

ERGA Assembly Report

v24.10.15

Tags: Other[INVALID TAG]

TxID	8153
ToLID	fHapBur2_h2
Species	Haplochromis burtoni
Class	Actinopteri
Order	Cichliformes

Genome Traits	Expected	Observed
Haploid size (bp)	845,713,155	886,825,585
Haploid Number	19 (source: ancestor)	20
Ploidy	2 (source: ancestor)	2
Sample Sex	Unknown	Unknown

EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 7.7.Q59

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

- . Observed Haploid Number is different from Expected

Curator notes

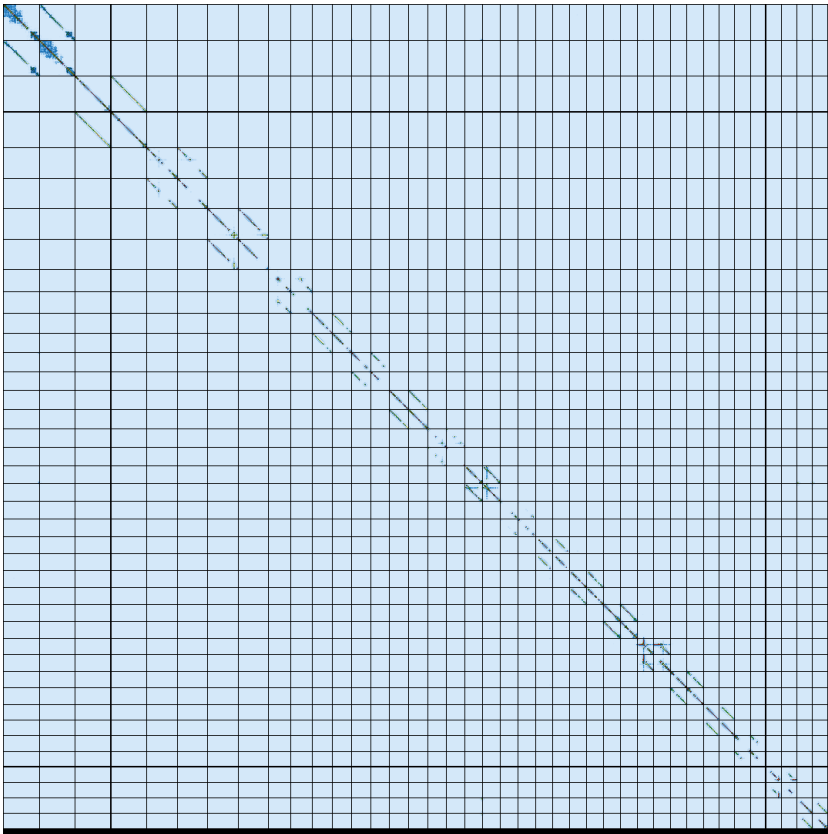
- . Interventions/Gb: 53
- . Contamination notes: ""
- . Other observations: "The assembly of Haplochromis burtoni (fHapBur2.1) was generated as part of the Vertebrate Genomes Project (<https://vertebrategenomesproject.org/>). Both haplotypes were analyzed and manually improved using Pretext. "

Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	892,868,092	886,825,585
GC %	41.07	41.09
Gaps/Gbp	136.64	155.61
Total gap bp	24,400	27,600
Scaffolds	128	115
Scaffold N50	46,284,737	40,573,942
Scaffold L50	7	8
Scaffold L90	16	18
Contigs	250	253
Contig N50	13,649,456	10,941,713
Contig L50	22	27
Contig L90	81	85
QV	59.4956	59.5779
Kmer compl.	94.1048	93.8129
BUSCO sing.	95.8%	95.7%
BUSCO dupl.	0.8%	0.7%
BUSCO frag.	0.9%	0.8%
BUSCO miss.	2.6%	2.7%

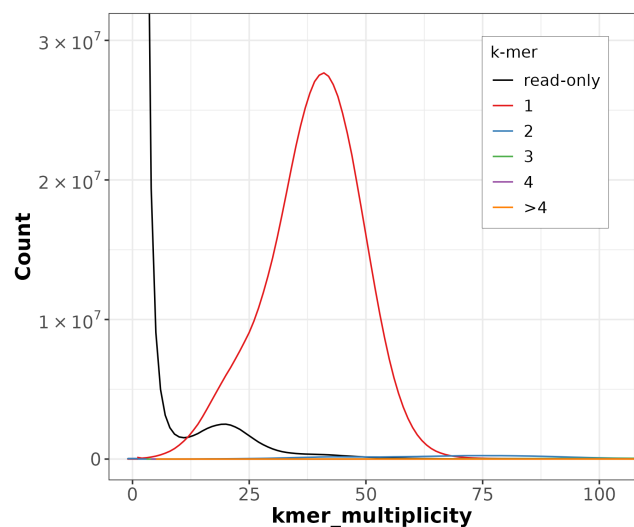
BUSCO: 5.8.2 (euk_genome_met, metaeuk) / Lineage: actinopterygii_odb12 (genomes:75, BUSCOs:7207)

