

ERGA Assembly Report

v24.10.15

Tags: Other[INVALID TAG]

TxID	8153
ToLID	fHapBur2_h1
Species	<i>Haplochromis burtoni</i>
Class	Actinopteri
Order	Cichliformes

Genome Traits	Expected	Observed
Haploid size (bp)	845,713,155	907,033,570
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: 6.7.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

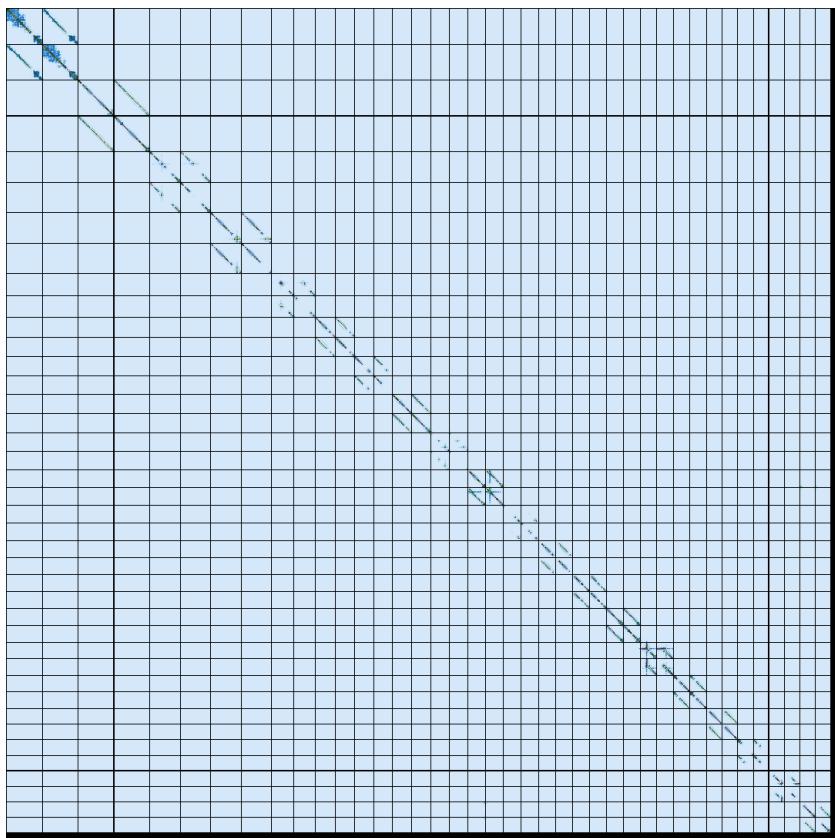
- Interventions/Gb: 53
- Contamination notes: ""
- Other observations: "The assembly of *Haplochromis burtoni* (fHapBur2.1) was generated as part of the Vertebrate Genomes Project (<https://vertebratogenomesproject.org/>). Both haplotypes were analyzed and manually improved using Pretext. "

Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	900,965,899	907,033,570
GC %	41.08	41.06
Gaps/Gbp	153.17	179.71
Total gap bp	27,600	32,600
Scaffolds	201	183
Scaffold N50	40,640,326	41,410,317
Scaffold L50	8	8
Scaffold L90	18	18
Contigs	339	346
Contig N50	9,768,771	9,972,013
Contig L50	28	24
Contig L90	93	93
QV	59.6904	59.6066
Kmer compl.	94.0401	94.3081
BUSCO sing.	95.9%	96.1%
BUSCO dupl.	0.8%	0.8%
BUSCO frag.	0.8%	0.8%
BUSCO miss.	2.6%	2.3%

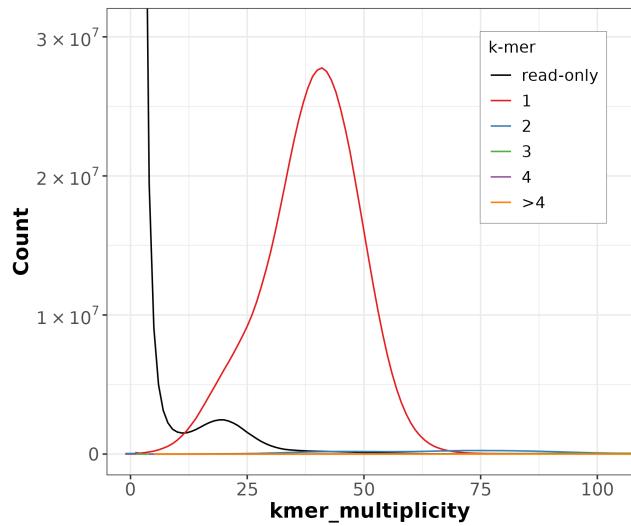
BUSCO: 5.8.2 (euk_genome_met, metaeuk) / Lineage: actinopterygii_odb12 (genomes:75, BUSCOs:7207)

