ERGA Assembly Report

v24.10.15

Tags: Other[INVALID TAG]

TxID	394696
ToLID	**fSebMen1_hap1**
Species	Sebastes mentella
Class	Actinopteri
Order	Perciformes

Genome Traits	Expected	Observed
Haploid size (bp)	796,775,342	836,362,942
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.Q57

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

Curator notes

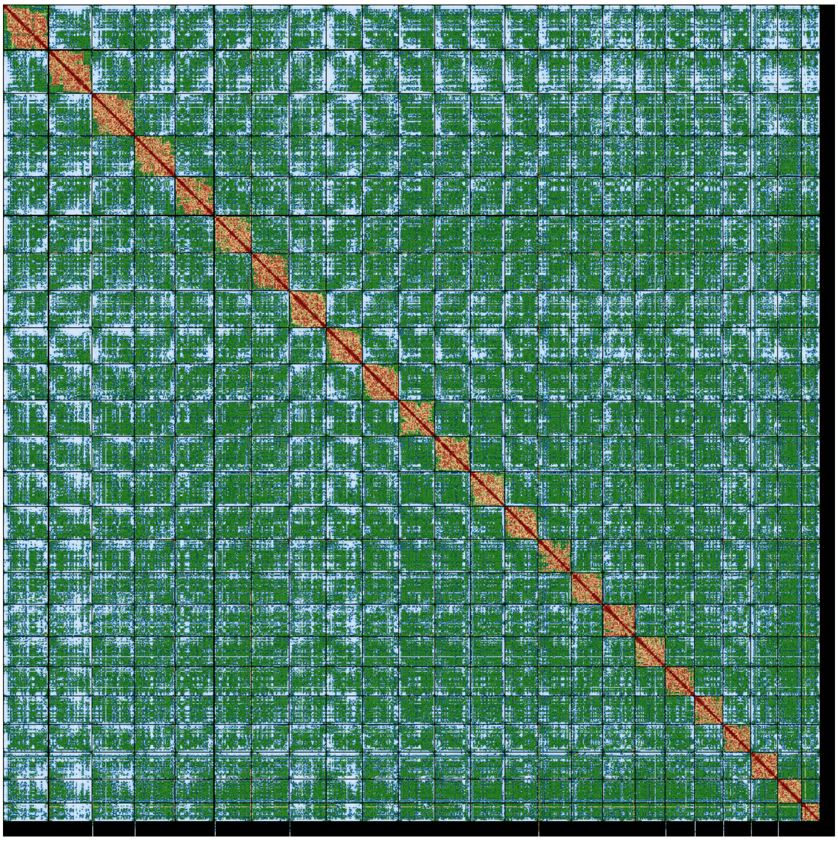
. Interventions/Gb: 178
. Contamination notes: ""
. Other observations: "The assembly of Sebastes mentella (fSebMen1) has been generated as part of the Vertebrate Genomes Project (https://vertebrategenomesproject.org/). Both haplotypes were analyzed and manually improved using Pretext. "

Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	822,650,995	836,362,942
GC %	40.84	40.88
Gaps/Gbp	482.59	554.78
Total gap bp	79,400	92,800
Scaffolds	519	510
Scaffold N50	34,728,012	36,014,244
Scaffold L50	11	11
Scaffold L90	22	22
Contigs	916	974
Contig N50	6,694,446	7,391,707
Contig L50	35	33
Contig L90	155	147
QV	57.7638	57.7708
Kmer compl.	93.6635	93.9941
BUSCO sing.	95.6%	97.1%
BUSCO dupl.	0.9%	1.5%
BUSCO frag.	0.8%	0.2%
BUSCO miss.	2.7%	1.2%

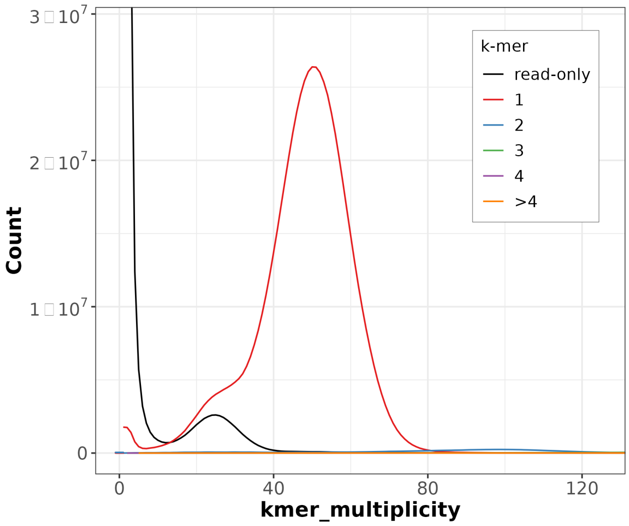
Warning! BUSCO versions or lineage datasets are not the same across results:
BUSCO: 5.8.2 (euk_genome_met, metaeuk) / Lineage: actinopterygii_odb12 (genomes:75, BUSCOs:7207)
BUSCO: 6.0.0 (euk_genome_min, miniprot) / Lineage: actinopterygii_odb12 (genomes:75, BUSCOs:7207)

