ERGA Assembly Report

v24.10.15

Tags: Other[INVALID TAG]

TxID	1182198
ToLID	**fPemSco2_hap2**
Species	Pempheris schomburgkii
Class	Actinopteri
Order	Acropomatiformes

Genome Traits	Expected	Observed
Haploid size (bp)	583,426,511	730,627,138
Haploid Number	24 (source: ancestor)	24
Ploidy	2 (source: ancestor)	2
Sample Sex	Unknown	Unknown

EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 6.7.Q60

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
. Assembly length loss > 3% for collapsed
. Not 90% of assembly in chromosomes for collapsed

Curator notes

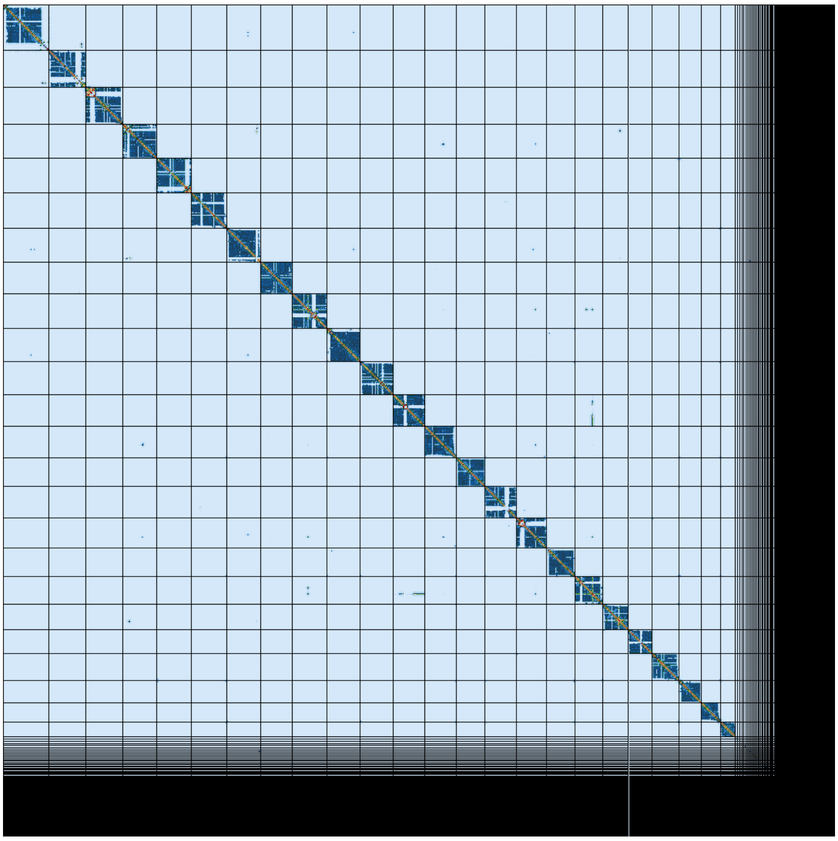
. Interventions/Gb: 173
. Contamination notes: ""
. Other observations: "The assembly of Pempheris schomburgkii (fPemSco2) was generated as part of the Vertebrate Genomes Project (https://vertebrategenomesproject.org/). Both haplotypes were analyzed and manually improved using Pretext "

Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	786,636,536	730,627,138
GC %	42.55	42.5
Gaps/Gbp	320.35	376.39
Total gap bp	50,400	55,000
Scaffolds	566	485
Scaffold N50	26,018,510	27,761,526
Scaffold L50	14	12
Scaffold L90	77	33
Contigs	818	760
Contig N50	6,121,453	6,025,865
Contig L50	39	37
Contig L90	238	214
QV	60.3562	60.5478
Kmer compl.	90.1707	89.8443
BUSCO sing.	95.9%	98.6%
BUSCO dupl.	0.9%	0.5%
BUSCO frag.	0.9%	0.1%
BUSCO miss.	2.3%	0.8%

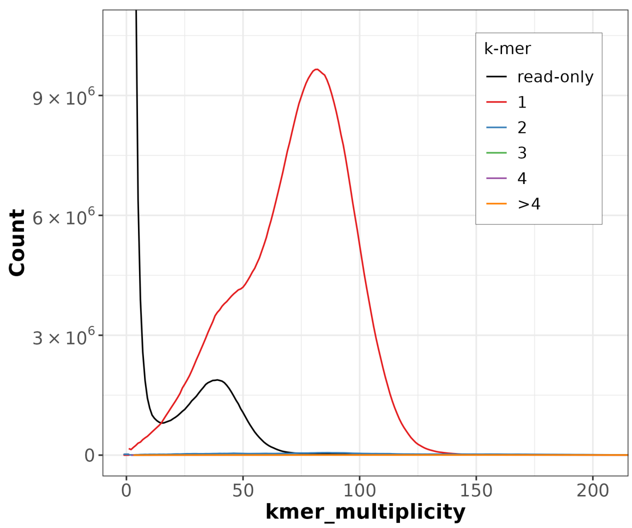
Warning! BUSCO versions or lineage datasets are not the same across results:
BUSCO: 5.8.2 (euk_genome_met, metaeuk) / Lineage: actinopterygii_odb12 (genomes:75, BUSCOs:7207)
BUSCO: 6.0.0 (euk_genome_min, miniprot) / Lineage: actinopterygii_odb12 (genomes:75, BUSCOs:7207)

