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High-quality genome assembly to identify structural variations in a quarantine plant parasitic nematode *Meloidogyne enterolobii*

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Meloidogyne enterolobii, a plant parasitic nematode

Root-knot nematodes, genus *Meloidogyne*, are obligatory plant endoparasites that threaten the global food supply. They cause lesions on the roots leading to a decrease in plant fitness or death.

M. enterolobii can circumvent non-chemical control methods and reproduce on cultivars that are resistant to the other members of the same genus.

Since 2023, *M. enterolobii* is part of the European Plant Protection Organisation (EPPO) Plant Quarantine Alert List.

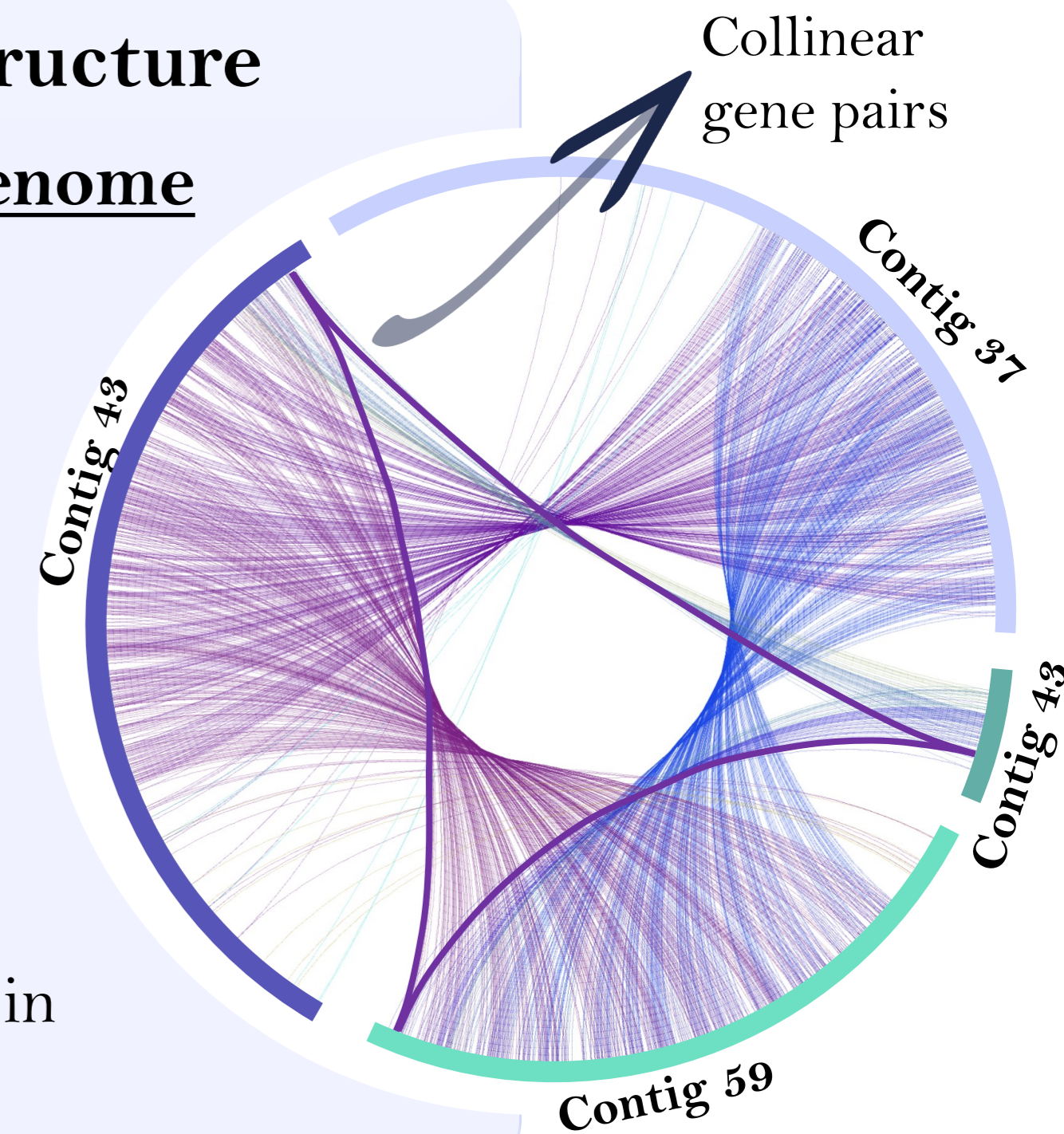
... with a complex structure

M. enterolobii has a **triploid genome**

94.8% of the protein-coding genes are duplicated.