HiC contact map of curated assembly

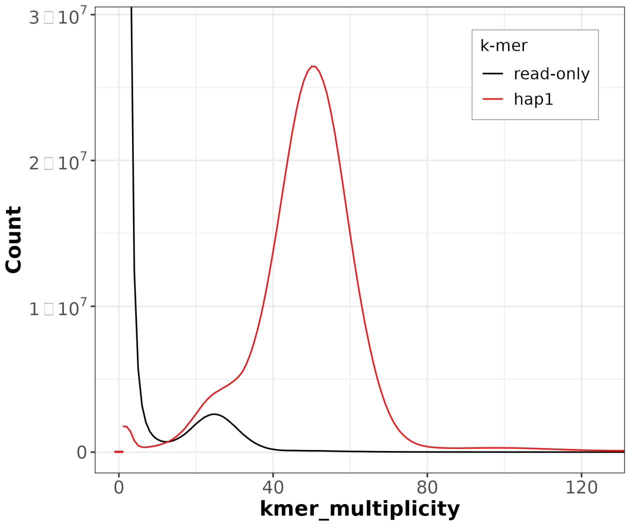


collapsed [LINK]

K-mer spectra of curated assembly

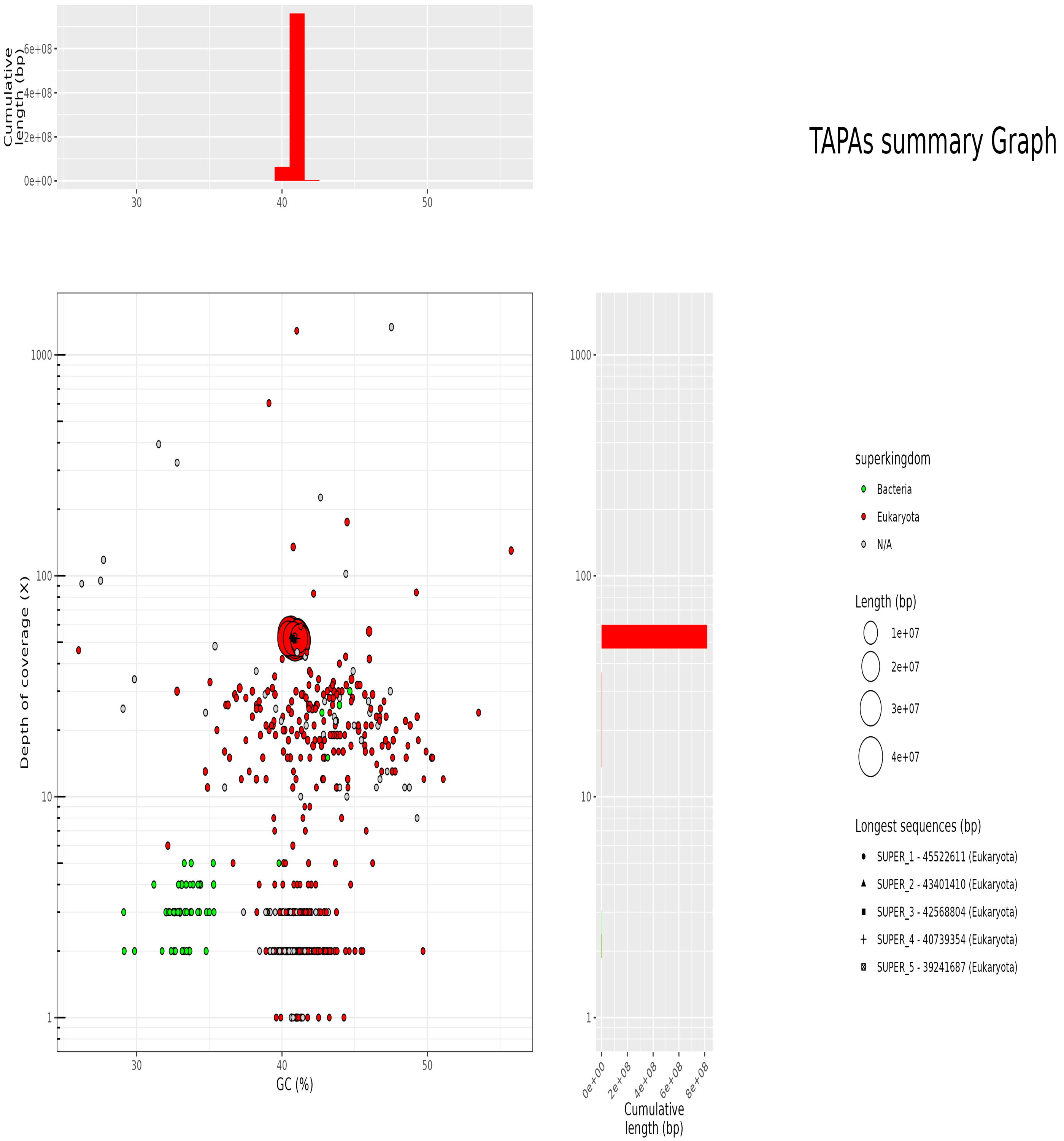


Distribution of k-mer counts per copy numbers found in asm



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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