

ERGA Assembly Report

v24.10.15

Tags: Other[INVALID TAG]

TxID	28791
ToLID	fCypLut1_hap1
Species	Cyprinella lutrensis
Class	Actinopteri
Order	Cypriniformes

Genome Traits	Expected	Observed
Haploid size (bp)	802,987,641	926,985,129
Haploid Number	25 (source: direct)	25
Ploidy	2 (source: ancestor)	2
Sample Sex	Unknown	Unknown

EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 6.7.Q57

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

Curator notes

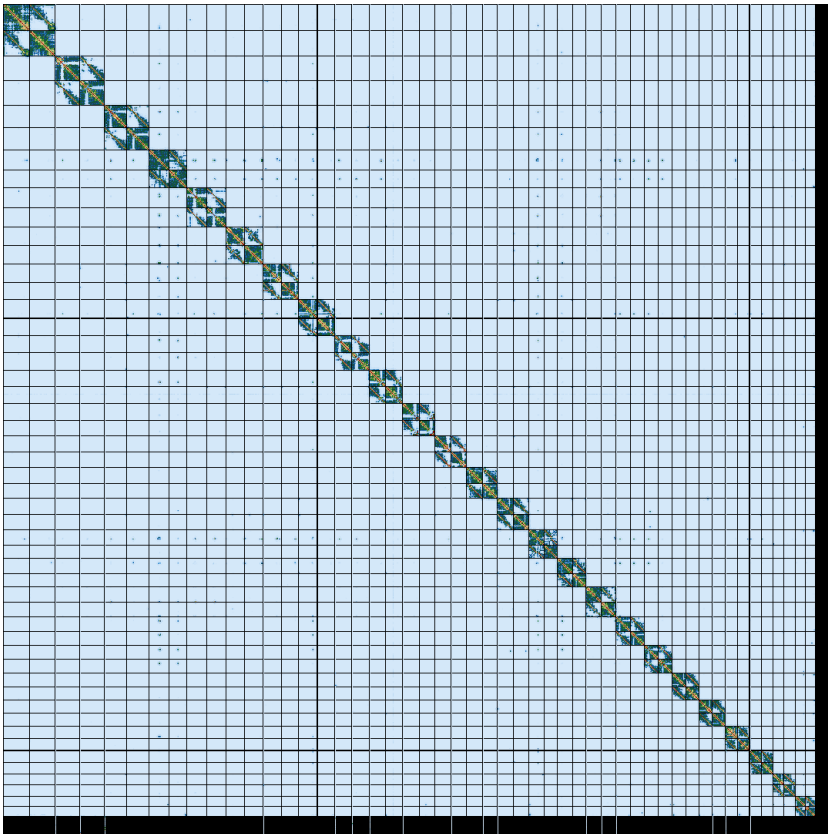
. Interventions/Gb: 154
. Contamination notes: ""
. Other observations: "The assembly of *Cyprinella lutrensis* (fCypLut1) was generated as part of the Vertebrate Genomes Project (<https://vertebrategenomesproject.org/>). Both haplotypes were analyzed and manually improved using Pretext. "

Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	905,396,741	926,985,129
GC %	38.58	38.61
Gaps/Gbp	875.86	900.77
Total gap bp	158,600	167,000
Scaffolds	470	456
Scaffold N50	36,464,699	36,156,036
Scaffold L50	9	11
Scaffold L90	21	23
Contigs	1,263	1,291
Contig N50	1,162,085	1,164,858
Contig L50	210	206
Contig L90	659	668
QV	57.4847	57.5044
Kmer compl.	74.3347	74.9648
BUSCO sing.	94.9%	
BUSCO dupl.	0.5%	
BUSCO frag.	1.2%	
BUSCO miss.	3.5%	

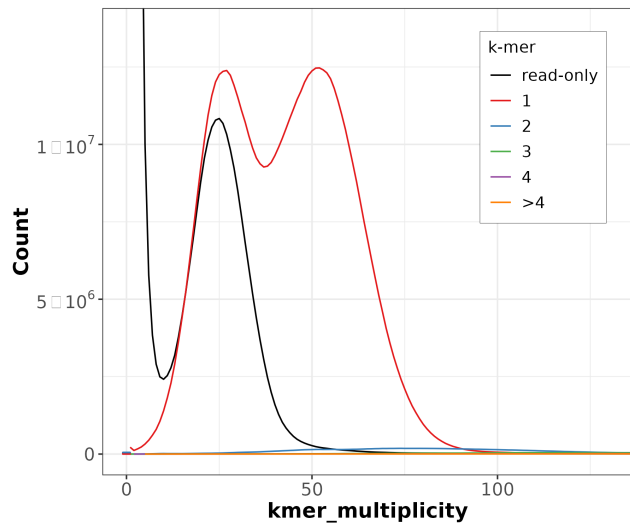
BUSCO: 5.8.2 (euk_genome_met, metaeuk) / Lineage: actinopterygii_odb12 (genomes:75, BUSCOs:7207)

