ERGA Assembly Report

v24.10.15

Tags: ATLASea[INVALID TAG]

TxID	88663
ToLID	**fBerSpl1**
Species	Beryx splendens
Class	Actinopteri
Order	Beryciformes

Genome Traits	Expected	Observed
Haploid size (bp)	788,070,465	827,657,184
Haploid Number	24 (source: direct)	24
Ploidy	2 (source: ancestor)	2
Sample Sex	Unknown	Unknown

EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 7.7.Q45

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

. Kmer completeness value is less than 90 for collapsed

Curator notes

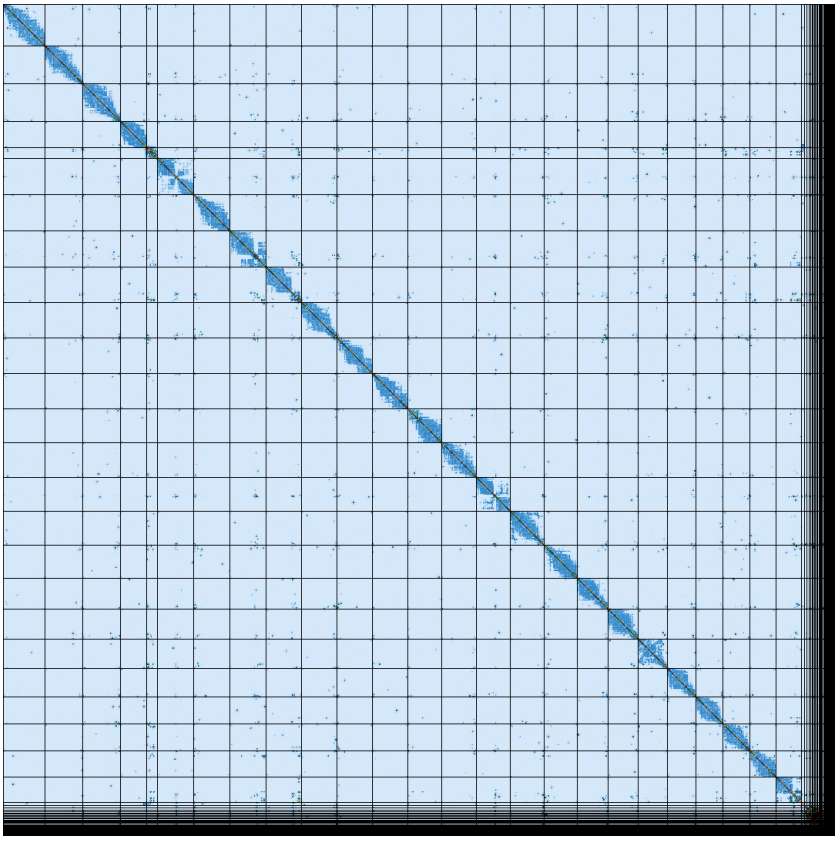
. Interventions/Gb: 63
. Contamination notes: ""
. Other observations: "The assembly of Beryx splendens (fBerSpl1) is based on 69X ONT data and 167X Arima Hi-C data generated as part of the ATLASea programme (https://www.atlasea.fr). The assembly process included the following steps: initial ONT assembly generation with Hifiasm, removal of contaminant sequences using Context, removal of haplotypic duplications using purge_dups, and Hi-C-based scaffolding with YaHS. No contigs were found to be contaminants (bacterial, archaeal, or viral). Additionally, 81 regions totaling 13.564 Mb (with the largest being 2.078 Mb) were identified as haplotypic duplications and removed. Mitochondrial genome was assembled using ptGAUL. Finally, the primary assembly was analyzed and manually improved using Pretext. Chromosome-scale scaffolds confirmed by Hi-C data were named in order of size. "

Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	828,025,693	827,657,184
GC %	44.75	44.75
Gaps/Gbp	9.66	13.29
Total gap bp	800	1,500
Scaffolds	110	101
Scaffold N50	34,063,000	34,063,000
Scaffold L50	12	12
Scaffold L90	23	23
Contigs	118	112
Contig N50	29,998,000	29,998,000
Contig L50	12	12
Contig L90	27	27
QV	45.1124	45.1127
Kmer compl.	79.2651	79.2649
BUSCO sing.	99.3%	98.3%
BUSCO dupl.	0.4%	0.4%
BUSCO frag.	0.0%	0.7%
BUSCO miss.	0.3%	0.6%

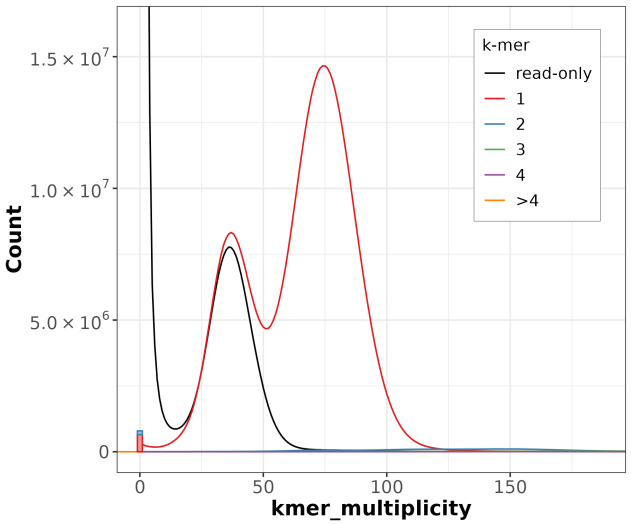
Warning! BUSCO versions or lineage datasets are not the same across results:
BUSCO: 6.0.0 (euk_genome_min, miniprot) / Lineage: actinopterygii_odb12 (genomes:75, BUSCOs:7207)
BUSCO: 5.8.2 (euk_genome_min, miniprot) / Lineage: actinopterygii_odb12 (genomes:75, BUSCOs:7207)

HiC contact map of curated assembly

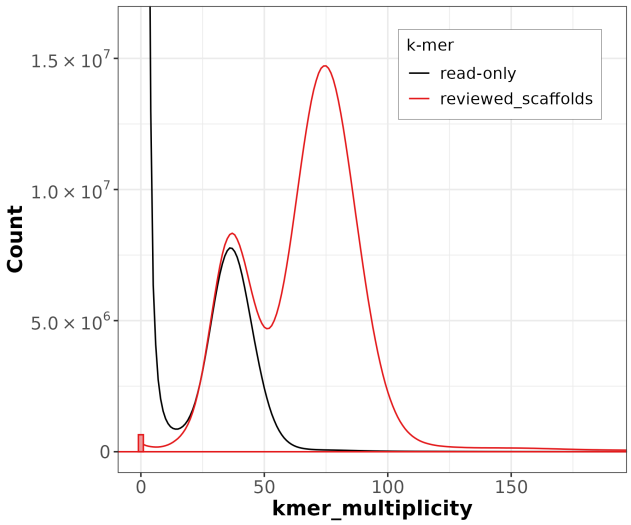


collapsed [LINK]