More than half of the genes (59.49%) are part of duplicated regions, probably as a result of whole genome duplication.

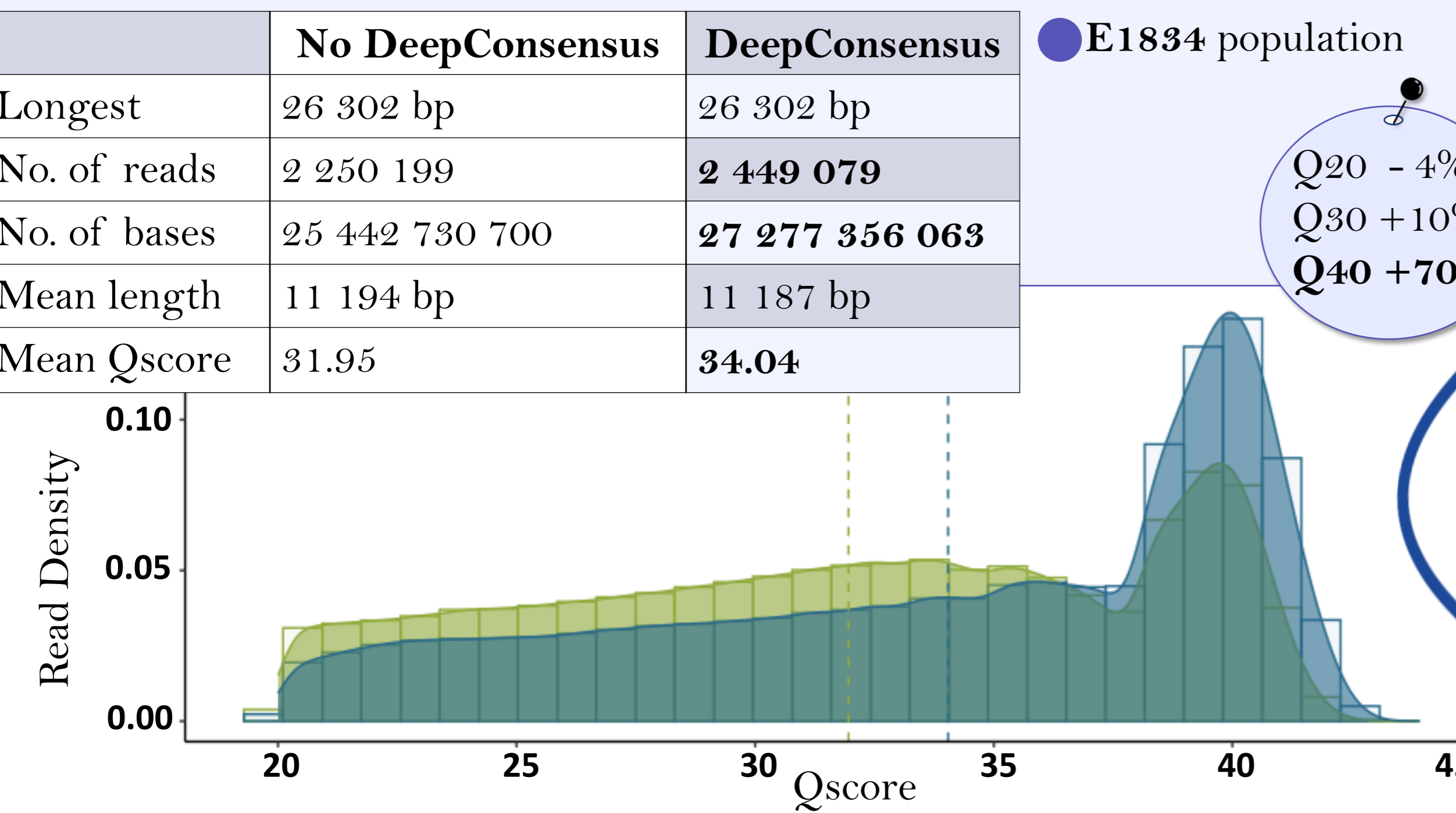
76.7% of these genes are present in three copies.



