

ERGA Assembly Report

v24.04.03_beta

Tags: ERGA-BGE

TxID	1303476
ToLID	rMedKot1
Species	Mediodactylus kotschyi
Class	Lepidosauria
Order	Squamata

Genome Traits	Expected	Observed
Haploid size (bp)	1,742,031,630	1,798,513,081
Haploid Number	21 (source: direct)	21
Ploidy	2 (source: ancestor)	2
Sample Sex	M	M

EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 7.8.Q68

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

Curator notes

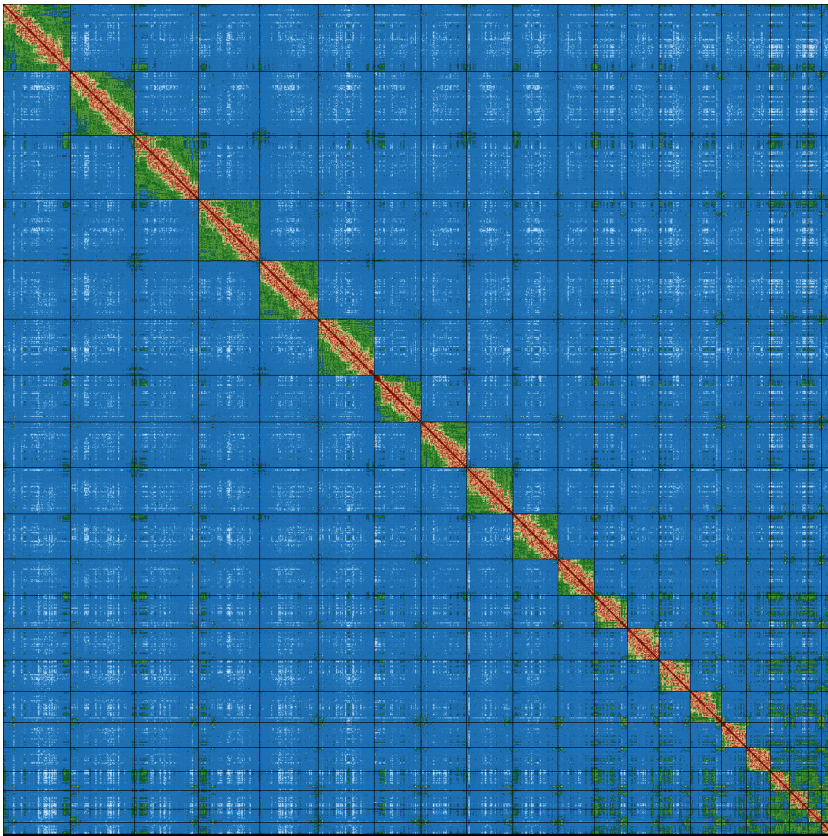
. Interventions/Gb: 36
. Contamination notes: "Contamination report for assembly labelled hap1; Total length of scaffolds removed: 314,784 (0.0 %); Scaffolds removed: 11 (9.6 %); Largest scaffold removed: (49,542); FCS-GX contaminant species (number of scaffolds; total length of scaffolds): Mitochondrion (11; 314,784)"
. Other observations: "Assembly was Hi-C phased; This is an assembly from homogametic specimen. No close relative could be identified to reliably assign the Z chromosome by syntenry."

Quality metrics table

Metrics	Pre-curation pri	Curated pri
Total bp	1,798,822,665	1,798,513,081
GC %	44.05	44.05
Gaps/Gbp	38.91	53.38
Total gap bp	14,000	19,200
Scaffolds	114	77
Scaffold N50	99,608,558	101,151,094
Scaffold L50	8	7
Scaffold L90	17	17
Contigs	184	173
Contig N50	47,144,669	47,144,669
Contig L50	14	14
Contig L90	50	50
QV	67.9	68.1
Kmer compl.	99.62	99.62
BUSCO sing.	93.3%	93.3%
BUSCO dupl.	1.5%	1.5%
BUSCO frag.	0.9%	0.9%
BUSCO miss.	4.3%	4.3%

