

ERGA Assembly Report

v24.09.10

Tags: ATLASea[INVALID TAG]

TxID	357811
ToLID	fApoImb1.1
Species	Apogon imberbis
Class	Actinopteri
Order	Kurtiformes

Genome Traits	Expected	Observed
Haploid size (bp)	794,137,431	819,133,141
Haploid Number	24 (source: ancestor)	18
Ploidy	2 (source: ancestor)	2
Sample Sex	Unknown	Unknown

EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 7.7.Q48

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

- . Observed Haploid Number is different from Expected
- . Kmer completeness value is less than 90 for collapsed

Curator notes

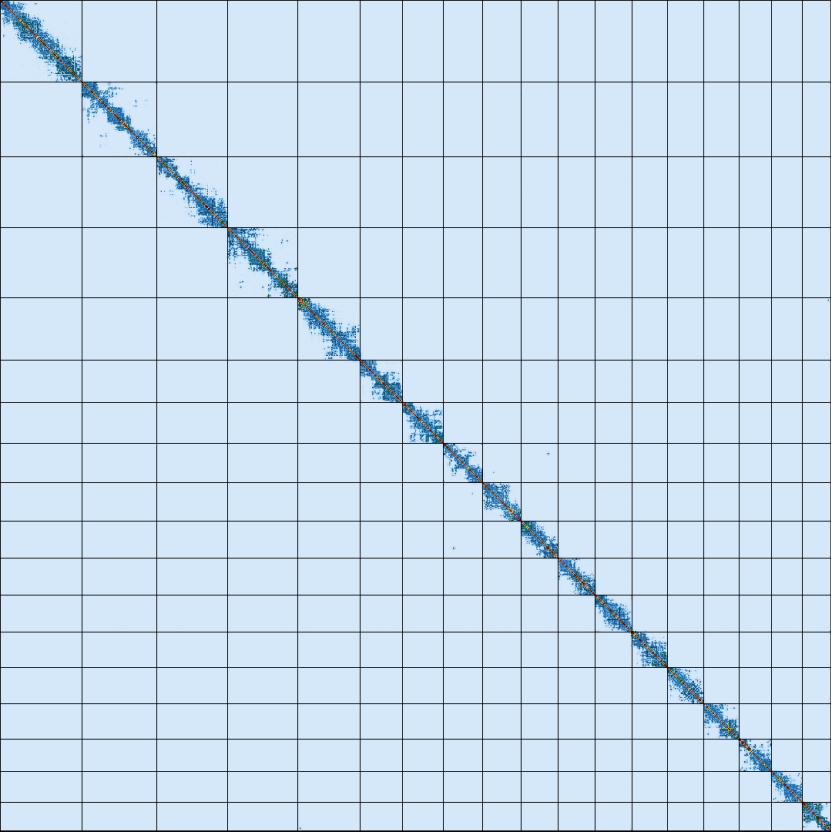
- . Interventions/Gb: 4
- . Contamination notes: "One bacterial sequence of 74 Kb detected. It was removed before scaffolding. "
- . Other observations: "Manual curation was minimal because we already had the chromosomes after scaffolding with yahs. The post-curation contamination screening plot corresponds to the assembly before bacterial sequences are removed. "

Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	819,152,605	819,133,141
GC %	39.9	39.9
Gaps/Gbp	3.66	6.1
Total gap bp	300	800
Scaffolds	38	33
Scaffold N50	40,310,727	40,310,727
Scaffold L50	7	7
Scaffold L90	16	16
Contigs	41	38
Contig N50	40,310,727	40,310,727
Contig L50	7	7
Contig L90	16	16
QV	48.2956	48.3336
Kmer compl.	82.7357	82.7356
BUSCO sing.	98.3%	98.3%
BUSCO dupl.	0.6%	0.6%
BUSCO frag.	0.2%	0.2%
BUSCO miss.	0.9%	0.9%

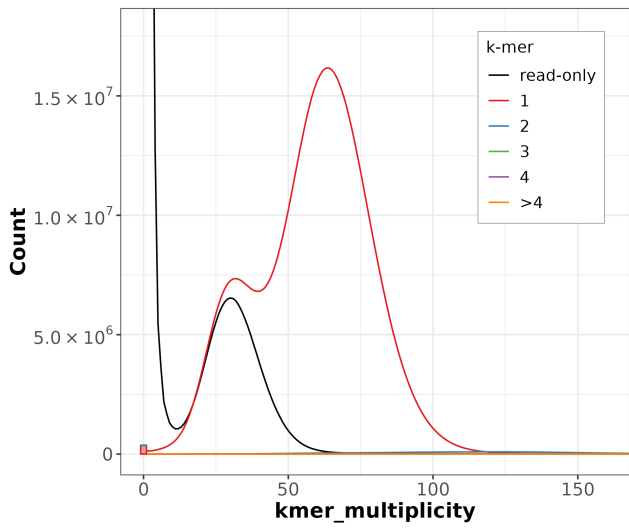
BUSCO 5.4.3 Lineage: actinopterygii_odb10 (genomes:26, BUSCOs:3640)

