

# ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	3237719
ToLID	<b>qqNelTrog1</b>
Species	<i>Nelima troglodytes</i>
Class	Arachnida
Order	Opiliones

Genome Traits	Expected	Observed
Haploid size (bp)	668,900,136	768,110,527
Haploid Number	10 (source: ancestor)	12
Ploidy	2 (source: ancestor)	2
Sample Sex	NA	NA

## EBP metrics summary and curation notes

Obtained EBP quality metric for hap1: 6.7.Q54

Obtained EBP quality metric for hap2: 6.7.Q54

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

- . Observed Haploid Number is different from Expected
- . Assembly length loss > 3% for hap1
- . Not 90% of assembly in chromosomes for hap1
- . Not 90% of assembly in chromosomes for hap2

## Curator notes

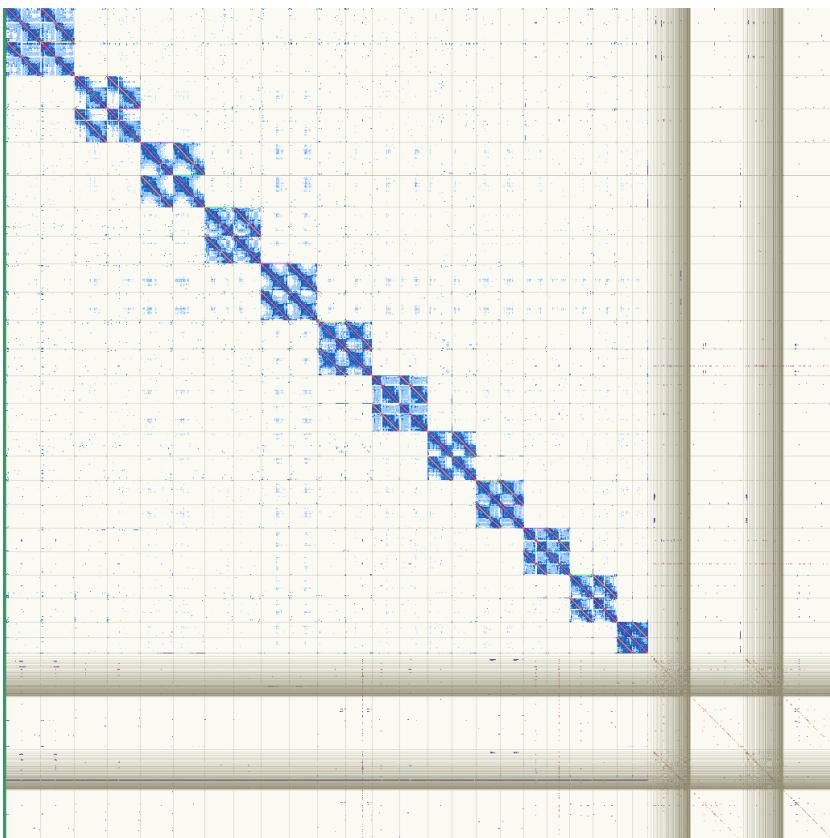
- . Interventions/Gb:
- . Contamination notes: "56,522,598 bp contained in 348 sequences were considered contaminants by FCS-GX and removed from hap1. Additionally, 23,775,017 bp contained in 43 sequences were also considered contaminants and removed from hap2. The longest removed contigs for hap1 and hap2 were 6,693,555 and 5,526,655 bp, respectively."
- . Other observations: "This genome assembly was produced by assembling ONT data with Hifiasm and then scaffolding with Yahs. Curation was made in diploid mode and we are planning to submit both haplotypes to the ENA. Curation made 22 cuts in contigs, 27 breaks at gaps and 66 joins"

# Quality metrics table

Metrics	Pre-curation hap1	Pre-curation hap2	Curated hap1	Curated hap2
Total bp	832,818,357	671,348,240	768,110,527	760,551,777
GC %	39.92	37.32	39.23	39.26
Gaps/Gbp	220.94	315.78	269.49	298.47
Total gap bp	36,800	42,400	41,400	45,400
Scaffolds	1,427	301	1,064	1,064
Scaffold N50	36,862,694	49,609,403	50,835,744	48,537,736
Scaffold L50	8	6	7	7
Scaffold L90	273	22	143	146
Contigs	1,611	513	1,271	1,291
Contig N50	4,053,437	4,188,491	3,941,584	3,223,771
Contig L50	51	44	49	57
Contig L90	437	200	334	357
QV	53.283	60.5424	54.5992	54.7591
Kmer compl.	96.8931	93.2094	92.6153	92.0134
BUSCO sing.	96.3%	95.5%	96.2%	96.2%
BUSCO dupl.	0.6%	0.7%	0.5%	0.5%
BUSCO frag.	1.7%	1.7%	1.8%	1.8%
BUSCO miss.	1.3%	2.0%	1.5%	1.5%

BUSCO: 6.0.0 (euk\_genome\_min, miniprot) / Lineage: arachnida\_odb12 (genomes:34, BUSCOs:1123)

