ERGA Assembly Report

v24.10.15

Tags: ATLASea[INVALID TAG]

TxID	246622
ToLID	**fAlpAfe1**
Species	Alphestes afer
Class	Actinopteri
Order	Perciformes

Genome Traits	Expected	Observed
Haploid size (bp)	981,953,298	1,004,081,665
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.Q50

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

Curator notes

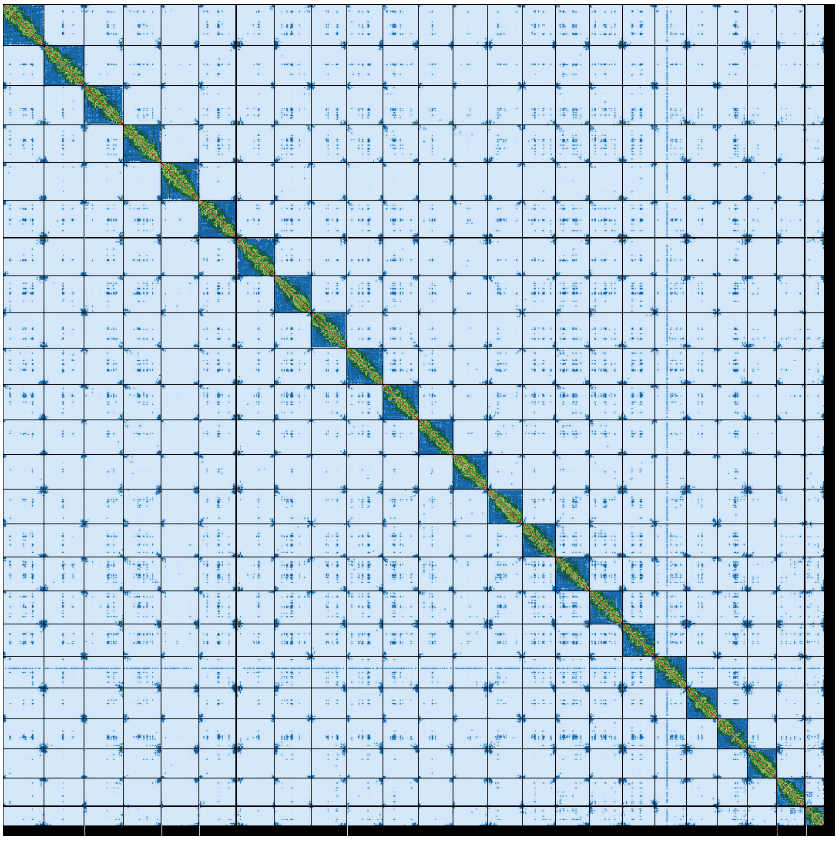
. Interventions/Gb: 26
. Contamination notes: ""
. Other observations: "The assembly of Alphestes afer (fAlpAfe1) is based on 46X PacBio data and 211X Arima Hi-C data generated as part of the ATLASea programme (https://www.atlasea.fr). The assembly process included the following steps: initial PacBio assembly generation with Hifiasm, removal of contaminant sequences using Context, removal of haplotypic duplications using purge_dups, and Hi-C-based scaffolding with YaHS. No contigs were found to be contaminants (bacterial, archaeal, or viral). Additionally, 92 regions totaling 7.467 Mb (with the largest being 0.661 Mb) were identified as haplotypic duplications and removed. 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	1,004,078,542	1,004,081,665
GC %	41.46	41.46
Gaps/Gbp	17.93	20.91
Total gap bp	1,800	2,500
Scaffolds	90	87
Scaffold N50	41,810,864	41,810,864
Scaffold L50	12	12
Scaffold L90	22	22
Contigs	108	108
Contig N50	40,355,020	40,355,020
Contig L50	12	12
Contig L90	23	23
QV	50.4332	50.4332
Kmer compl.	93.8076	93.8076
BUSCO sing.	99.5%	99.5%
BUSCO dupl.	0.2%	0.2%
BUSCO frag.	0.0%	0.0%
BUSCO miss.	0.3%	0.3%

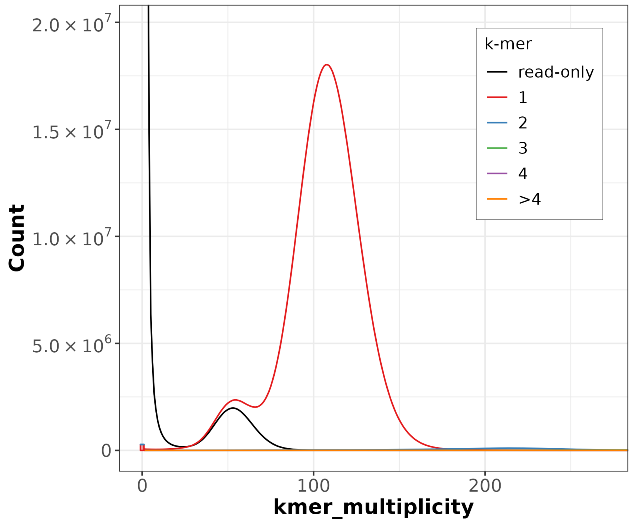
BUSCO: 6.0.0 (euk_genome_min, miniprot) / Lineage: actinopterygii_odb12 (genomes:75, BUSCOs:7207)

