ERGA Assembly Report

v24.10.15

Tags: Other[INVALID TAG]

TxID	2803083
ToLID	**sPotMar1_h2**
Species	Potamotrygon marinae
Class	Chondrichthyes
Order	Myliobatiformes

Genome Traits	Expected	Observed
Haploid size (bp)	4,702,183,164	4,218,244,870
Haploid Number	33 (source: ancestor)	32
Ploidy	2 (source: ancestor)	2
Sample Sex	Unknown	Unknown

EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 7.8.Q63

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

. Observed Haploid Number is different from Expected

. Assembly length loss > 3% for collapsed

Curator notes

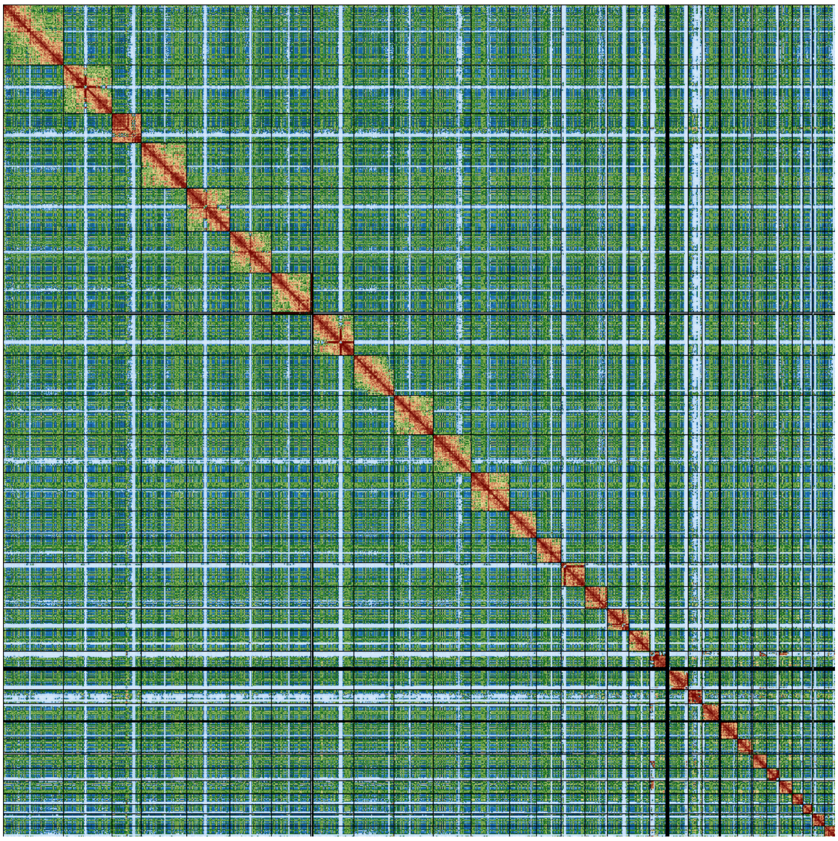
. Interventions/Gb: 67
. Contamination notes: ""
. Other observations: "The assembly of Potamotrygon marinae (sPotMar1) was generated as part of the Vertebrate Genomes Project (https://vertebrategenomesproject.org/). Both haplotypes were analyzed and manually improved using Pretext. "

Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	4,432,826,445	4,218,244,870
GC %	41.4	41.36
Gaps/Gbp	207.54	248.44
Total gap bp	184,000	209,600
Scaffolds	967	50
Scaffold N50	137,101,827	192,842,538
Scaffold L50	11	10
Scaffold L90	63	25
Contigs	1,887	1,098
Contig N50	12,387,240	13,340,777
Contig L50	90	81
Contig L90	568	430
QV	63.6893	63.9831
Kmer compl.	93.6111	92.2768
BUSCO sing.	91.6%	
BUSCO dupl.	1.9%	
BUSCO frag.	1.9%	
BUSCO miss.	4.6%	

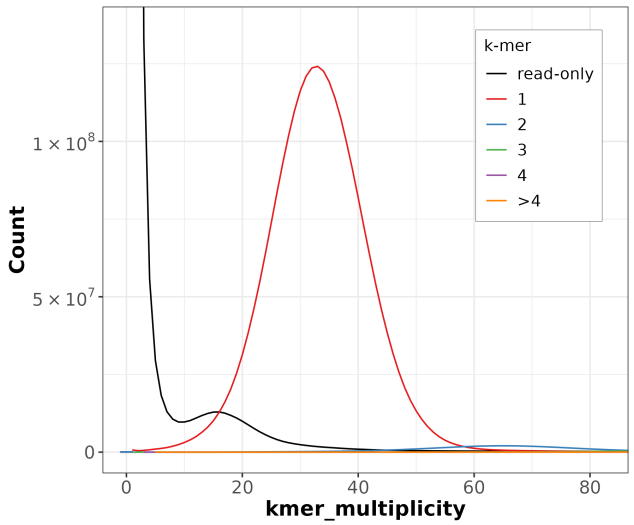
BUSCO: 5.8.2 (euk_genome_min, miniprot) / Lineage: vertebrata_odb12 (genomes:119, BUSCOs:3390)

