ERGA Assembly Report

v24.10.15

Tags: Other[INVALID TAG]

TxID	8265
ToLID	**fPseAme1_Hap2**
Species	Pseudopleuronectes americanus
Class	Actinopteri
Order	Pleuronectiformes

Genome Traits	Expected	Observed
Haploid size (bp)	458,814,187	561,814,457
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: 6.7.Q55

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

. Observed Haploid size (bp) has >20% difference with Expected

. Kmer completeness value is less than 90 for collapsed
. More than 1000 gaps/Gbp for collapsed

Curator notes

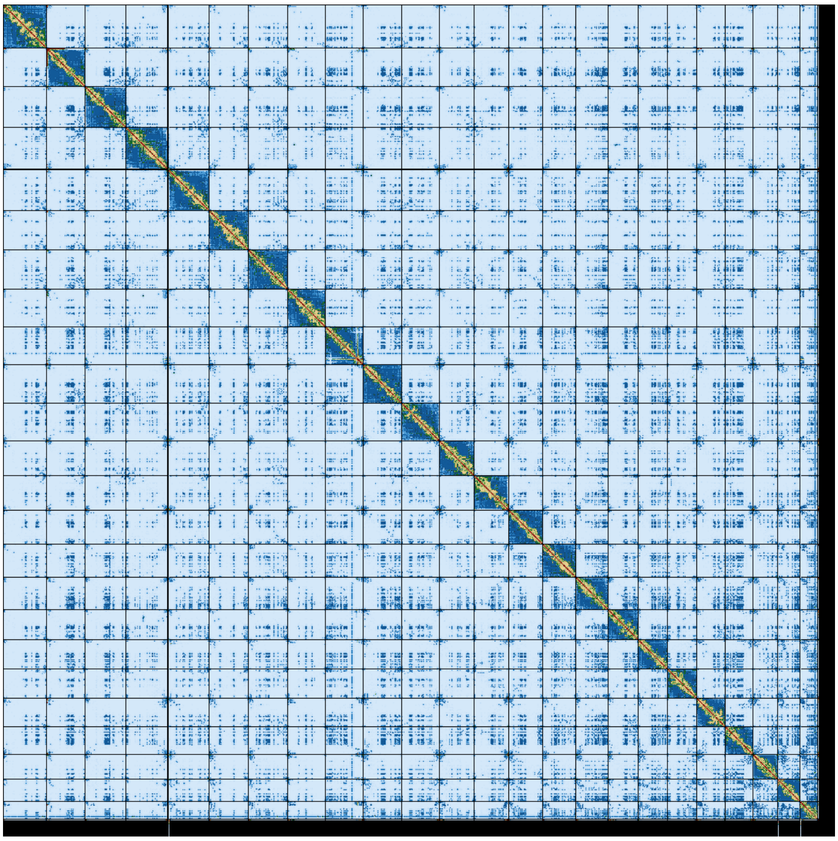
. Interventions/Gb: 88
. Contamination notes: ""
. Other observations: "The assembly of Pseudopleuronectes americanus (fPseAme1) was generated as part of the Vertebrate Genomes Project (https://vertebrategenomesproject.org/). Both haplotypes were analyzed and manually improved using Pretext "

Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	572,201,698	561,814,457
GC %	42.32	42.33
Gaps/Gbp	1,649.77	1,683.83
Total gap bp	188,800	189,200
Scaffolds	417	284
Scaffold N50	23,518,535	25,422,776
Scaffold L50	11	11
Scaffold L90	22	21
Contigs	1,361	1,230
Contig N50	1,967,681	1,908,931
Contig L50	78	79
Contig L90	453	430
QV	54.8872	55.0102
Kmer compl.	90.2596	89.8051
BUSCO sing.	97.8%	97.5%
BUSCO dupl.	1.2%	1.0%
BUSCO frag.	0.2%	0.2%
BUSCO miss.	0.8%	1.4%

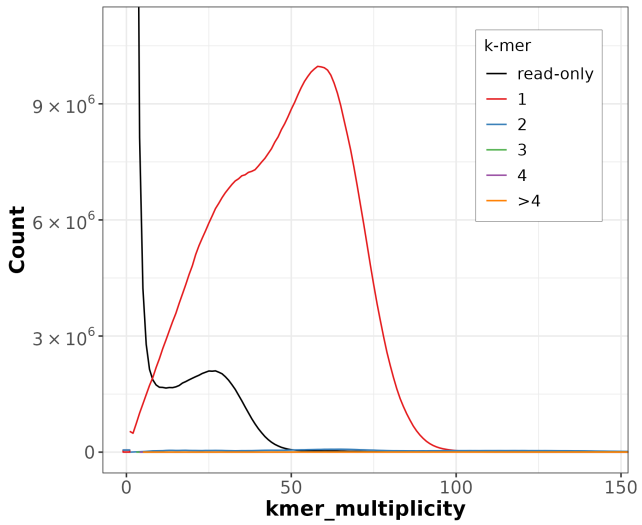
BUSCO: 6.0.0 (euk_genome_min, miniprot) / Lineage: actinopterygii_odb12 (genomes:75, BUSCOs:7207)