HiC contact map of curated assembly

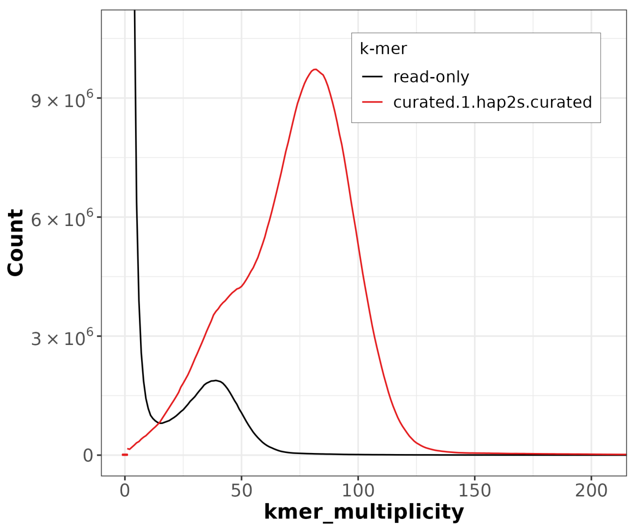


collapsed [LINK]

K-mer spectra of curated assembly

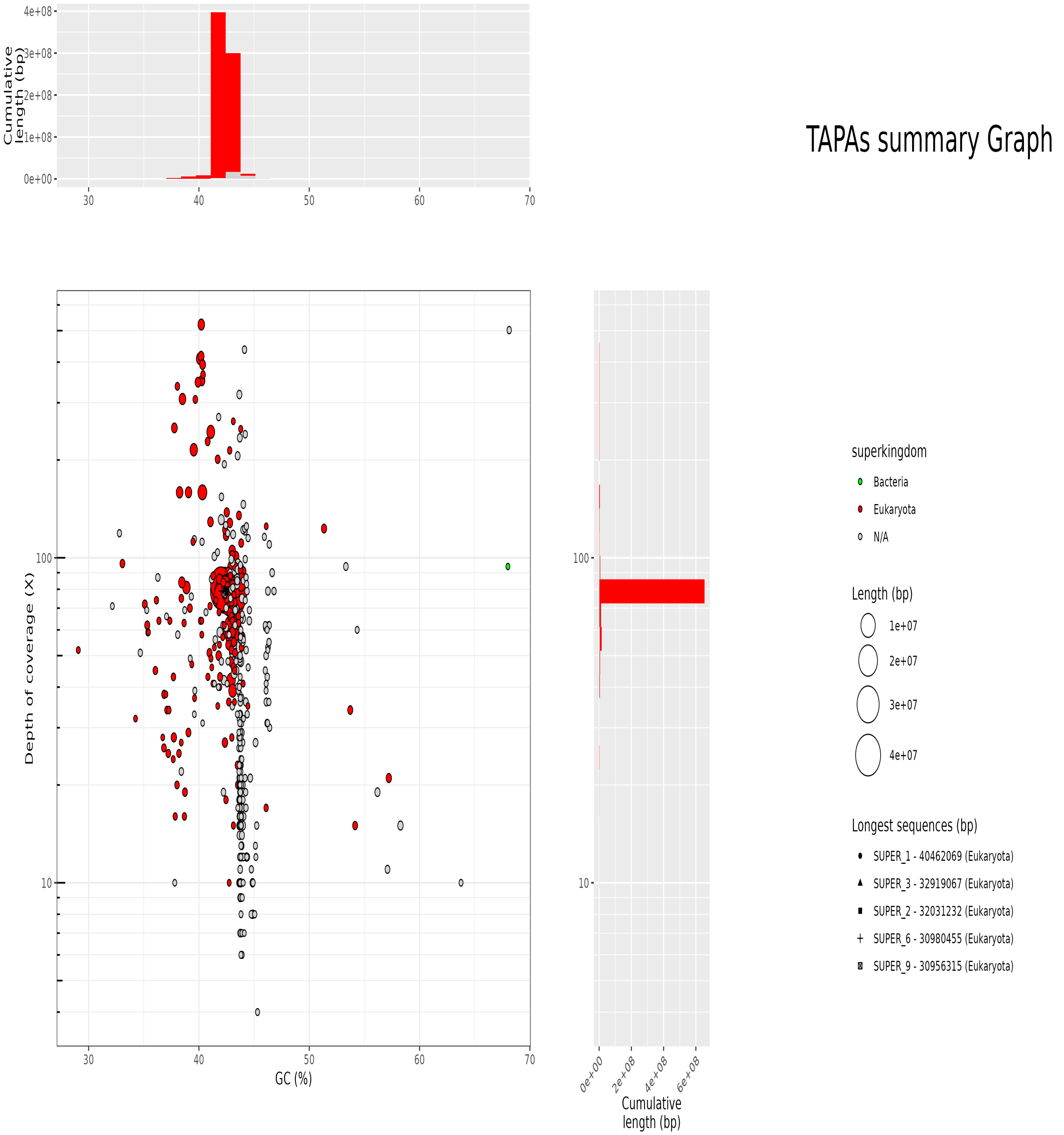


Distribution of k-mer counts per copy numbers found in asm



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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