HiC contact map of curated assembly

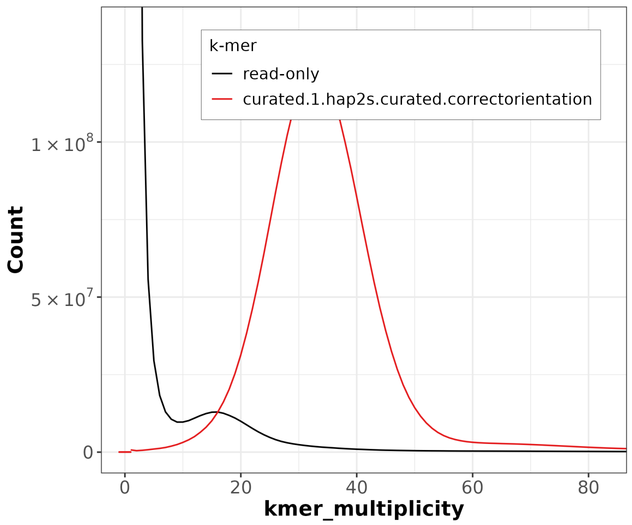


collapsed [LINK]

K-mer spectra of curated assembly

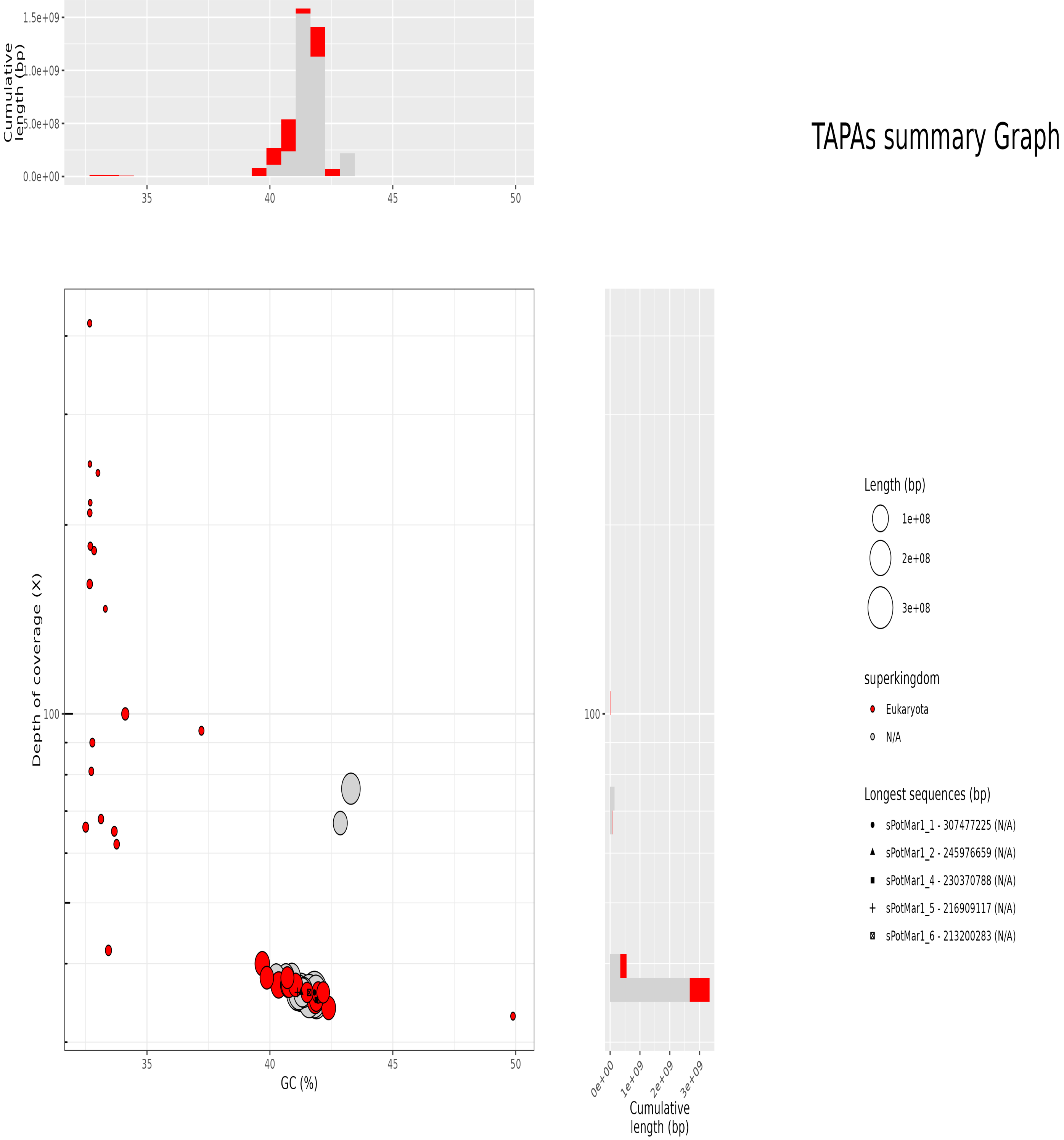


Distribution of k-mer counts per copy numbers found in asm



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: Jean-Marc Aury
Affiliation: Genoscope

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