ERGA Assembly Report

v24.09.10

Tags: ATLASea[INVALID TAG]

TxID	488663	
ToLID	xgNatHebr1.1	
Species	Naticarius hebraeus	
Class	Gastropoda	
Order	Littorinimorpha	

Genome Traits	Expected	Observed
Haploid size (bp)	2,242,301,173	2,232,923,658
Haploid Number	17 (source: ancestor)	18
Ploidy	2 (source: ancestor)	2
Sample Sex	Unknown	Unknown

EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 6.8.Q57

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

. Observed Haploid Number is different from Expected

Curator notes

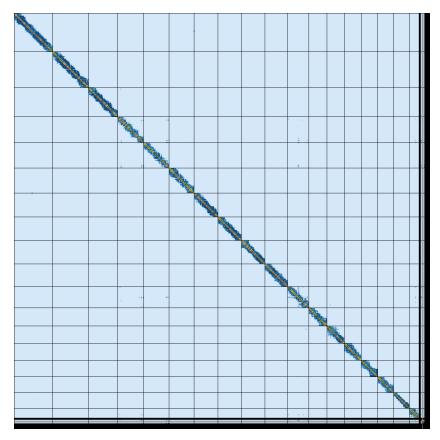
- . Interventions/Gb: 2
- . Contamination notes: "none "
- . Other observations: "none "

Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	2,232,953,292	2,232,923,658
GC %	42.19	42.19
Gaps/Gbp	484.56	487.25
Total gap bp	108,200	109,400
Scaffolds	170	150
Scaffold N50	125,934,709	125,934,709
Scaffold L50	8	8
Scaffold L90	16	16
Contigs	1,252	1,238
Contig N50	4,029,449	4,029,449
Contig L50	159	159
Contig L90	593	593
QV		57.2806
Kmer compl.		96.0756
BUSCO sing.	97.3%	97.3%
BUSCO dupl.	0.8%	0.8%
BUSCO frag.	0.8%	0.8%
BUSCO miss.	1.1%	1.1%

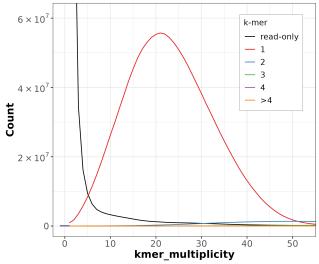
BUSCO 5.4.3 Lineage: eukaryota_odb10 (genomes:70, BUSCOs:255)

HiC contact map of curated assembly

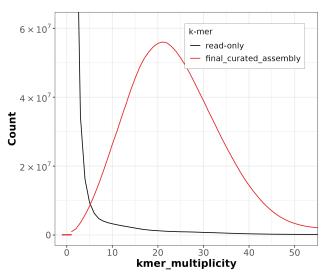


collapsed [LINK]

K-mer spectra of curated assembly

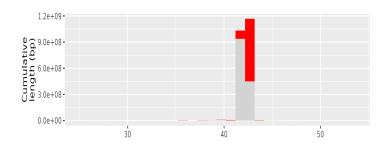


Distribution of k-mer counts per copy numbers found in asm

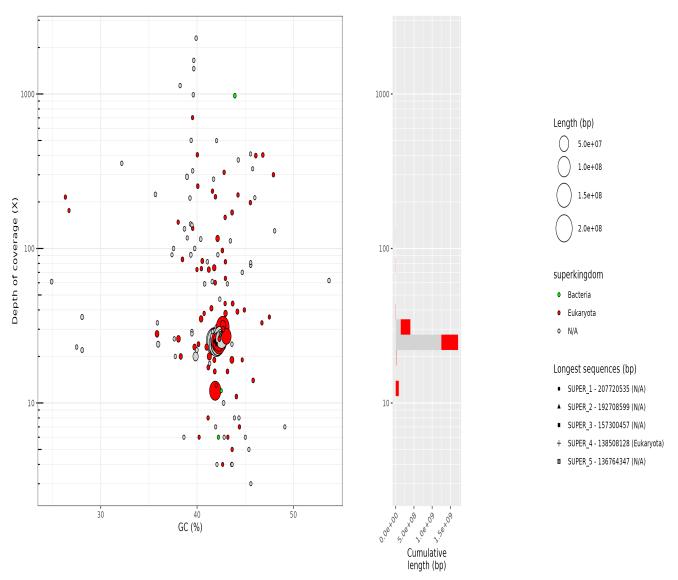


Distribution of k-mer counts coloured by their presence in reads/assemblies

Post-curation contamination screening



TAPAs summary Graph



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 (4-enz)
Coverage	30	50

Assembly pipeline

Curation pipeline

Submitter: Arnaud Couloux Affiliation: Genoscope

Date and time: 2024-11-16 15:01:58 CET