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	576,263,513
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.Q54

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

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

. More than 1000 gaps/Gbp for collapsed

Curator notes

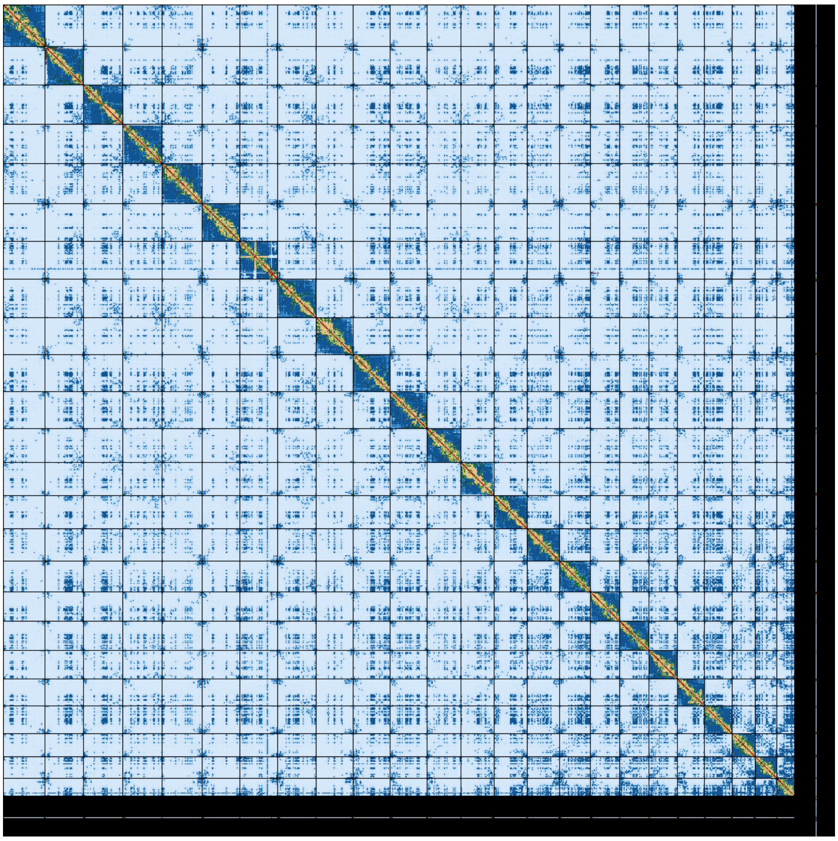
. Interventions/Gb: 47
. Contamination notes: ""
. Other observations: "The assembly of Pseudopleuronectes americanus (fPseAme1) was generated as part of the Vertebrate Genomes Project (https://vertebrategenomesproject.org/). Both haplotypes were analyzed and manually improved using Pretext "

Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	564,700,661	576,263,513
GC %	42.3	42.33
Gaps/Gbp	1,659.29	1,624.26
Total gap bp	187,400	187,200
Scaffolds	336	704
Scaffold N50	25,873,033	25,411,836
Scaffold L50	10	11
Scaffold L90	20	22
Contigs	1,273	1,640
Contig N50	2,088,214	1,863,158
Contig L50	70	83
Contig L90	417	488
QV	54.8425	54.696
Kmer compl.	90.0777	90.1077
BUSCO sing.	95.3%	94.7%
BUSCO dupl.	0.8%	1.3%
BUSCO frag.	0.7%	0.7%
BUSCO miss.	3.2%	3.2%

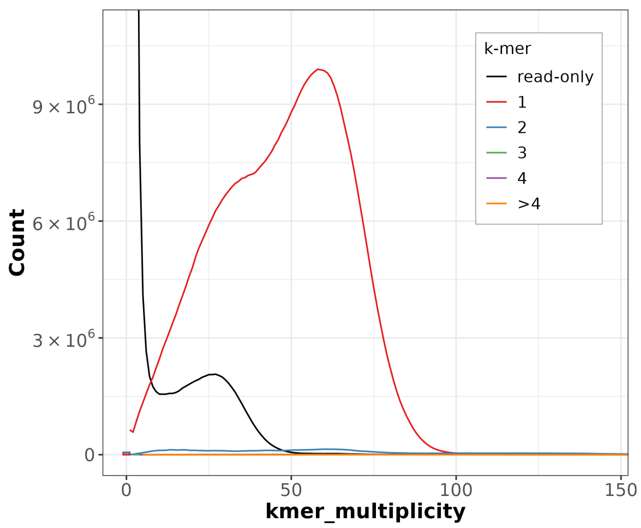
BUSCO: 5.8.2 (euk_genome_met, metaeuk) / Lineage: actinopterygii_odb12 (genomes:75, BUSCOs:7207)