Data available for the study

We have produced high-fidelity genome data (PacBio Hifi) for 7 different geographical isolates of *M. enterolobii*. Each isolate differs in its host range.

Improving PacBio Hifi Long-Reads with DeepConsensus



Workflow strategies for variant calling

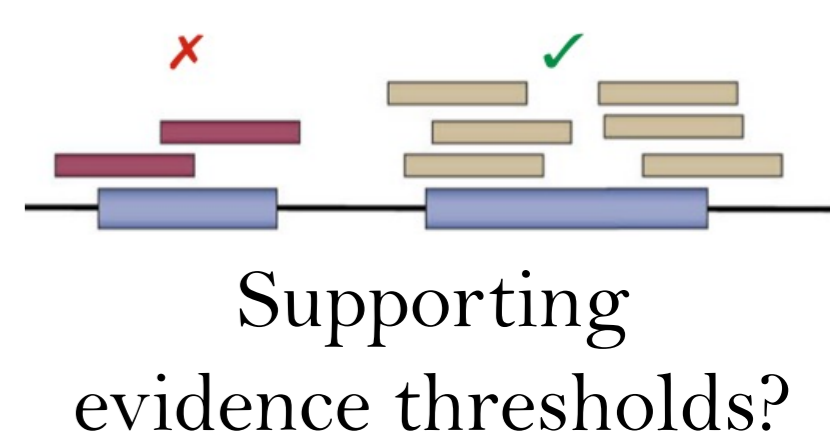
Coordinate-sorted BAM file for *M. enterolobii* populations

Discovering SVs signatures with multiple independent algorithms



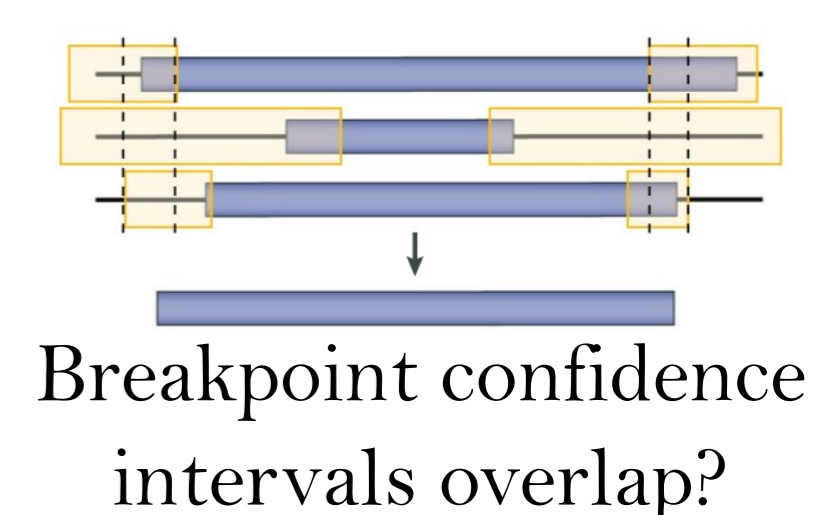
Filtering Structural Variants

- Supporting reads
- Length ($50 < x < 2\text{Mb}$)
- Allele frequency ($x > 0.3$)