# HiC contact map of curated assembly

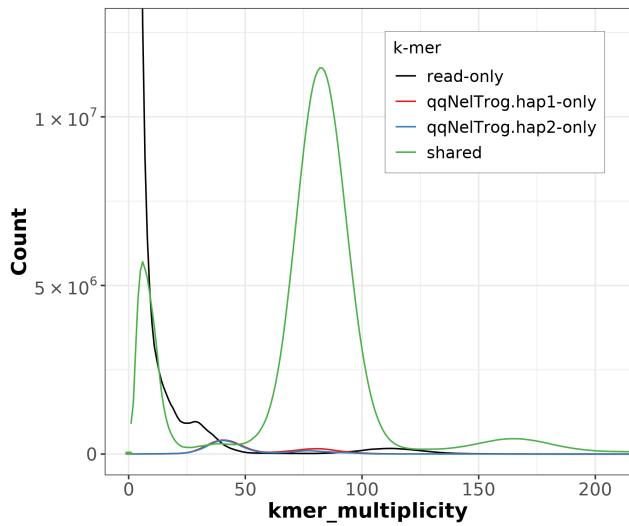


**hap1** [\[LINK\]](#)

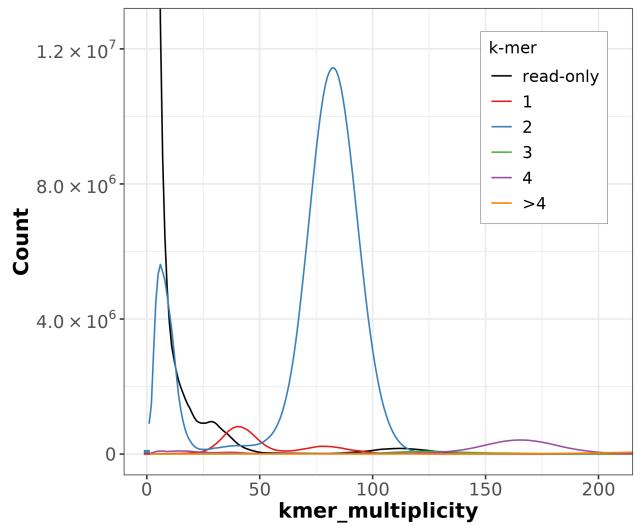
**hap2** HiC PNG is missing!

**hap2** File link is missing!

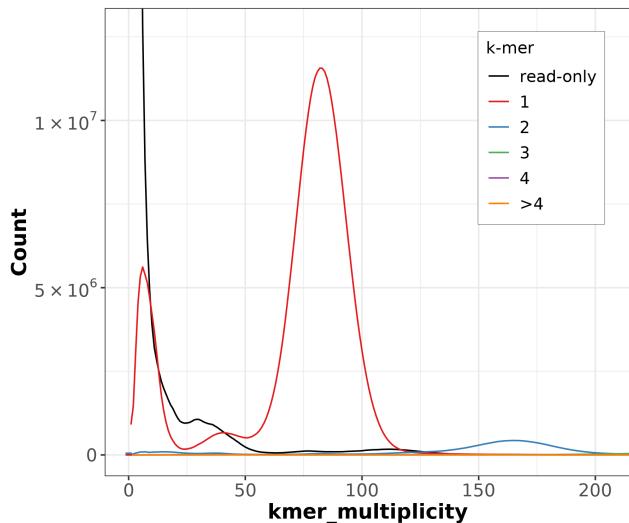
# K-mer spectra of curated assembly



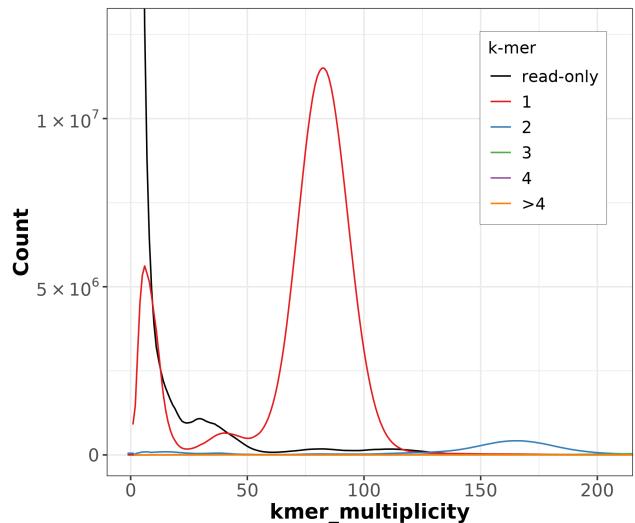
Distribution of k-mer counts coloured by their presence in reads/assemblies



Distribution of k-mer counts per copy numbers found in asm (dpl.)



Distribution of k-mer counts per copy numbers found in **hap1** (hapl.)



Distribution of k-mer counts per copy numbers found in **hap2** (hapl.)

# Post-curation contamination screening

## Data profile

	Data	ONT	Arima Hi-C
Coverage	174	125	

## Assembly pipeline

- **CLAWS**
  - |\_ ver: v3.1
  - |\_ key param: NA
- **Filtlong**
  - |\_ ver: v0.2.1
  - |\_ key param: --minlen 1000
  - |\_ key param: --min\_mean\_q 80
  - |\_ key param: --target\_bases 60000000000
- **Hifiasm**
  - |\_ ver: 0.24.0
  - |\_ key param: --ont
  - |\_ key param: --telo-m TTAGG
- **Yahs**
  - |\_ ver: 1.2a
  - |\_ key param: -mq 10
  - |\_ key param: --no-contig-ec
- **FOAM**
  - |\_ ver: 0.5
  - |\_ key param: NA

## Curation pipeline

- **FCS-GX**
  - |\_ ver: None
  - |\_ key param: NA
- **PretextViewAI**
  - |\_ ver: 1.0.5
  - |\_ key param: NA

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