

# Genome organization of *Caenorhabditis brenneri*

Anastasia A. Teterina<sup>1,2</sup>, John H. Willis<sup>1</sup>, Charles F. Baer<sup>3</sup>, Patrick C. Phillips<sup>1</sup>

teterina@uoregon.edu



<sup>1</sup> Institute of Ecology and Evolution, University of Oregon, Eugene, OR, USA; <sup>2</sup> Center of Parasitology, Severtsov Institute of Ecology and Evolution RAS, Moscow, Russia; <sup>3</sup> Department of Biology, University of Florida, Gainesville, USA

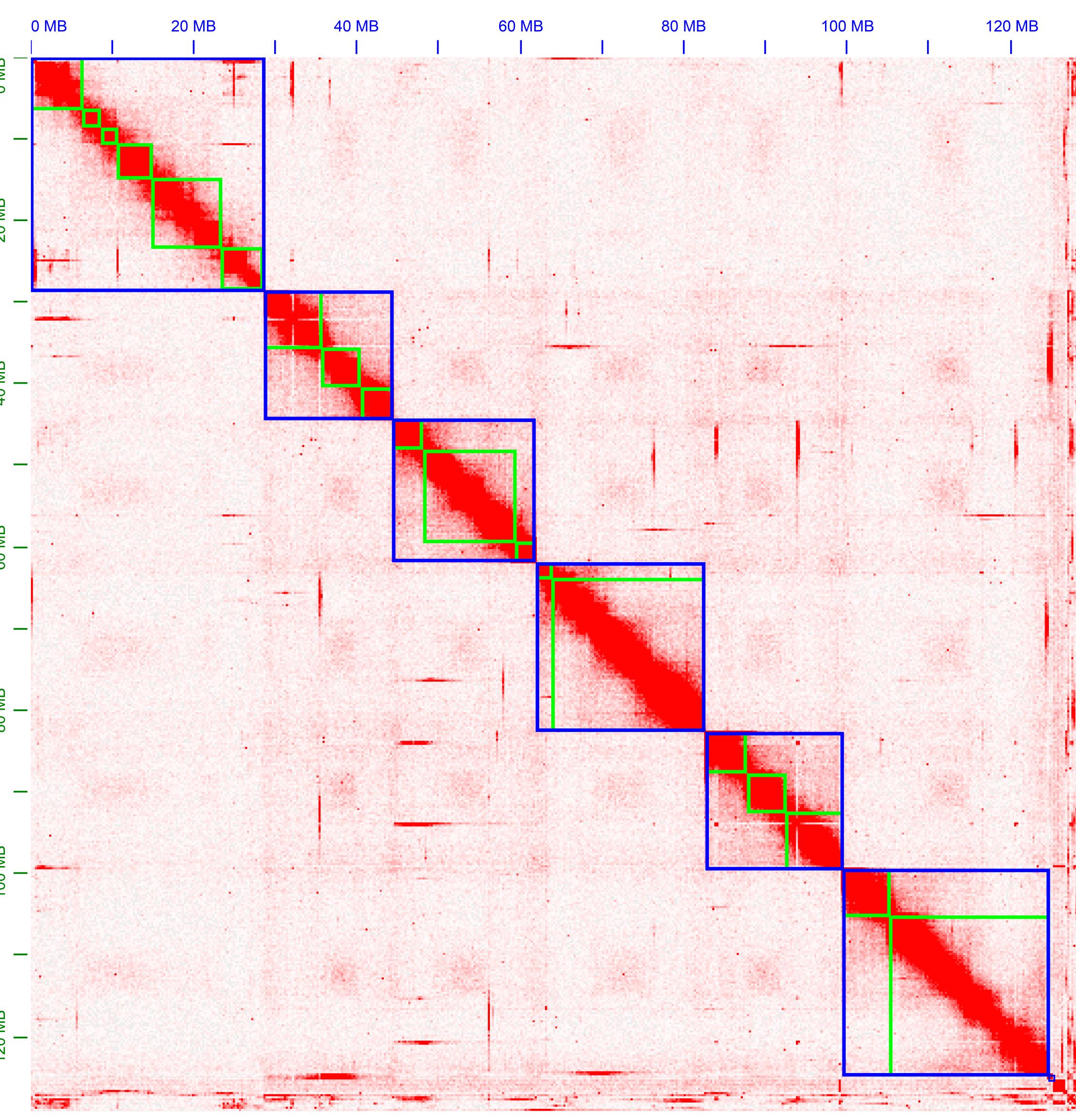
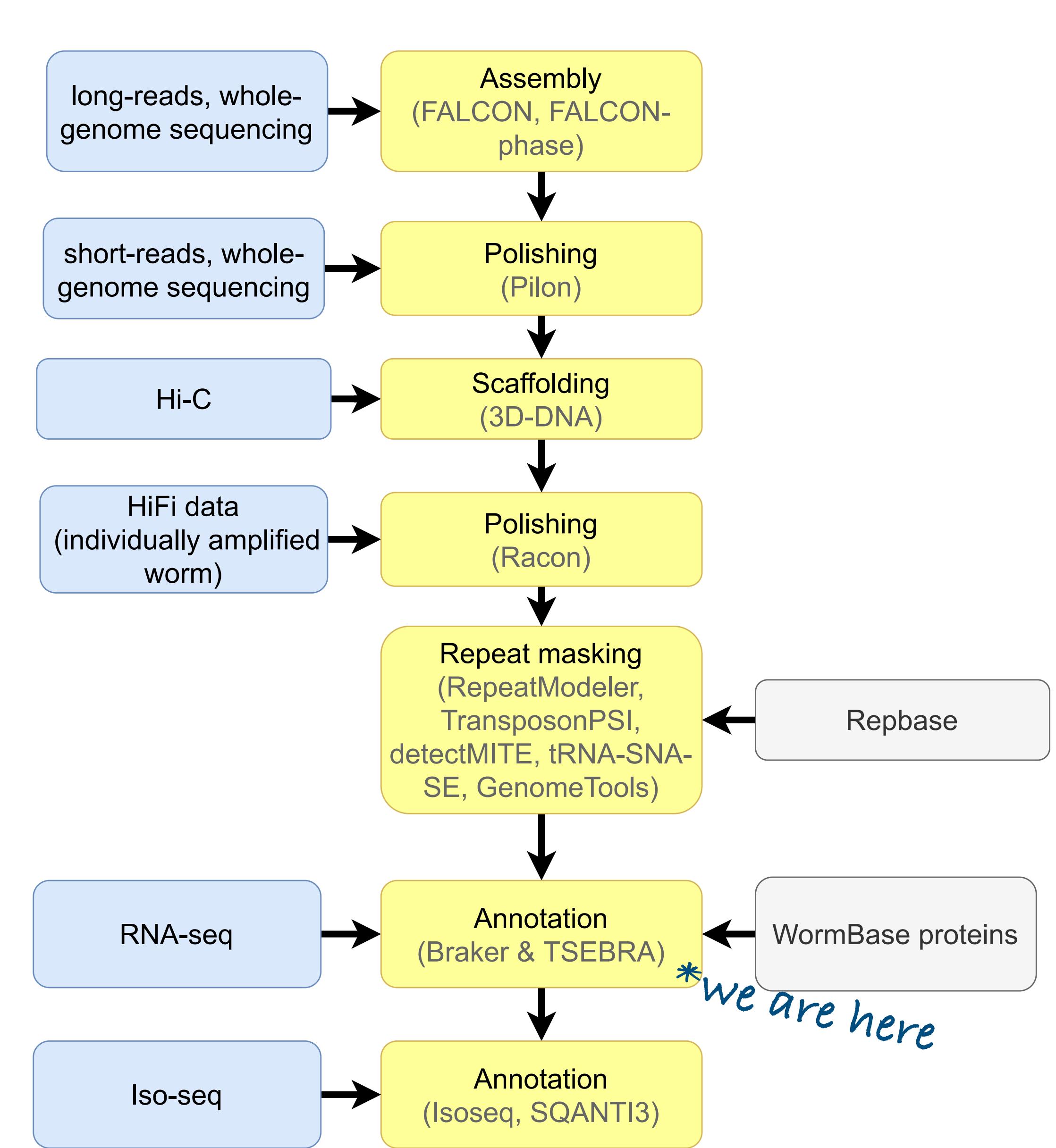
## Sample and genome assembly