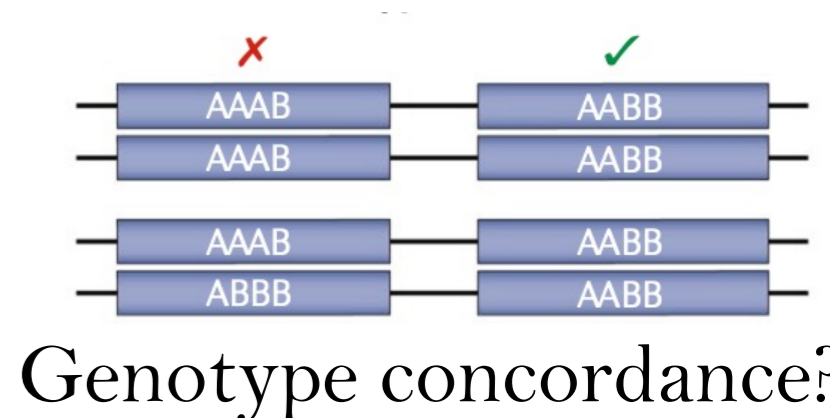
Merging and breakpoint refinement

- Jasmine



Per-sample re-genotyping and refinement

- SV Jedi Graph

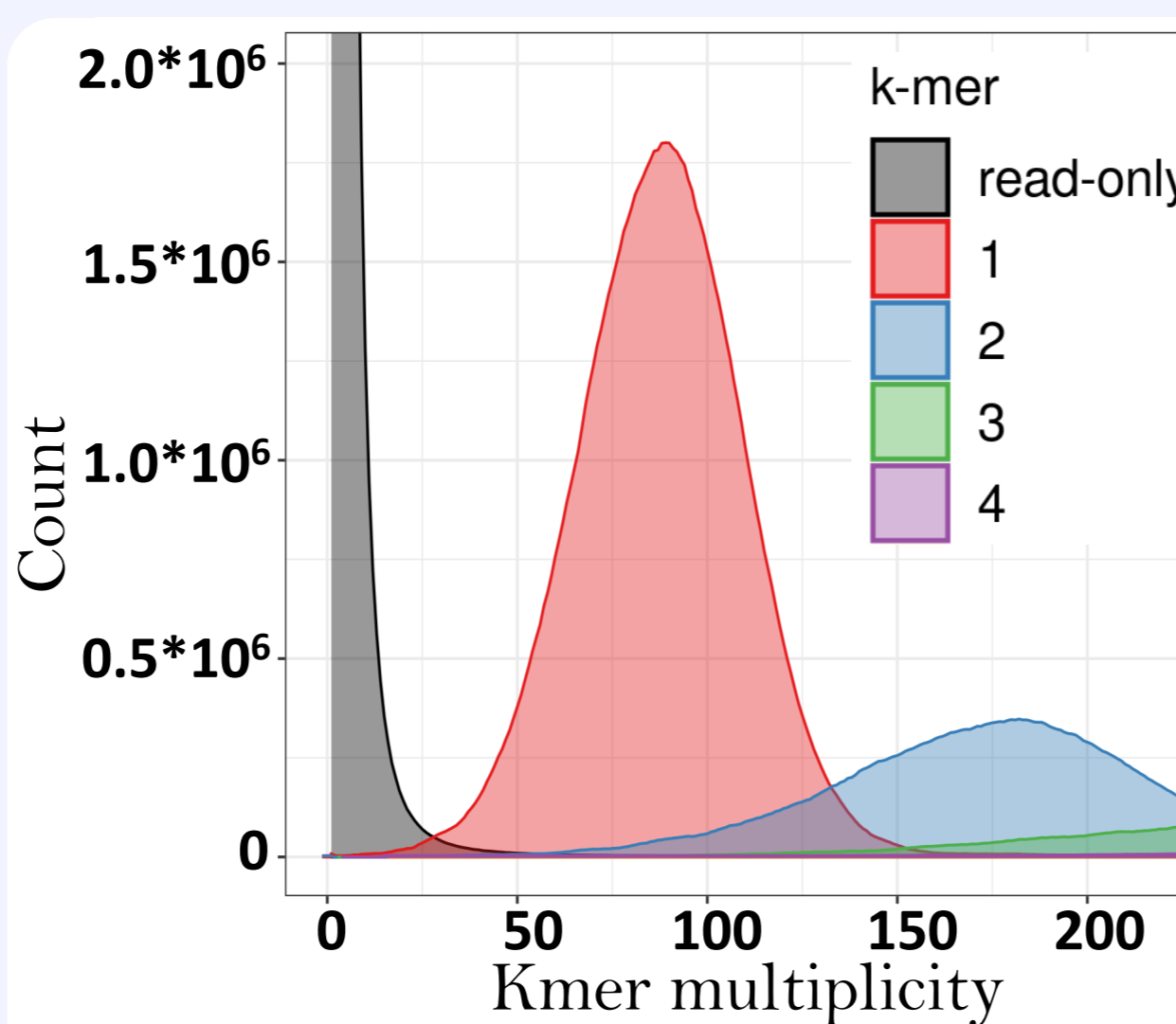


Population-level VCF creation

The most contiguous assembly so far for *M. enterolobii*

Assembly Size (Mb)	273
No. Contigs	556
Minimum (bp)	14 620
Maximum (bp)	8 284 238
N50 (bp)	2 114 331

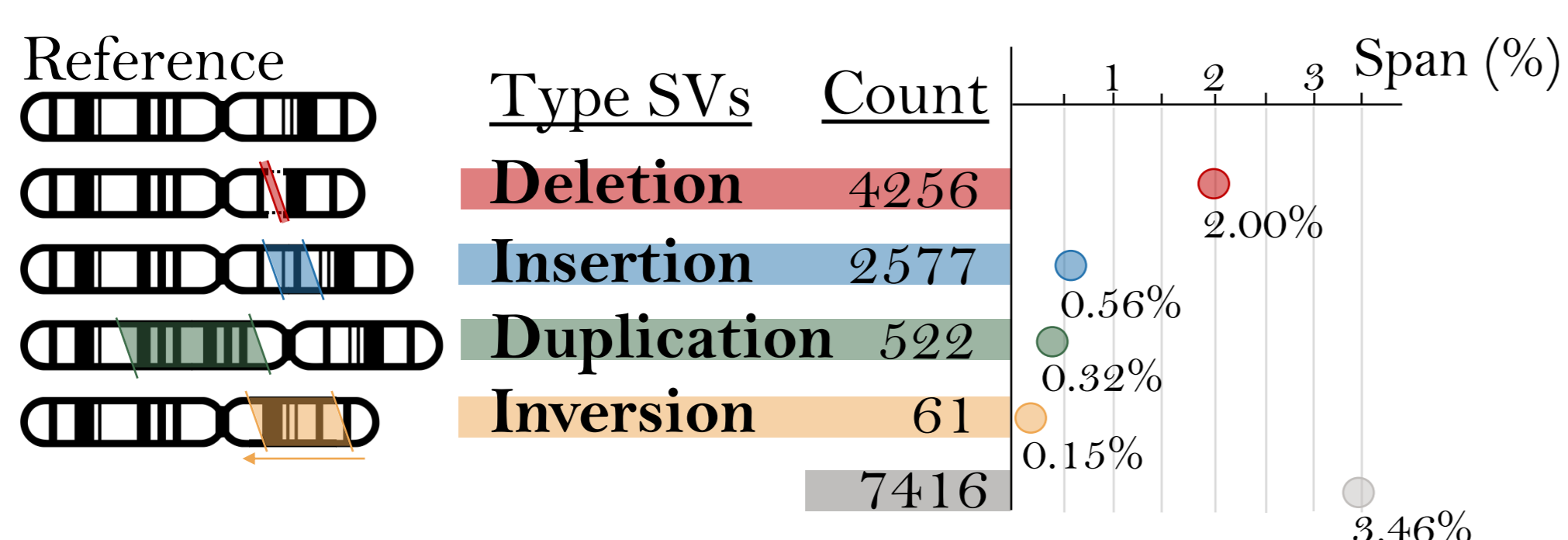
The assembly has been done with the assembler Peregrine-2021.



- GC content of 31%
- Merquy completeness score of 99.61%
- New reference for *M. ent*

Preliminary results & Perspectives

- 7416 SVs per sample spanning 3.46% of the reference genome



- Investigate the relationship between genomic variations (**Structural Variations and Single Nucleotide Polymorphisms**) and phenotypic variations (**host range compatibility and geographic distribution**).

Acknowledgements

