ERGA Assembly Report

v24.10.15

Tags: ATLASea[INVALID TAG]

TxID	2999897
ToLID	**fChaFls1**
Species	Chaunax flavomaculatus
Class	Actinopteri
Order	Lophiiformes

Genome Traits	Expected	Observed
Haploid size (bp)	653,830,877	673,279,983
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:

Curator notes

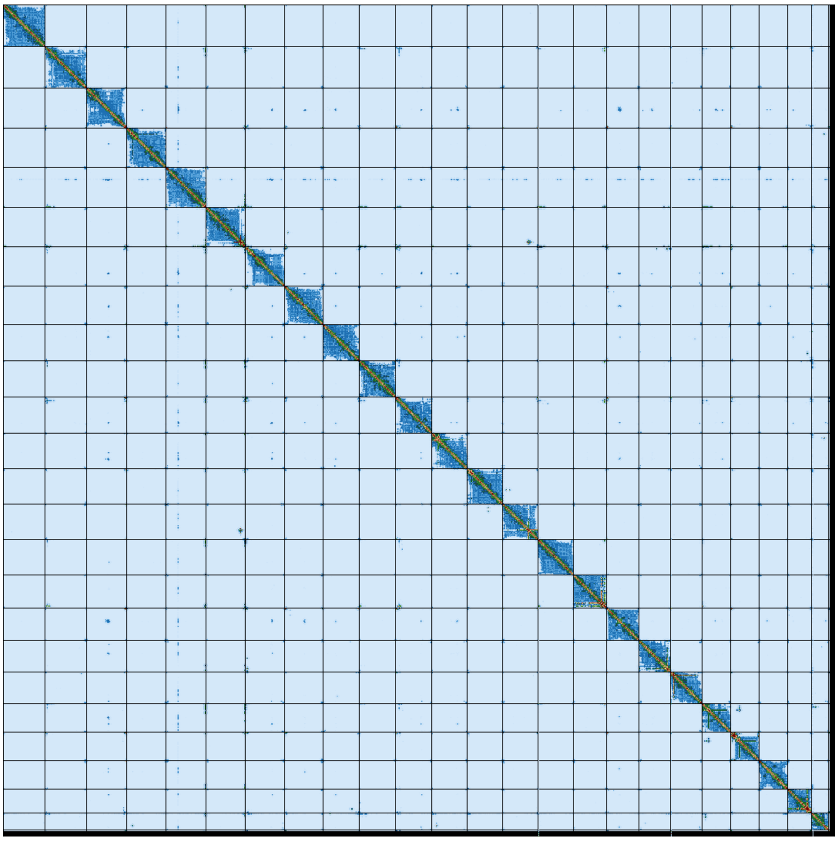
. Interventions/Gb: 27
. Contamination notes: ""
. Other observations: "The assembly of Chaunax flavomaculatus (fChaFls1) is based on 72X PacBio data and 295X OmniC Hi-C data generated as part of the ATLASea programme (https://www.atlasea.fr). The assembly process included the following steps: initial 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, 59 regions totaling 14.392 Mb (with the largest being 3.65 Mb) were identified as haplotypic duplications and removed. Mitochondrial genome was assembled using OATK. During manual curation, 1 haplotypic region was removed, totaling 0.86Mb (with the largest being 0.86Mb). 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	674,143,051	673,279,983
GC %	40.48	40.48
Gaps/Gbp	53.4	71.29
Total gap bp	3,600	6,300
Scaffolds	66	53
Scaffold N50	29,178,781	29,178,781
Scaffold L50	11	11
Scaffold L90	22	21
Contigs	102	101
Contig N50	23,300,000	23,300,000
Contig L50	13	13
Contig L90	37	37
QV	49.2948	49.2944
Kmer compl.	90.339	90.3307
BUSCO sing.	98.8%	99.0%
BUSCO dupl.	0.7%	0.6%
BUSCO frag.	0.1%	0.1%
BUSCO miss.	0.4%	0.4%

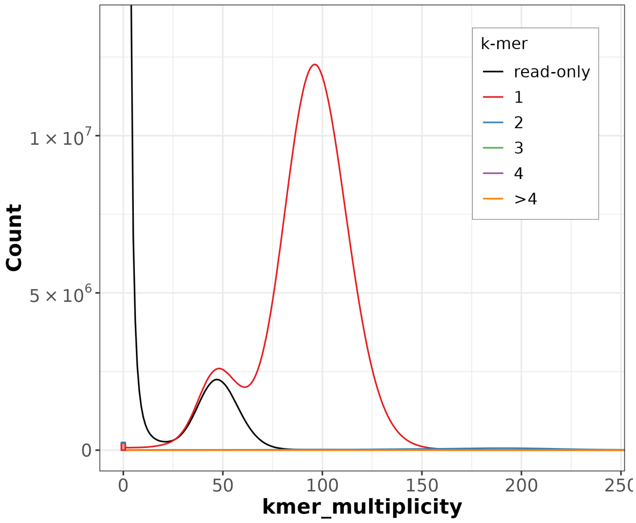
BUSCO: 6.0.0 (euk_genome_min, miniprot) / Lineage: actinopterygii_odb12 (genomes:75, BUSCOs:7207)