HiC contact map of curated assembly

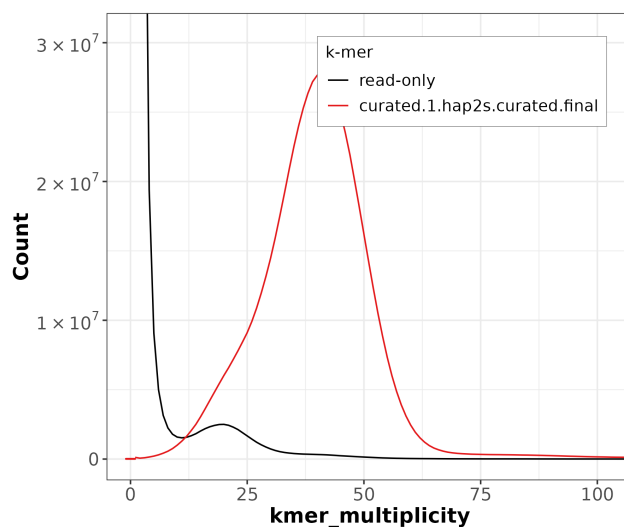


collapsed [\[LINK\]](#)

K-mer spectra of curated assembly

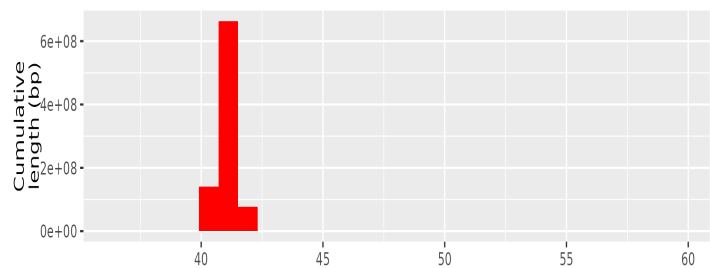


Distribution of k-mer counts per copy numbers found in asm

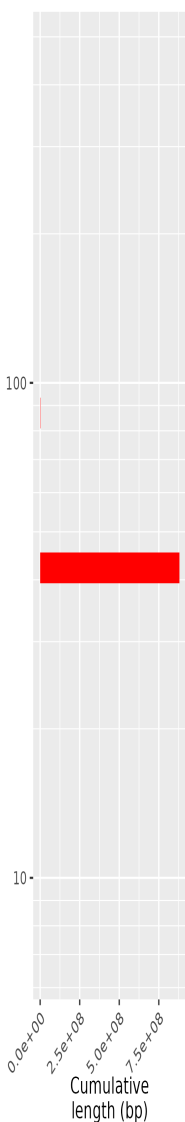
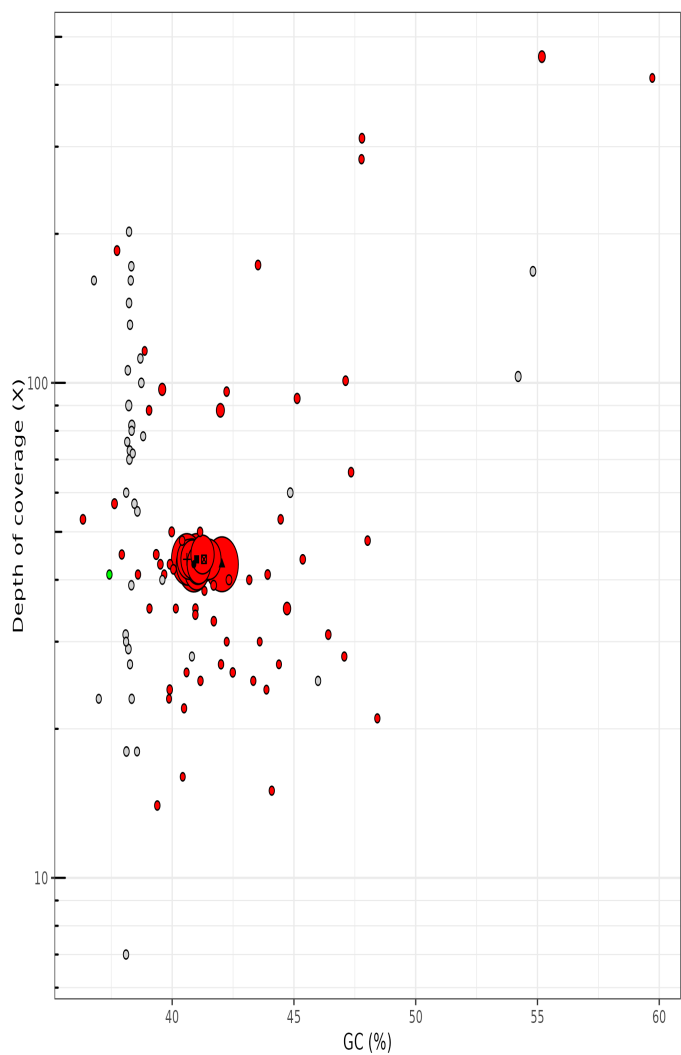


Distribution of k-mer counts coloured by their presence in reads/assemblies

Post-curation contamination screening



TAPAs summary Graph



superkingdom

- Bacteria
- Eukaryota
- N/A

Length (bp)

- 2e+07
- 4e+07
- 6e+07

Longest sequences (bp)

- fHapBur2_2 - 77150240 (Eukaryota)
- ▲ fHapBur2_1 - 75642445 (Eukaryota)
- fHapBur2_3 - 65018418 (Eukaryota)
- + fHapBur2_4 - 64911583 (Eukaryota)
- ▣ fHapBur2_5 - 46284737 (Eukaryota)

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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