HiC contact map of curated assembly

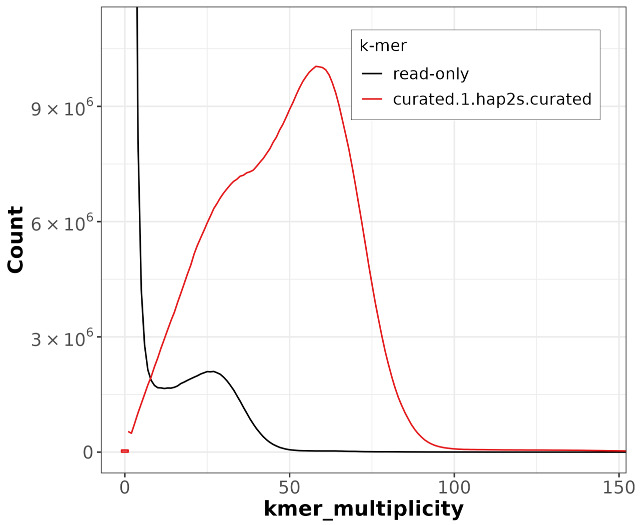


collapsed [LINK]

K-mer spectra of curated assembly

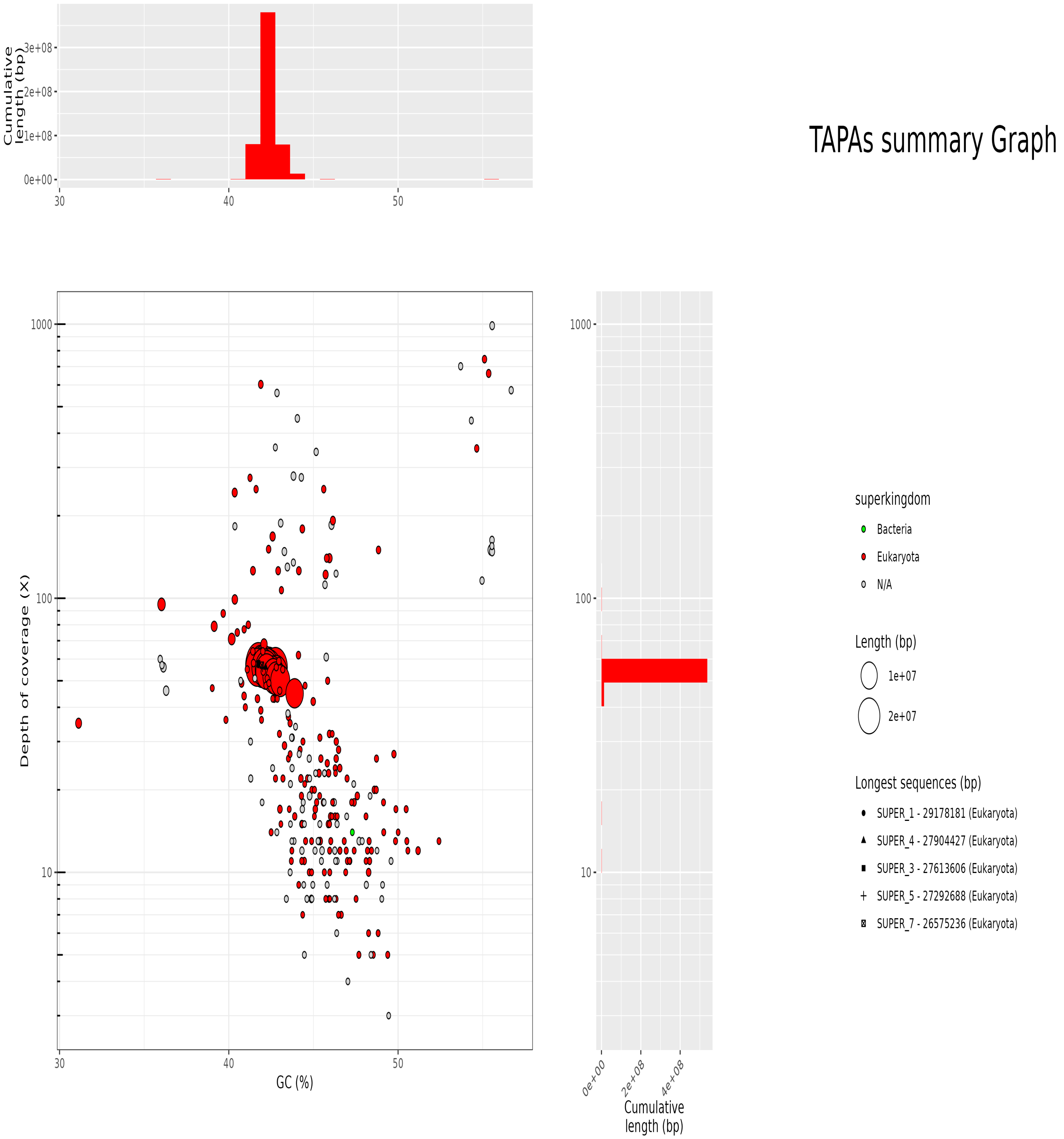


Distribution of k-mer counts per copy numbers found in asm



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	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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