HiC contact map of curated assembly

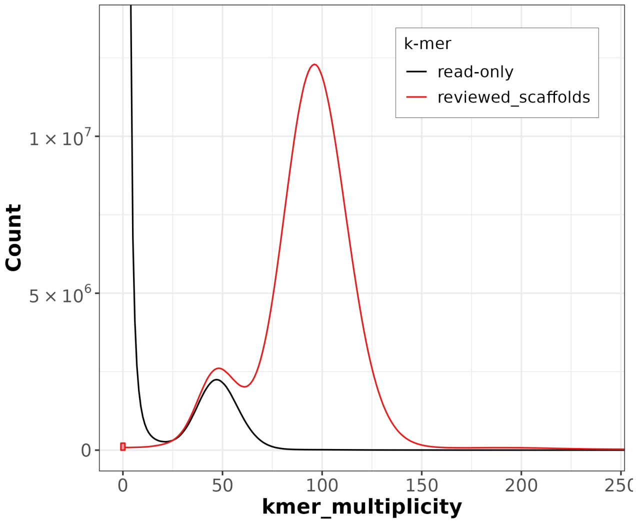


collapsed [LINK]

K-mer spectra of curated assembly

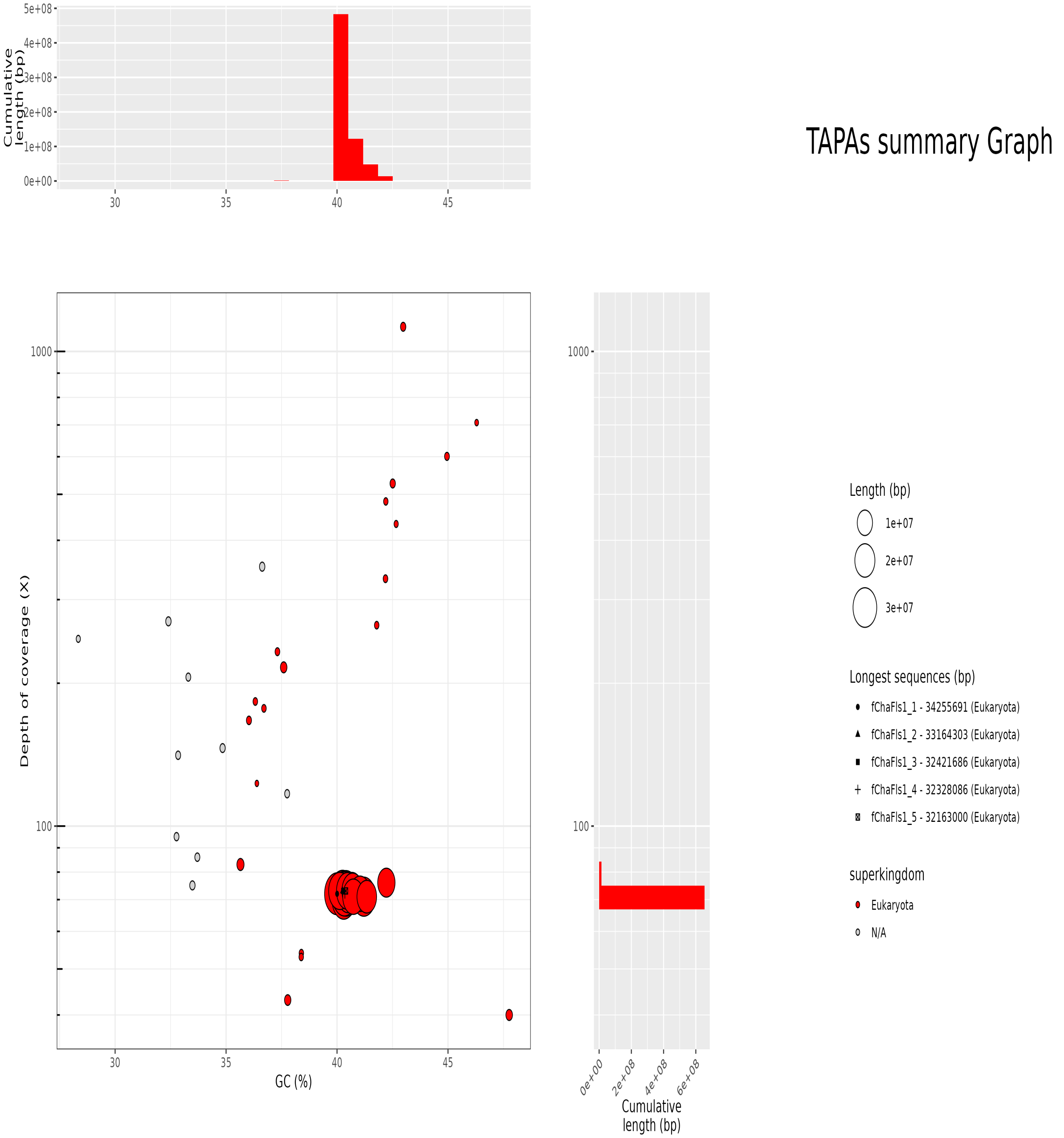


Distribution of k-mer counts per copy numbers found in asm



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	72	295

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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