ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	387912
ToLID	**mCroZim1**
Species	Crocidura zimmermanni
Class	Mammalia
Order	Eulipotyphla

Genome Traits	Expected	Observed
Haploid size (bp)	2,224,927,356	2,571,728,606
Haploid Number	17 (source: direct)	20
Ploidy	2 (source: ancestor)	2
Sample Sex	Unknown	Unknown

EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 7.8.Q62

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

. Observed Haploid Number is different from Expected

Curator notes

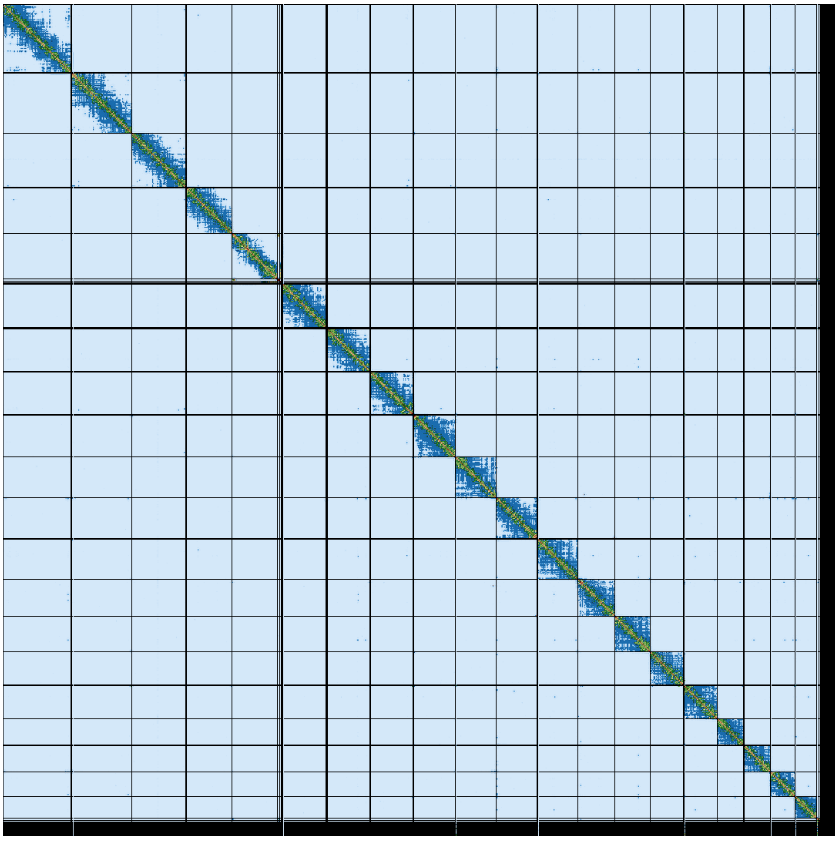
. Interventions/Gb: 2
. Contamination notes: ""
. Other observations: "The assembly of Crocidura zimmermanni (mCroZim1.1) is based on 37X PacBio data and 189X Arima Hi-C data generated as part of the European Reference Genome Atlas (ERGA, https://www.erga-biodiversity.eu/) via the Biodiversity Genomics Europe project (BGE, https://biodiversitygenomics.eu/). The assembly process included the following steps: initial PacBio assembly generation with Hifiasm, removal of contaminant sequences using Context, removal of haplotypic duplications using purge_dups, and Hi-C-based scaffolding with YaHS. In total, 8 contigs were identified as contaminants (bacterial), totaling 690.5 Kb (with the largest being 117.9 Kb). Additionally, 195 regions totaling 76.2 Mb (with the largest being 20.8 Mb) were identified as haplotypic duplications and removed. The mitochondrial genome was assembled using OATK. Finally, the primary assembly was analyzed and manually improved using Pretext. During manual curation, no regions were tagged as allelic duplications nor contaminants ; 24 sequences were tagged Unloc, their orientation is uncertain ; Chromosome-scale scaffolds confirmed by Hi-C data were named in order of size. "

Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	2,571,745,479	2,571,728,606
GC %	39.85	39.85
Gaps/Gbp	62.6	62.6
Total gap bp	16,100	16,400
Scaffolds	151	146
Scaffold N50	127,229,103	127,229,103
Scaffold L50	9	9
Scaffold L90	18	18
Contigs	312	307
Contig N50	28,351,139	28,351,139
Contig L50	25	25
Contig L90	97	97
QV	62.0833	62.0867
Kmer compl.	92.9631	92.9629
BUSCO sing.	90.6%	90.6%
BUSCO dupl.	2.2%	2.2%
BUSCO frag.	0.9%	0.9%
BUSCO miss.	6.3%	6.3%

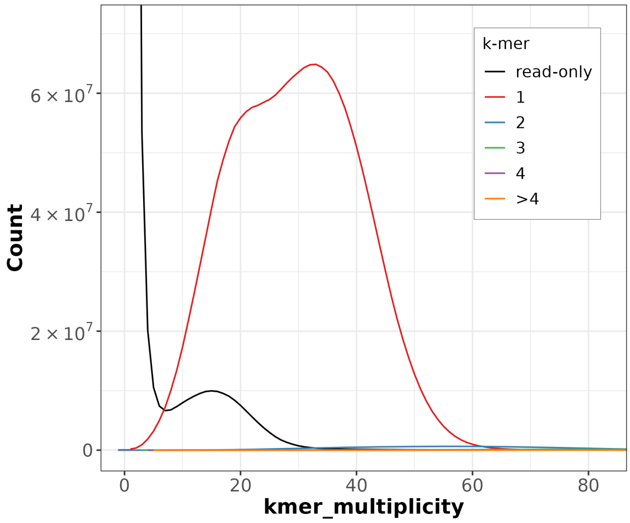
BUSCO: 5.4.3 (euk_genome_met, metaeuk) / Lineage: laurasiatheria_odb10 (genomes:52, BUSCOs:12234)