K-mer spectra of curated assembly

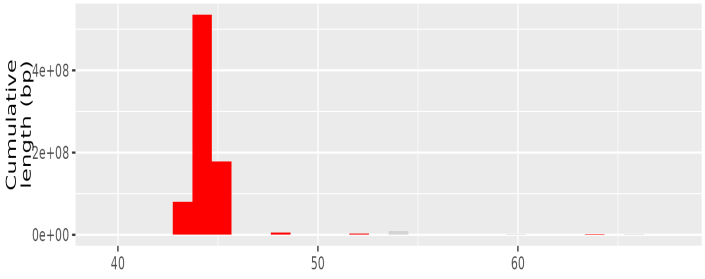


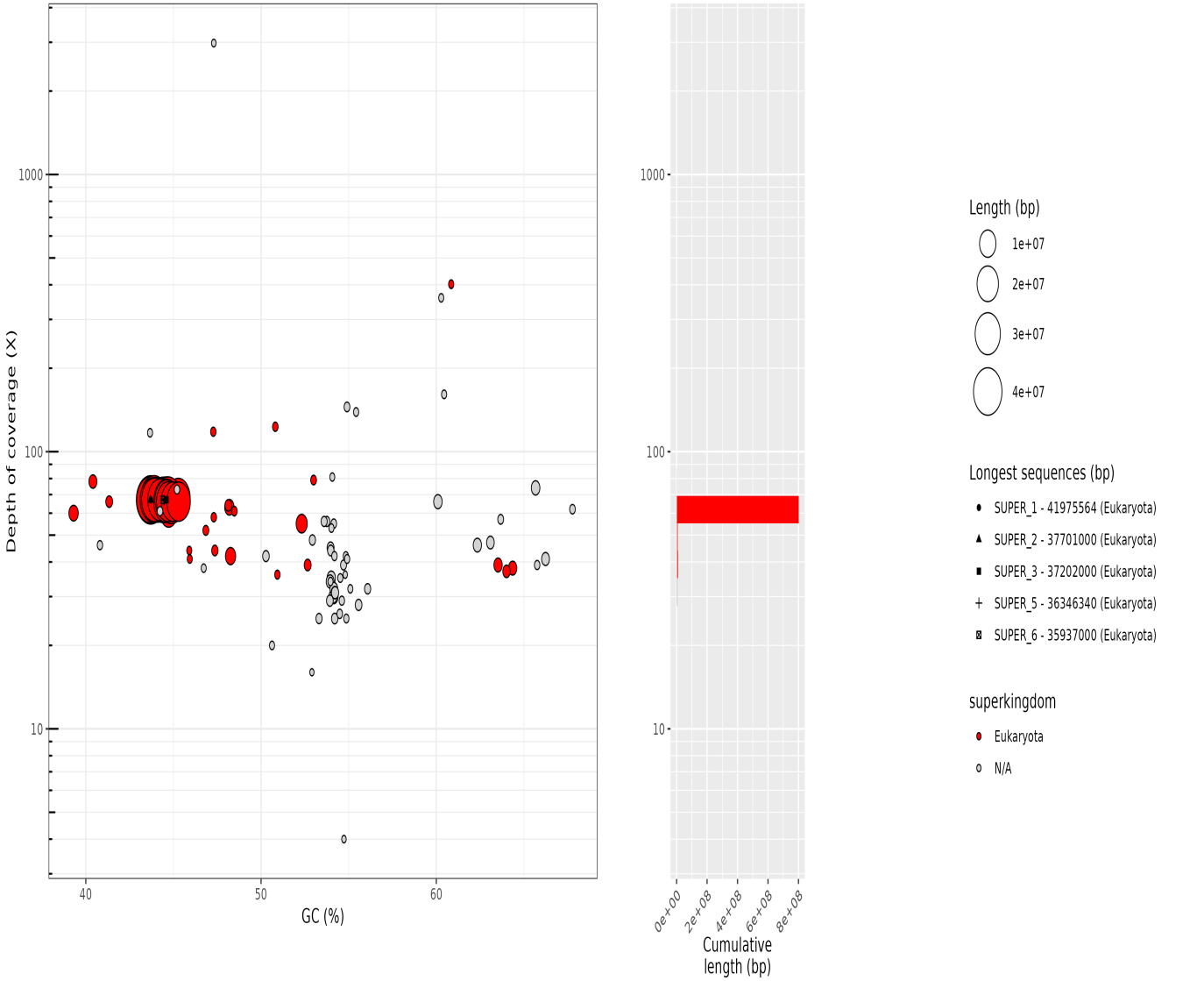
Distribution of k-mer counts per copy numbers found in asm



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	Long reads	Arima
Coverage	69	167

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: 2026-09-07 22:37:19 CEST