ERGA Assembly Report

v24.10.15

Tags: Other[INVALID TAG]

TxID	8153
ToLID	**fHapBur1**
Species	Astatotilapia burtoni
Class	Actinopteri
Order	Cichliformes

Genome Traits	Expected	Observed
Haploid size (bp)	827,591,195	1,778,393,173
Haploid Number	19 (source: ancestor)	40
Ploidy	2 (source: ancestor)	2
Sample Sex	Unknown	Unknown

EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 6.7.Q59

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

. Observed Haploid size (bp) has >20% difference with Expected
. Observed Haploid Number is different from Expected

. BUSCO single copy value is less than 90% for collapsed
. BUSCO duplicated value is more than 5% for collapsed

Curator notes

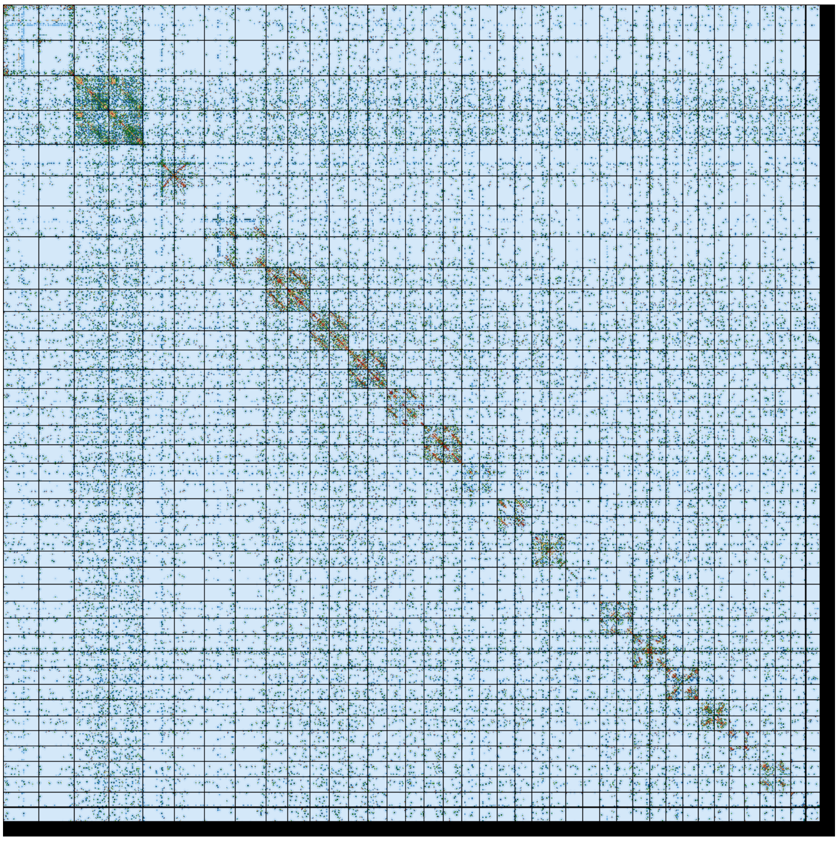
. Interventions/Gb: 39
. Contamination notes: ""
. Other observations: "The assembly of Astatotilapia burtoni (fHapBur1) was generated as part of the Vertebrate Genomes Project (https://vertebrategenomesproject.org/). Both haplotypes were analyzed and manually improved using Pretext "

Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	1,778,387,773	1,778,393,173
GC %	41.05	41.05
Gaps/Gbp	188.37	203.55
Total gap bp	67,000	72,400
Scaffolds	448	438
Scaffold N50	46,594,217	40,434,971
Scaffold L50	13	16
Scaffold L90	33	36
Contigs	783	800
Contig N50	8,965,086	8,466,078
Contig L50	60	62
Contig L90	209	222
QV	59.1748	59.1748
Kmer compl.	99.3767	99.3767
BUSCO sing.	2.5%	2.2%
BUSCO dupl.	95.0%	95.3%
BUSCO frag.	0.7%	0.7%
BUSCO miss.	1.7%	1.8%

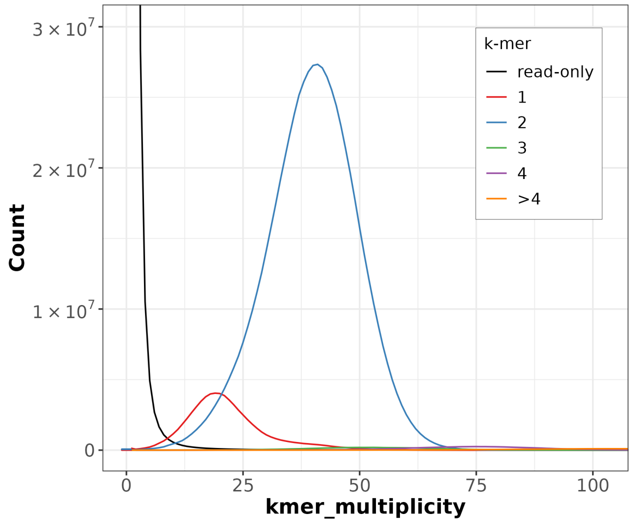
BUSCO: 5.8.2 (euk_genome_met, metaeuk) / Lineage: actinopterygii_odb12 (genomes:75, BUSCOs:7207)