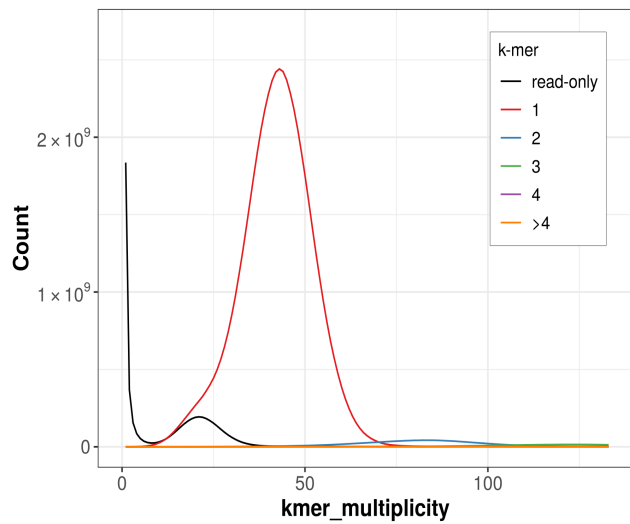
BUSCO 5.3.0 Lineage: sauropsida_odb10 (genomes:76, BUSCOs:7480)

HiC contact map of curated assembly

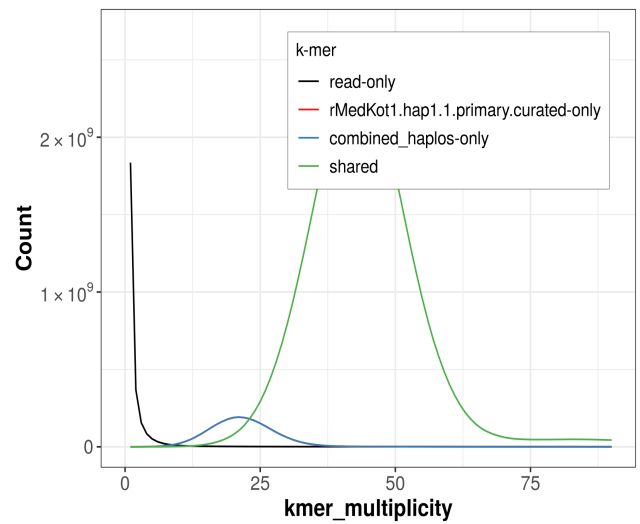


pri [\[LINK\]](#)