HiC contact map of curated assembly

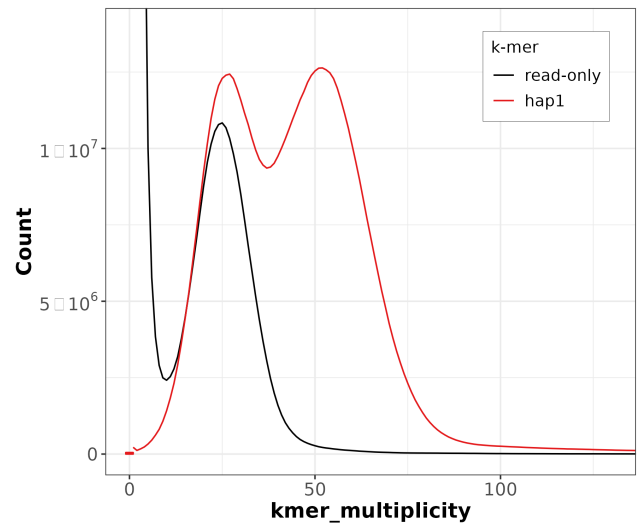


collapsed [\[LINK\]](#)

K-mer spectra of curated assembly

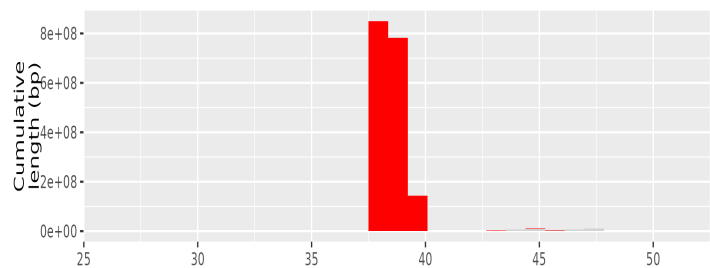


Distribution of k-mer counts per copy numbers found in asm



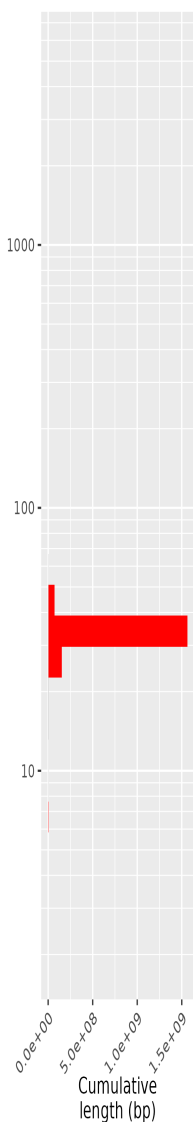
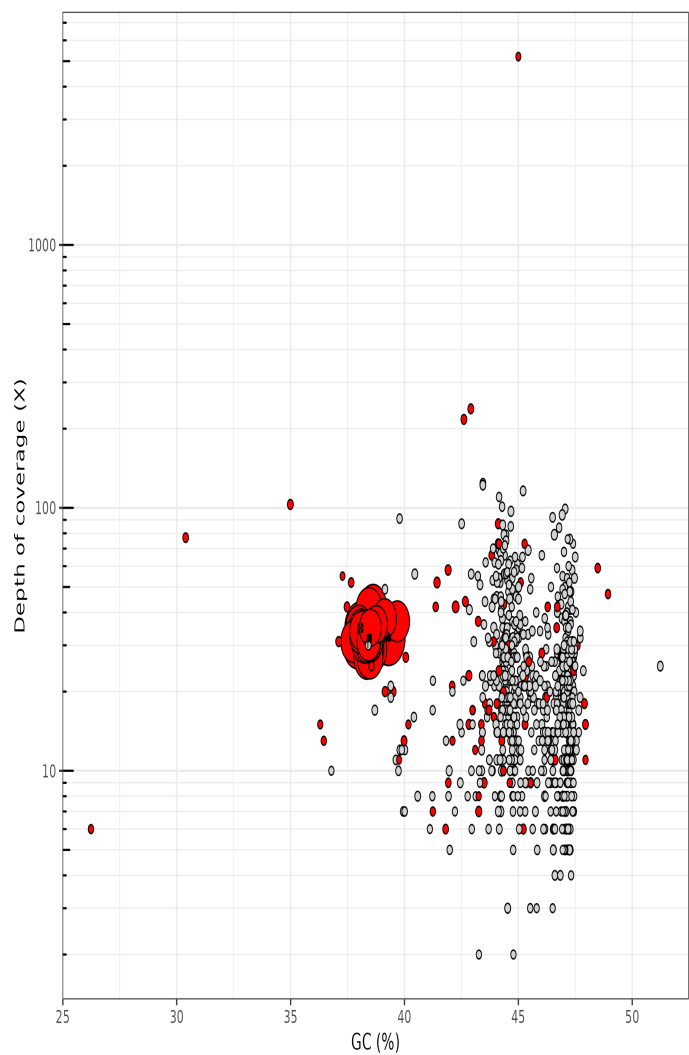
Distribution of k-mer counts coloured by their presence in reads/assemblies

Post-curation contamination screening

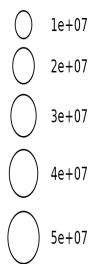


TAPAs summary Graph

(1 0X contig has been hidden)



Length (bp)



superkingdom



Longest sequences (bp)

- Hap1_fCypLut1_1 - 57444818 (Eukaryota)
- ▲ Hap2_fCypLut1_1 - 56629774 (Eukaryota)
- Hap1_fCypLut1_2 - 53729220 (Eukaryota)
- + Hap2_fCypLut1_2 - 53125133 (Eukaryota)
- ▣ Hap1_fCypLut1_3 - 49364229 (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	Long reads	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: 2025-10-20 08:59:17 CEST