HiC contact map of curated assembly

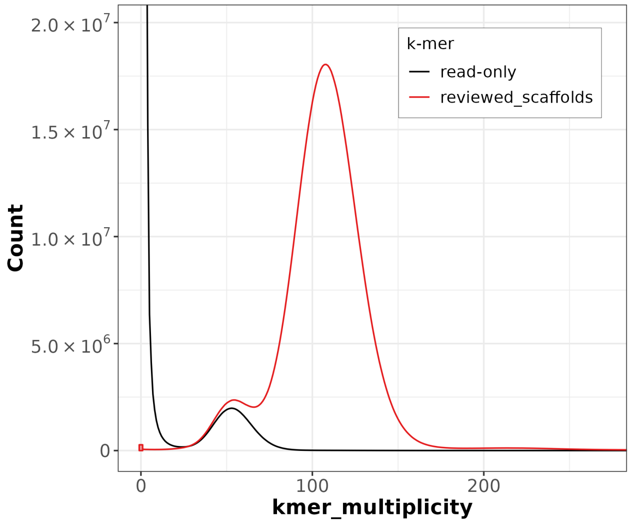


collapsed [LINK]

K-mer spectra of curated assembly

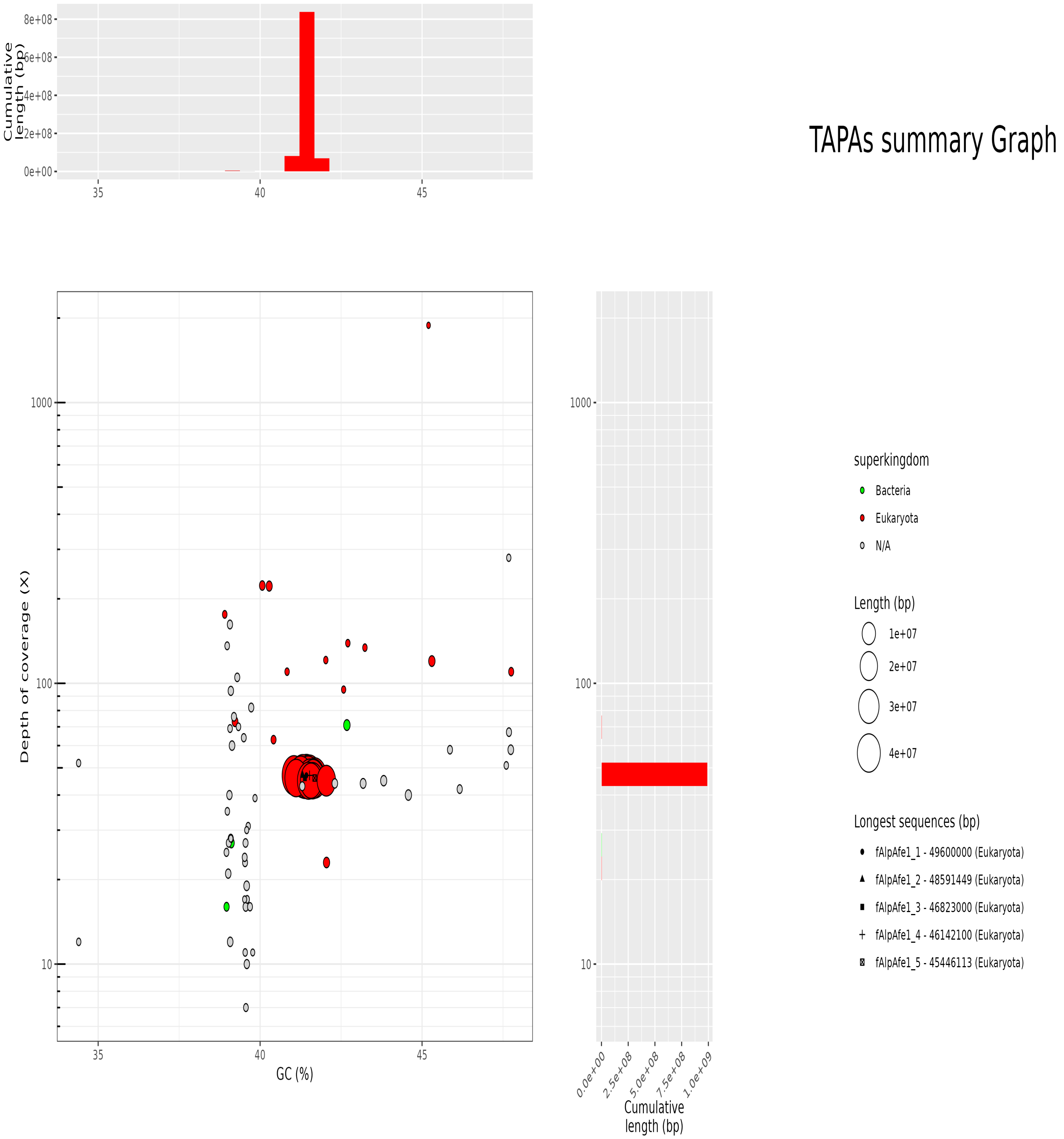


Distribution of k-mer counts per copy numbers found in asm



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	Arima
Coverage	46	211

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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