HiC contact map of curated assembly

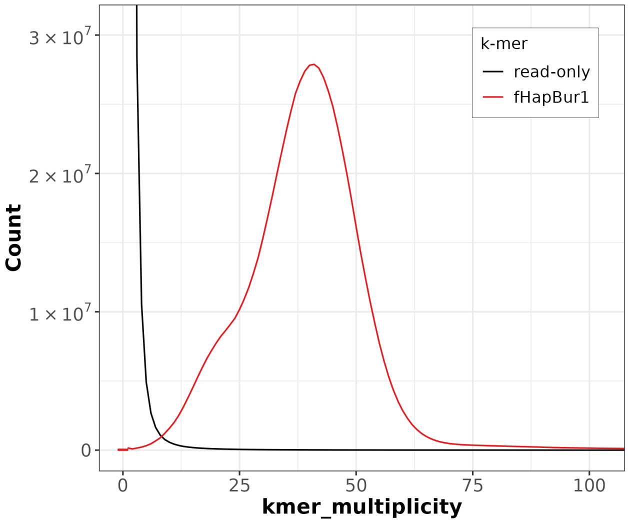


collapsed [LINK]

K-mer spectra of curated assembly

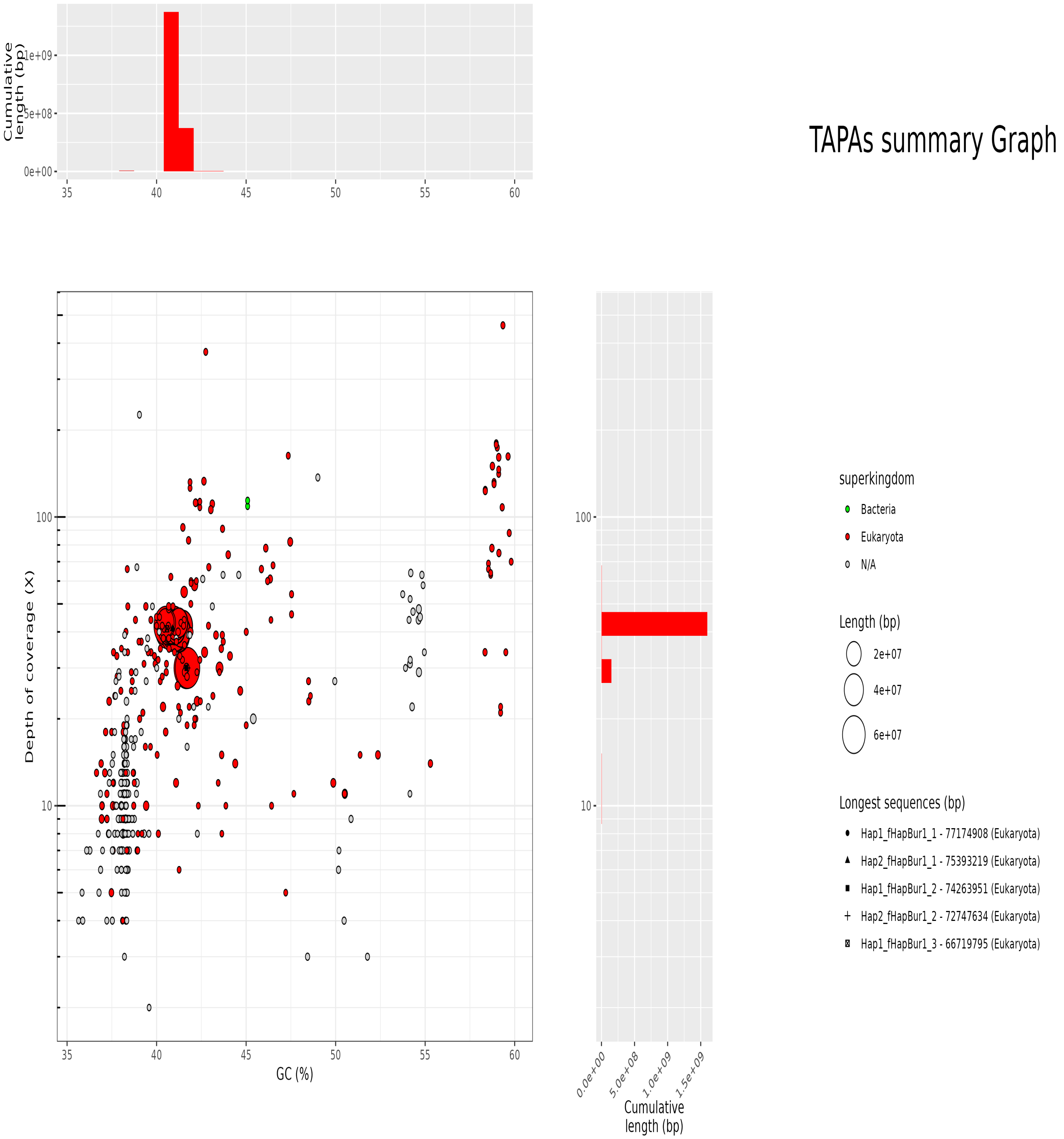


Distribution of k-mer counts per copy numbers found in asm



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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