*Caenorhabditis brenneri* is an outcrossing species of nematodes in the 'Elegans' supergroup (Rhabditida) formally described by Sudhaus & Kiontke in 2007.

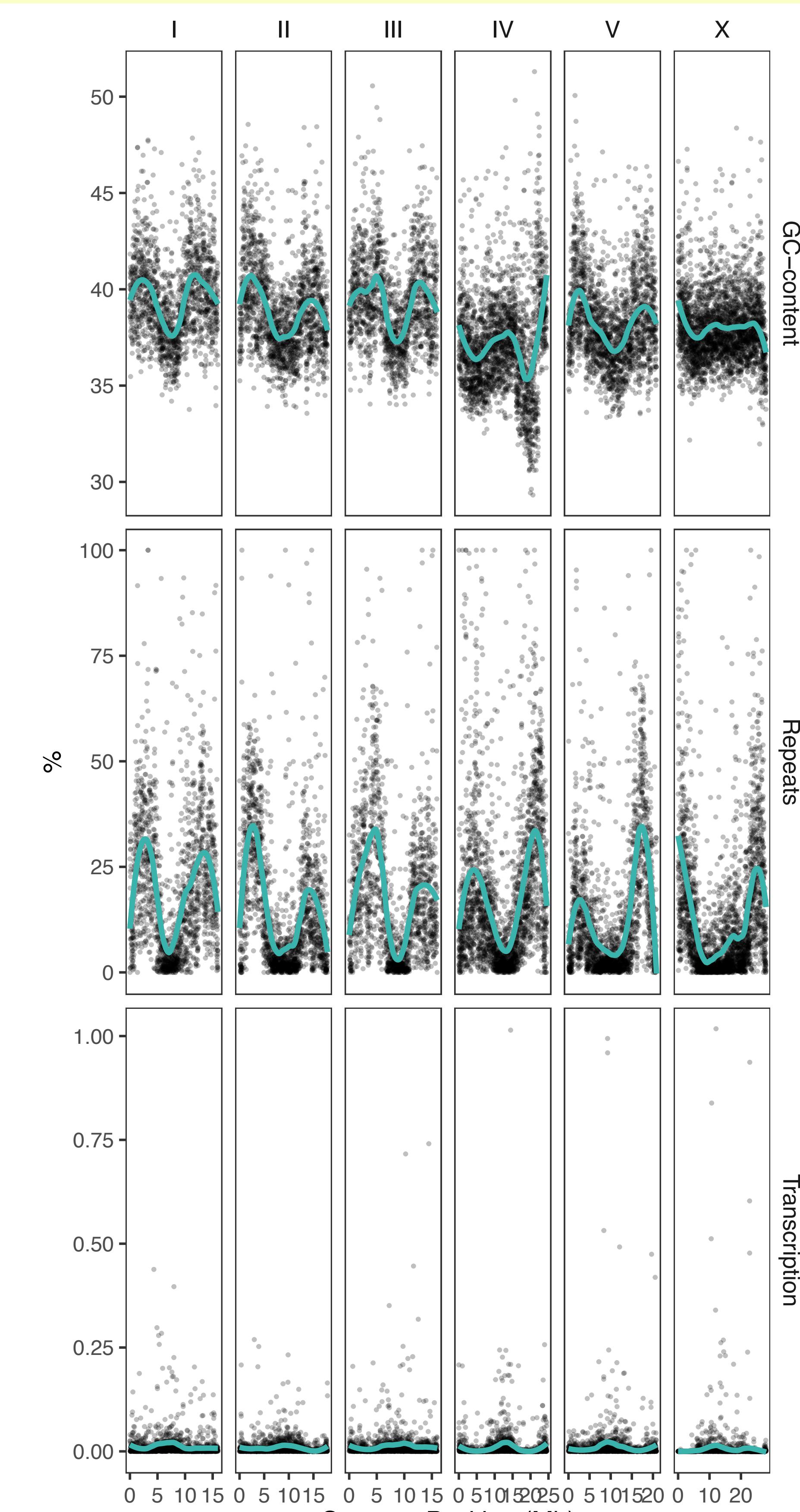
*C. brenneri* is one of the most genetically diverse eukaryotes, roughly every tenth nucleotide is polymorphic, which makes it comparable to hyperdiverse bacteria (Dey et al. 2013).