HiC contact map of curated assembly

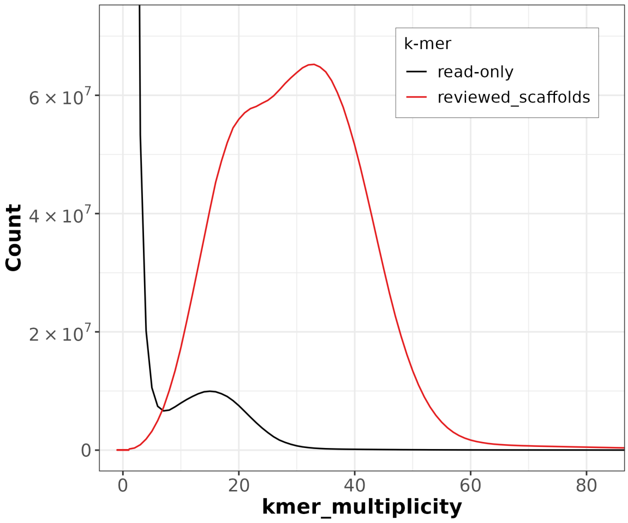


collapsed [LINK]

K-mer spectra of curated assembly

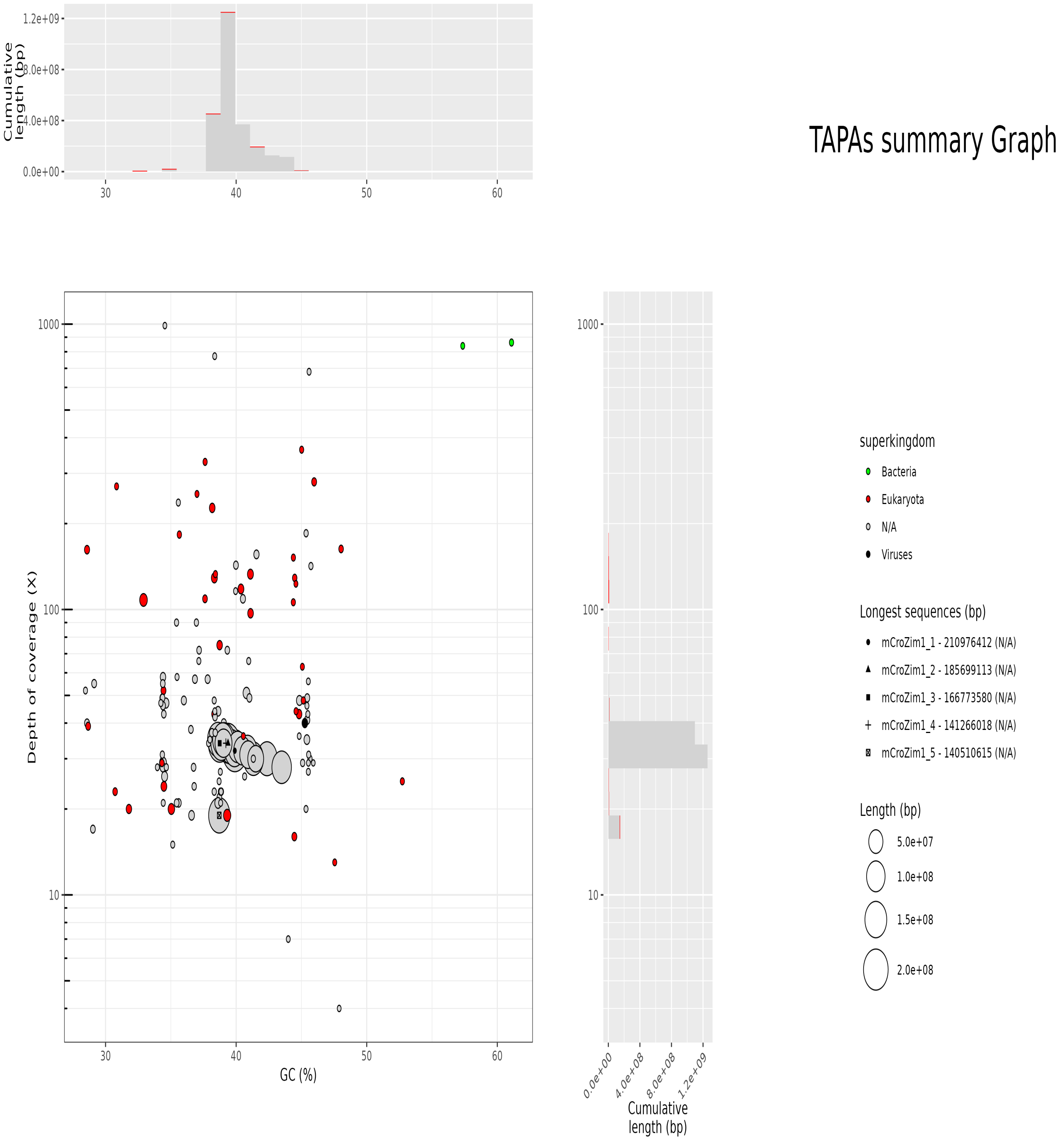


Distribution of k-mer counts per copy numbers found in asm



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	37	189

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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