HiC contact map of curated assembly

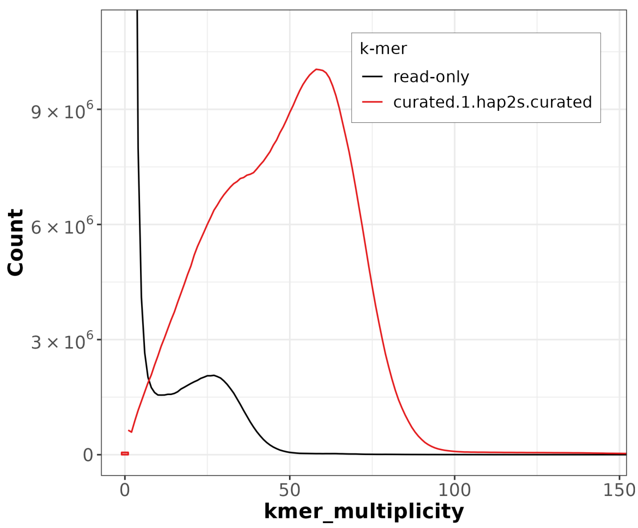


collapsed [LINK]

K-mer spectra of curated assembly

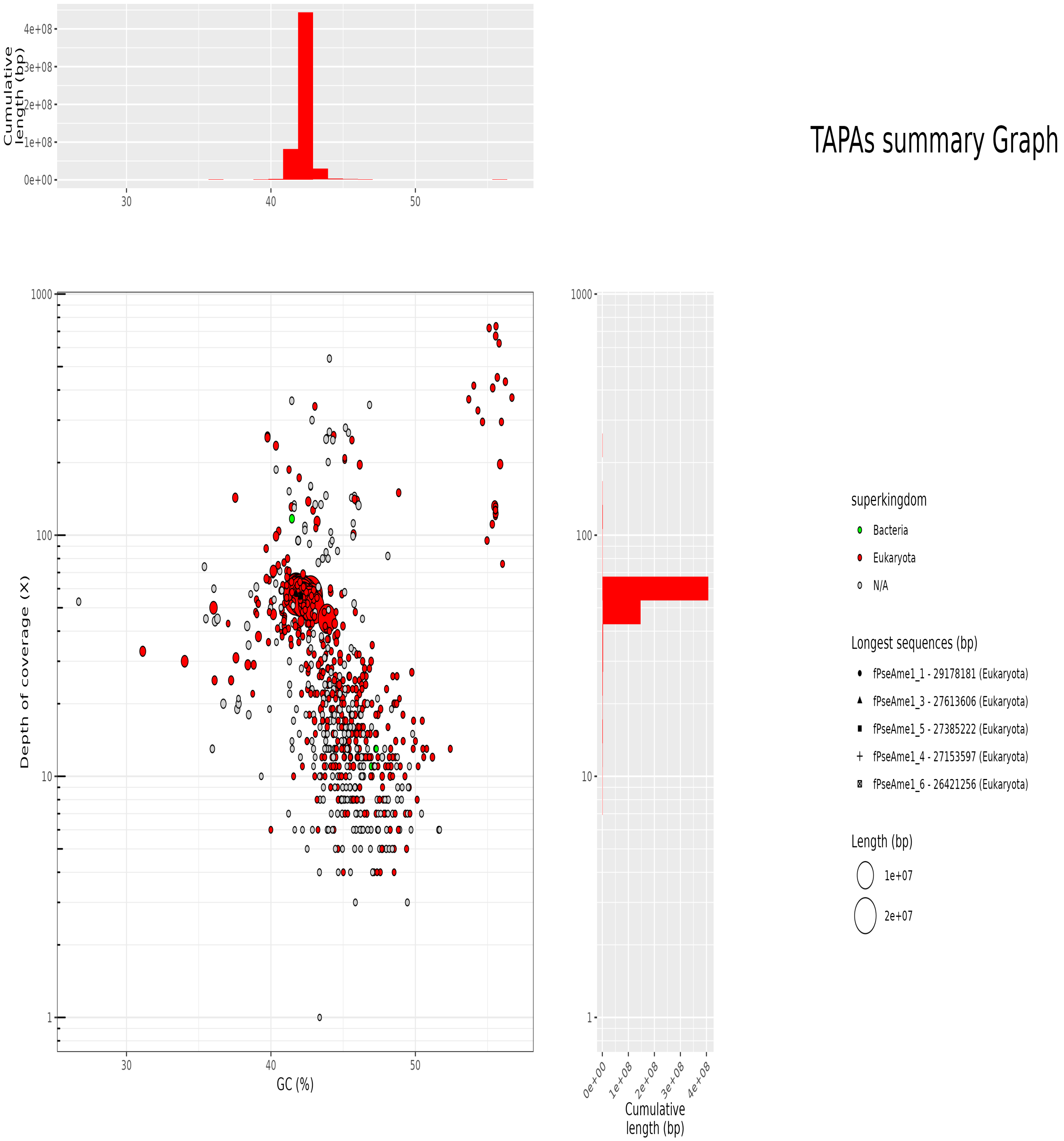


Distribution of k-mer counts per copy numbers found in asm



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

Post-curation contamination screening



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
```

Submitter: Emilie Teodori
Affiliation: Genoscope

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