We created an inbred strain VX0223 to remove the residual heterozygosity of *C. brenneri* (300 generations of inbreeding!).

Using various types of genomic data (see our pipeline on the right), we generated a new chromosome-scale assembly of *C. brenneri*. We are planning to use this reference to study diversity of *C. brenneri* population at the genome-scale.



Contact map of Hi-C interactions. Green boxes represent contigs, blue ones show scaffolds



### Assembly statistics

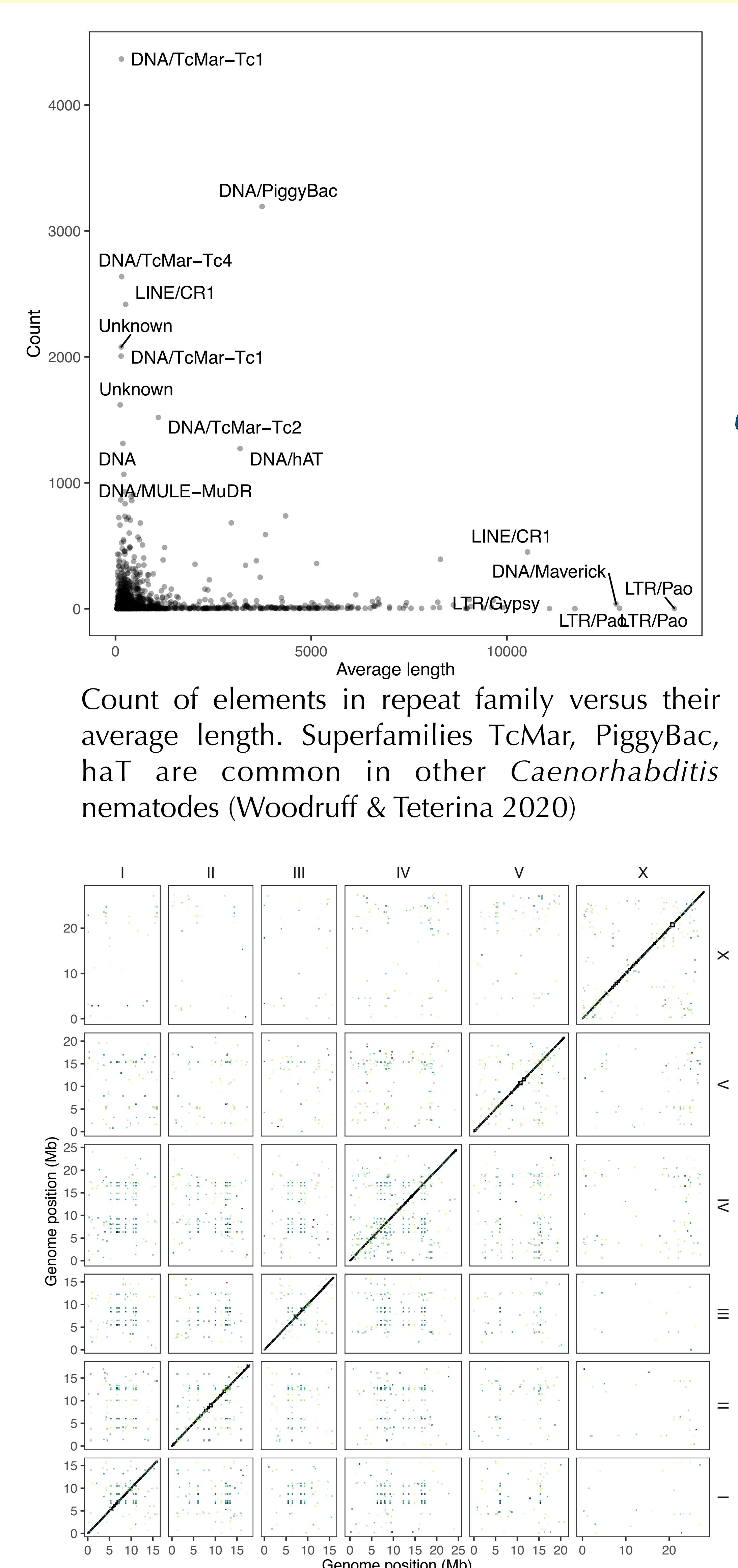
Size: 123.19Mb  
L50/N50: 3/20.8Mb  
L75/N75: 5/15.9Mb  
GC%: 38.39

