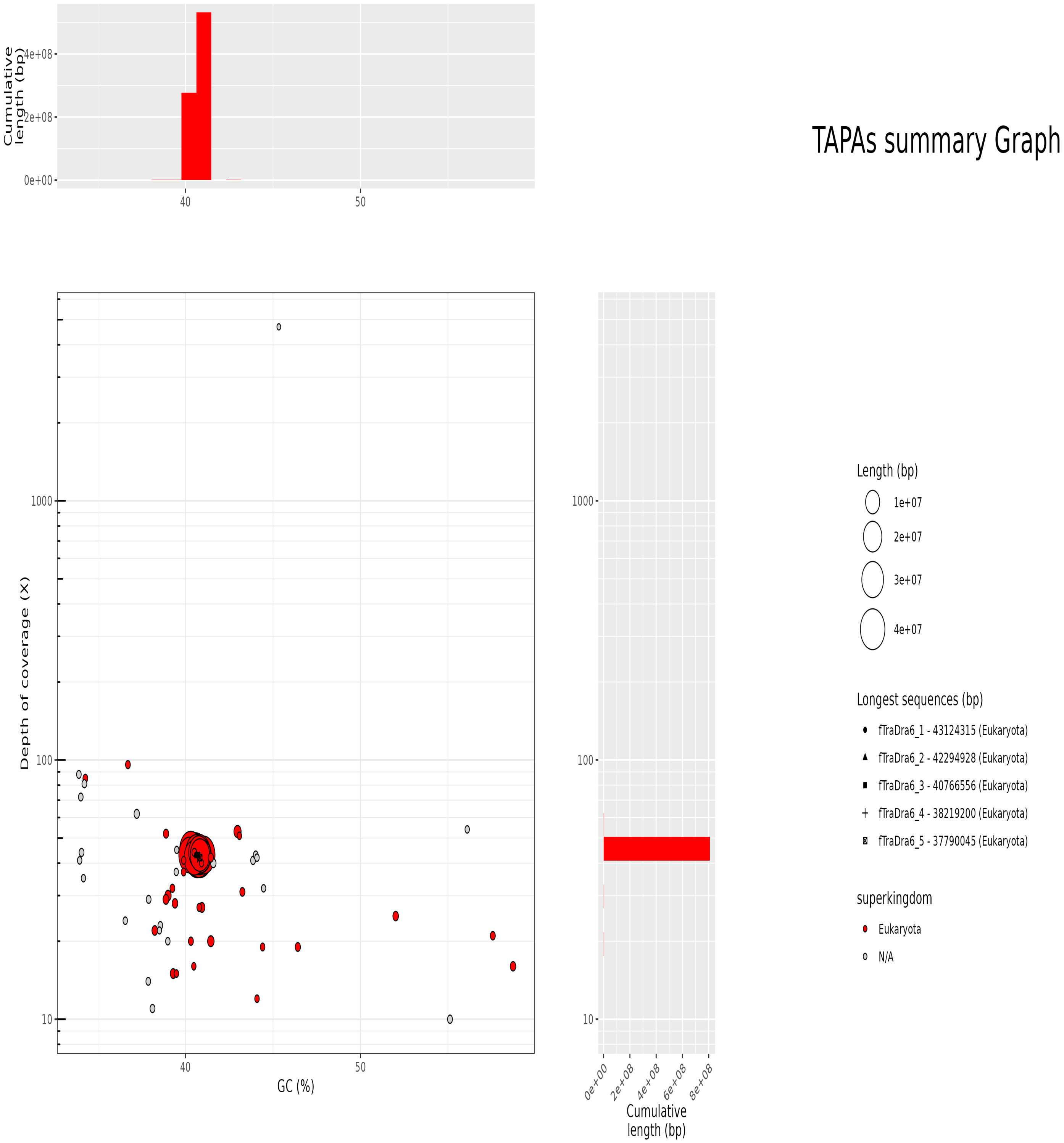


Distribution of k-mer counts per copy numbers found in asm



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

Post-curation contamination screening



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	Omnic
Coverage	43	279

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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