### ERGA Assembly Report

v24.09.10

Tags: ERGA-BGE

TxID	9659	
ToLID	mMarFoi2	
Species	Martes foina	
Class	Mammalia	
Order	Carnivora	

Genome Traits	Expected	Observed	
Haploid size (bp)	2,439,340,219	2,388,581,548	
Haploid Number	19 (source: direct)	19	
Ploidy	2 (source: ancestor)	2	
Sample Sex	XY	XY	

#### EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 7.8.Q56

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

#### Curator notes

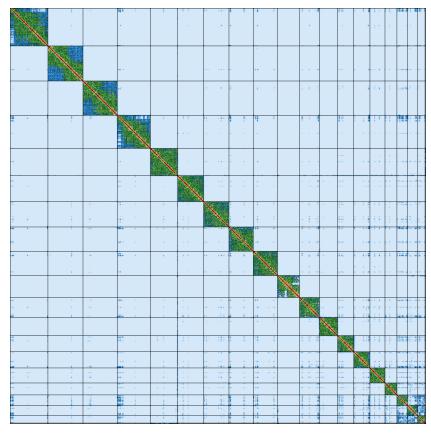
- . Interventions/Gb: 4 . Contamination notes: "No contaminants detected in the Nextdenovo assembly selected for curation."
- . Other observations: "Curation and review made 0 cuts in contigs, 3 breaks at a gap and 7 joins. SUPER\_Y sequence accounts for 5,617,504 bp. The final assembly contains 2 unplaced scaffolds shorter than the HiC map resolution. Link points to a folder cotaining the pretext map and the final savestate for the curated assembly. Mitogenome was successfully assembled into a circular contig of 16,591 bp and high sequence accuracy."

# Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed	
Total bp	2,388,579,948	2,388,581,548	
GC %	41.74	41.74	
Gaps/Gbp	20.93	24.28	
Total gap bp	10,000	11,600	
Scaffolds	27	22	
Scaffold N50	146,036,623	146,036,623	
Scaffold L50	7	7	
Scaffold L90	16	15	
Contigs	77	80	
Contig N50	64,160,893	64,160,893	
Contig L50	13	13	
Contig L90	39	39	
QV	56.1982	56.1982	
Kmer compl.	98.0977	98.0977	
BUSCO sing.	97.0%	97.0%	
BUSCO dupl.	1.1% 1.2%		
BUSCO frag.	0.8%	0.8%	
BUSCO miss.	1.1%	1.0%	

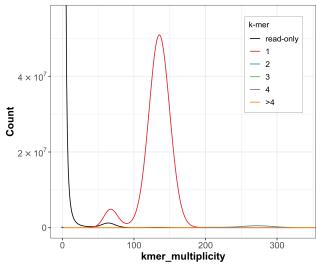
BUSCO 5.4.0 Lineage: vertebrata\_odb10 (genomes:67, BUSCOs:3354)

HiC contact map of curated assembly

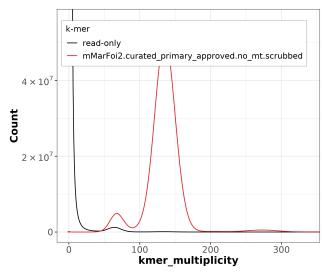


collapsed [LINK]

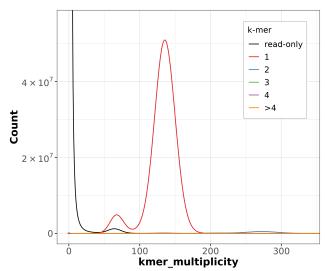
## K-mer spectra of curated assembly



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



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



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

## Post-curation contamination screening

## Data profile

Data	ONT	Illumina	OmniC
Coverage	114x	80x	102x

## Assembly pipeline

```
- CLAWS pipeline
    _ ver: 2.2.0
    _ key param: NA
- Trim_galore
    |_ ver: 0.6.7
    |_ key param: NA
- Filtlong
    |_ ver: 0.2.1
    | key param: NA
- flye
    |_ ver: 2.9.1
    _ key param: NA

    nextdenovo

    _ ver: 2.5.0
    _ key param: NA
hypo
   |_ ver: 1.0.3
   _ key param: NA
- purge_dups
    _ ver: 1.2.6
    _ key param: NA
- YaHS
    _ ver: 1.2a
    _ key param: NA
- FOAM pipeline
    |_ ver: 0.5
    |_ key param: NA
- mitos
   |_ ver: 2.1.3
    | key param: NA
```

## Curation pipeline

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Date and time: 2024-10-29 20:44:32 CET