### BUSCO (nematoda\_odb9)

Complete: 95.5%  
Single copy: 94.6%  
Duplicated: 0.9%  
Fragmented: 2.2%  
Missing: 2.3%

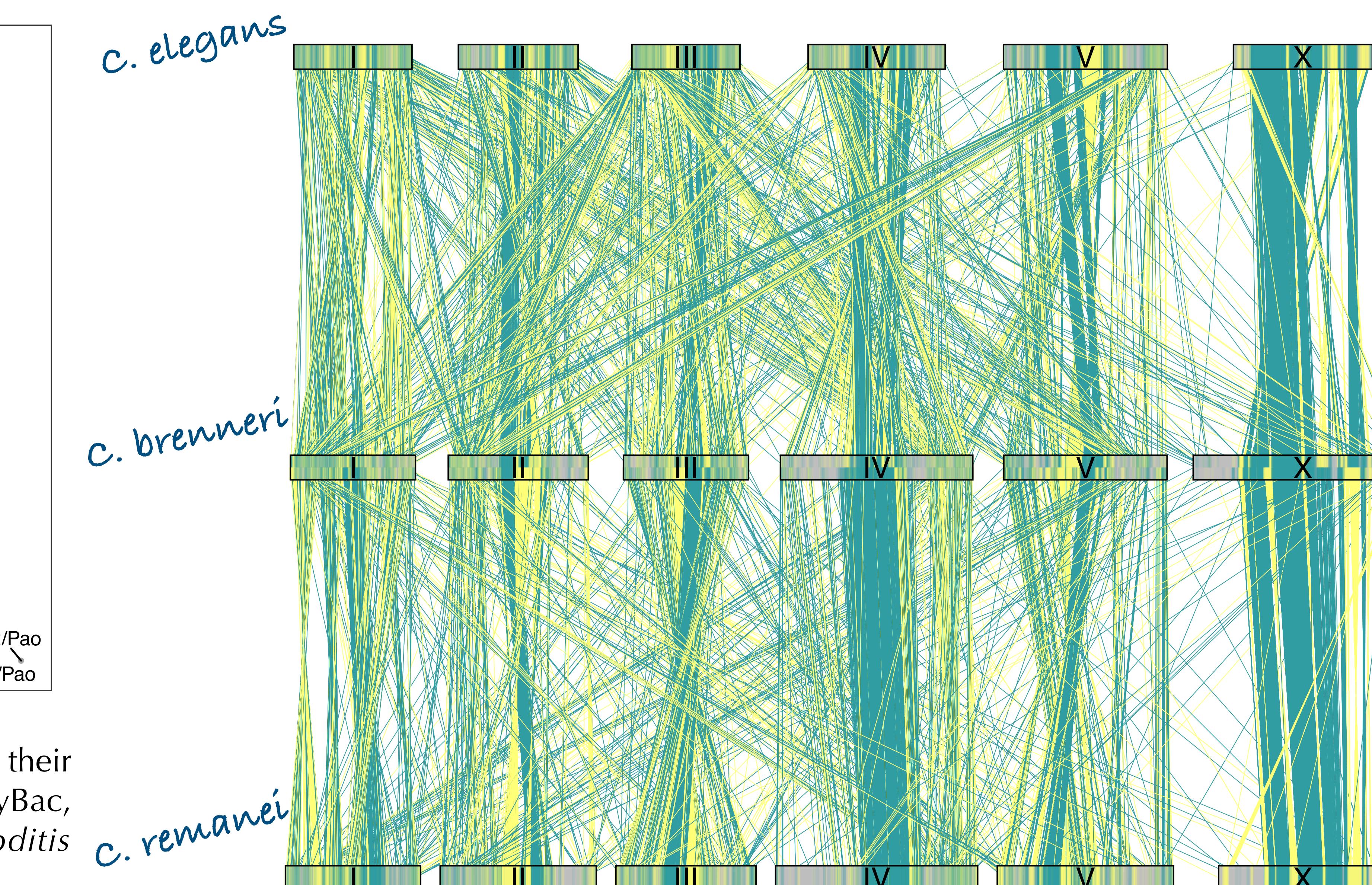
Percent of G/C bases, repetitive elements, and transcripts estimated per 10Kb windows. Similar to other *Caenorhabditis* species, *C. brenneri* has a domain-like chromosome organization