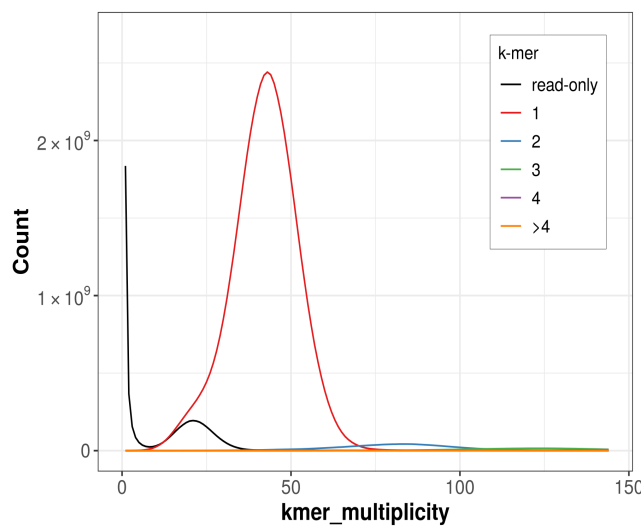
K-mer spectra of curated assembly



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

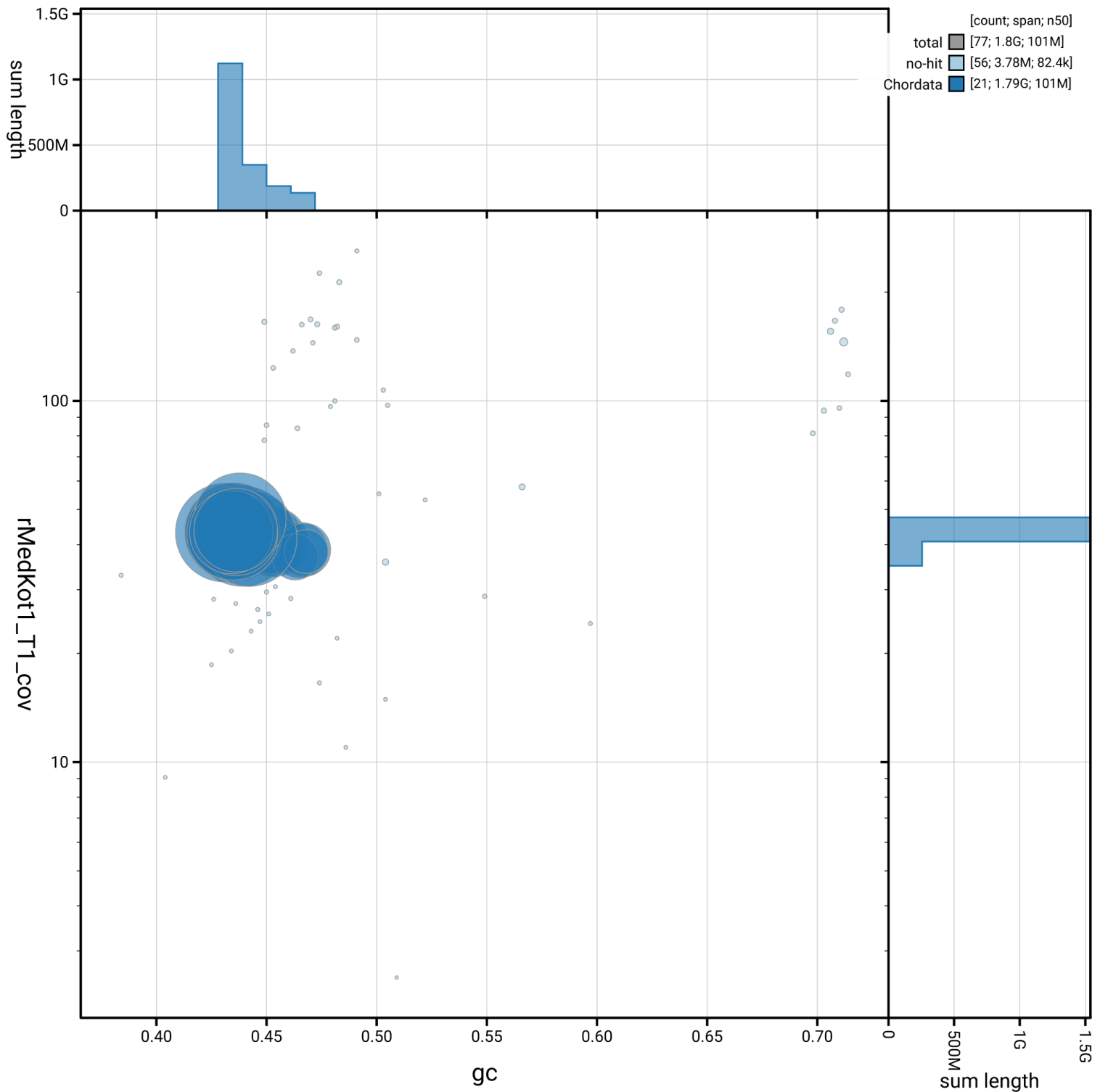


Distribution of k-mer counts coloured by their presence in reads/assemblies



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

Post-curation contamination screening



pri. 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 v2
Coverage	42x	306x

Assembly pipeline

- **hifiasm-hic**
 - |_ *ver*: 0.19.8-r603
 - |_ *key param*: --h1/--h2
- **yahs**
 - |_ *ver*: 1.2.2
 - |_ *key param*: NA

Curation pipeline

- **hifiasm-hic**
 - |_ *ver*: 0.19.8-r603
 - |_ *key param*: --h1/--h2
- **yahs**
 - |_ *ver*: 1.2.2
 - |_ *key param*: NA
- **TreeVal**
 - |_ *ver*: 1.2.1
 - |_ *key param*: NA

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