HiC contact map of curated assembly

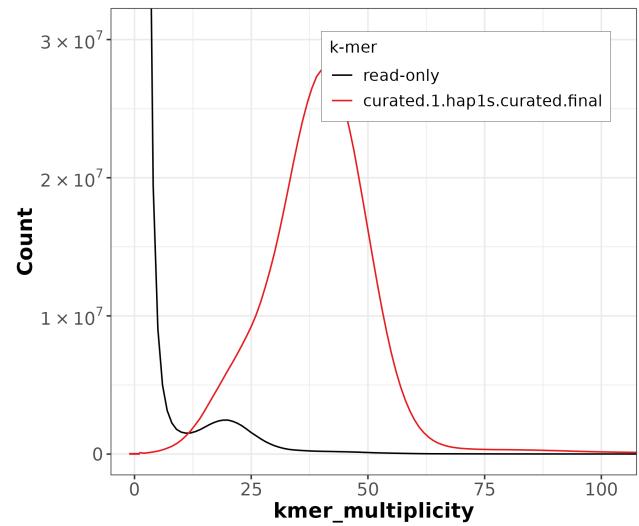


collapsed [\[LINK\]](#)

K-mer spectra of curated assembly

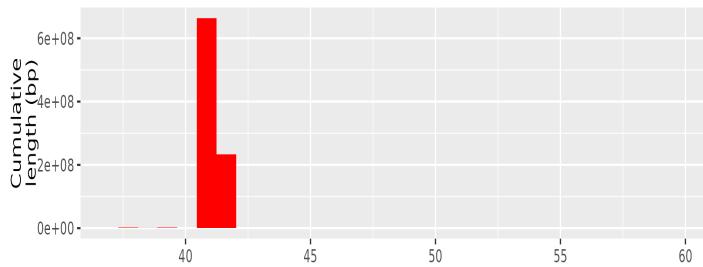


Distribution of k-mer counts per copy numbers found in asm

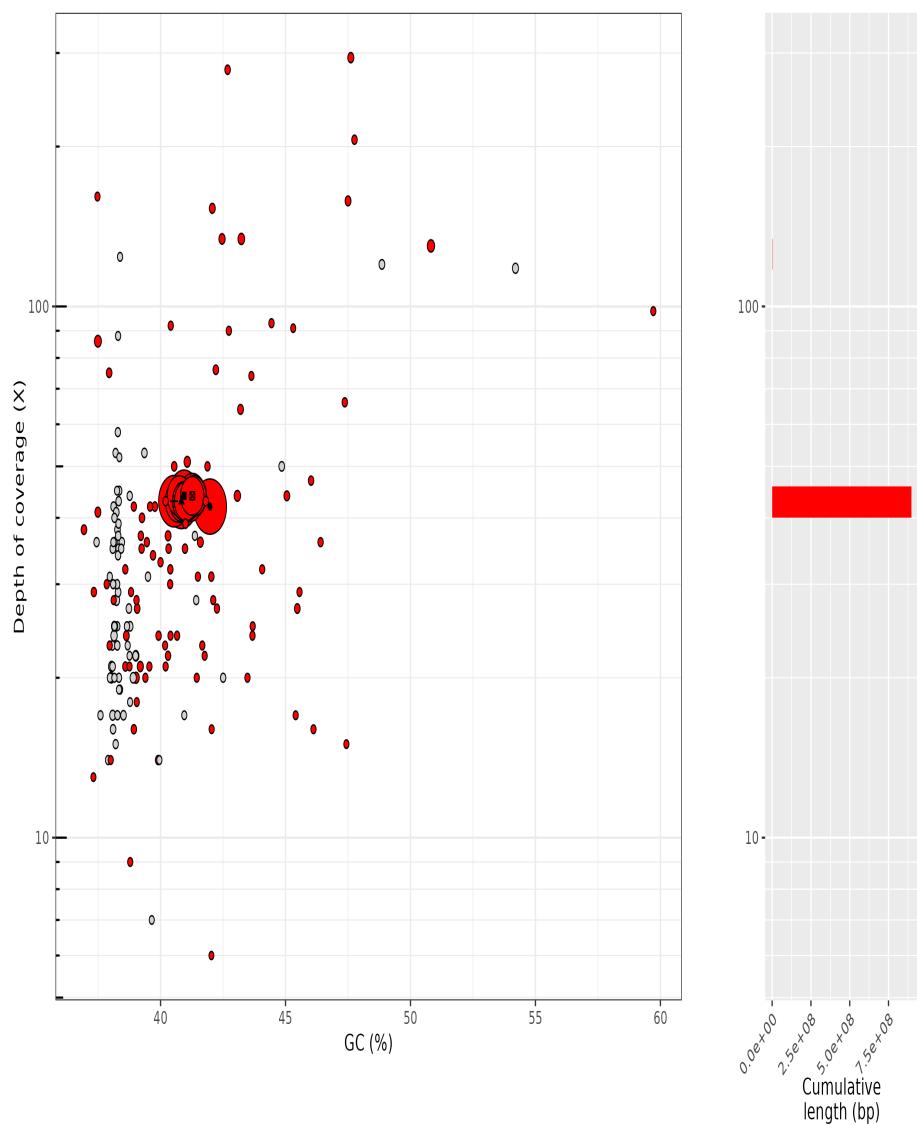


Distribution of k-mer counts coloured by their presence in reads/assemblies

Post-curation contamination screening



TAPAs summary Graph



Length (bp)

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

superkingdom

- Eukaryota
- N/A

Longest sequences (bp)

- fHapBur2_1 - 78276036 (Eukaryota)
- ▲ fHapBur2_2 - 77460584 (Eukaryota)
- fHapBur2_3 - 66706600 (Eukaryota)
- ✚ fHapBur2_4 - 66487641 (Eukaryota)
- ▣ fHapBur2_5 - 47784665 (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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Date and time: 2025-08-04 14:45:18 CEST