Only 15.8% of the *C. brenneri* genome is repetitive, which is lower than in most other outcrossing species and similar to *C. bovis* (Stevens et al. 2020). Such a low number of repeats may be the result of highly effective selection against transposons due to the large population size of *C. brenneri*. Alternatively, the current pipeline may under-detect repeats due to significant divergence among them.



Count of elements in repeat family versus their average length. Superfamilies TcMar, PiggyBac, haT are common in other *Caenorhabditis* nematodes (Woodruff & Teterina 2020)

## Genomic features



Genome alignments of *C. elegans* (top), *C. brenneri*, and *C. remanei* (bottom). Lines show alignments longer than 1000 bp. with identity > 65%, the same orientation is teal, the opposite is yellow. The X chromosome is the most conservative, and it's noticeably longer in *C. brenneri*. The central domains have more extended synthetic blocks

## Future directions

- Analysis of repetitive sequences, comparison with other species
- Genome annotation with full-length transcripts, and isoform analysis
- Best practices for population genomics with individually amplified worms
- Analysis of the structural variation in the population
- Evolution and diversity of repetitive elements

## References

- Sudhaus W, Kiontke K. Comparison of the cryptic nematode species *Caenorhabditis brenneri* sp. n. and *C. remanei* (Nematoda: Rhabditidae) with the stem species pattern of the *Caenorhabditis Elegans* group. Zootaxa. 2007 Apr 25;1456(1):45-62.
- Dey A, Chan CK, Thomas CG, Cutter AD. Molecular hyperdiversity defines populations of the nematode *Caenorhabditis brenneri*. PNAS. 2013 Jul 2;110(27):11056-60.
- Stevens L, Rooke S, Falzon LC, Machuka EM, Momanyi K, Murungi MK, Njoroge SM, Odinga CO, Ogendo A, Ogola J, FRvre EM. The genome of *Caenorhabditis bovis*. Current Biology. 2020 Mar 23;30(6):1023-31.
- Woodruff GC, Teterina AA. Degradation of the Repetitive Genomic Landscape in a Close Relative of *Caenorhabditis elegans*. MBE. 2020 Sep;37(9):2549-67.