HiC contact map of curated assembly

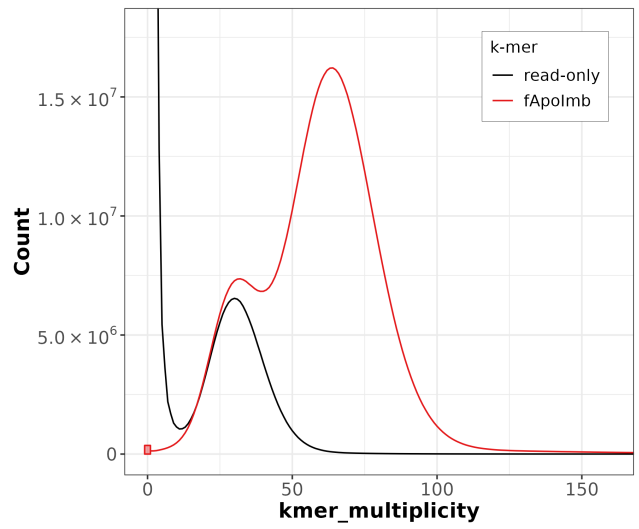


collapsed [\[LINK\]](#)

K-mer spectra of curated assembly

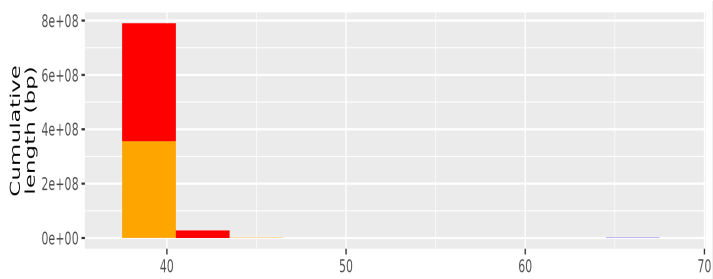


Distribution of k-mer counts per copy numbers found in asm



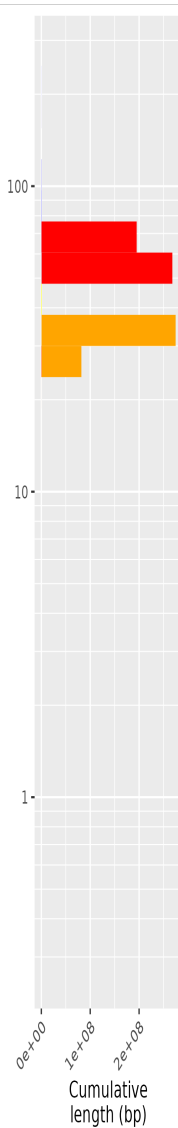
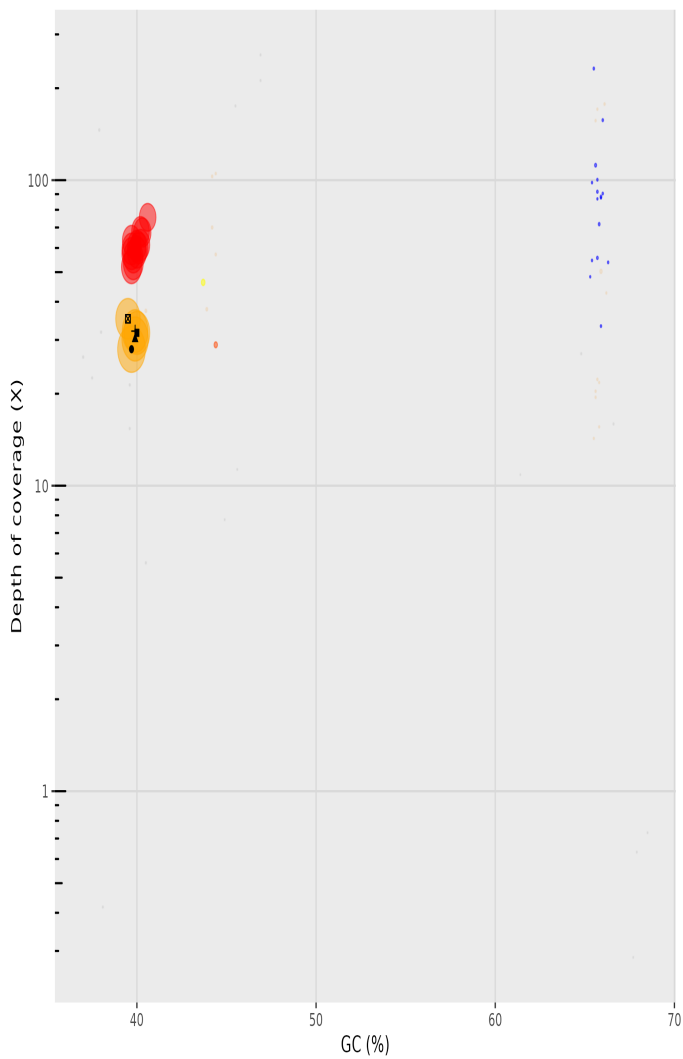
Distribution of k-mer counts coloured by their presence in reads/assemblies

Post-curation contamination screening



Decap Summary Graph

(12 0X contigs have been hidden)



MetaBAT binning
 <cluster>_<cumul.length>_<assignment>_<superkingdom>

- Clust10_462173867_N/A_N/A_Eukaryota
- Clust8_355493808_N/A_N/A_Eukaryota
- Clust5_1309144_Escherichia_coli_Bacteria
- Clust6_914879_N/A_N/A_Eukaryota
- Clust11_754271_N/A_N/A_Eukaryota
- other bins
- NULL

Longest sequences (bp)

- 81116326 (Clust8)
- ▲ 73440976 (Clust8)
- 69701495 (Clust8)
- + 69061070 (Clust8)
- 62173941 (Clust8)

Length (bp)

- 2e+07
- 4e+07
- 6e+07
- 8e+07

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	ONT	Arima
Coverage	93	128	60

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: 2024-11-19 14:41:01 CET