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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.

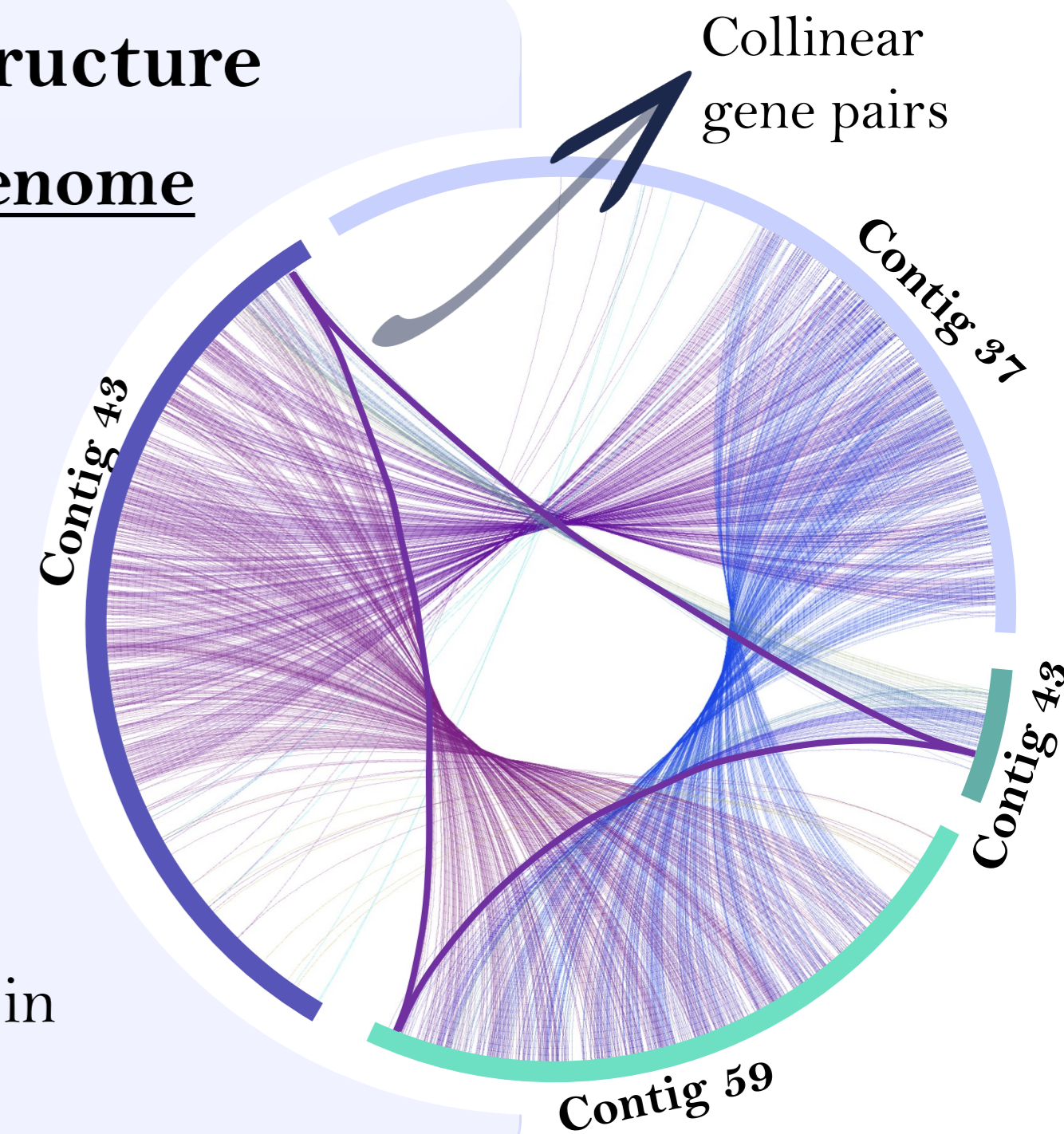
## ... with a complex structure

*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.

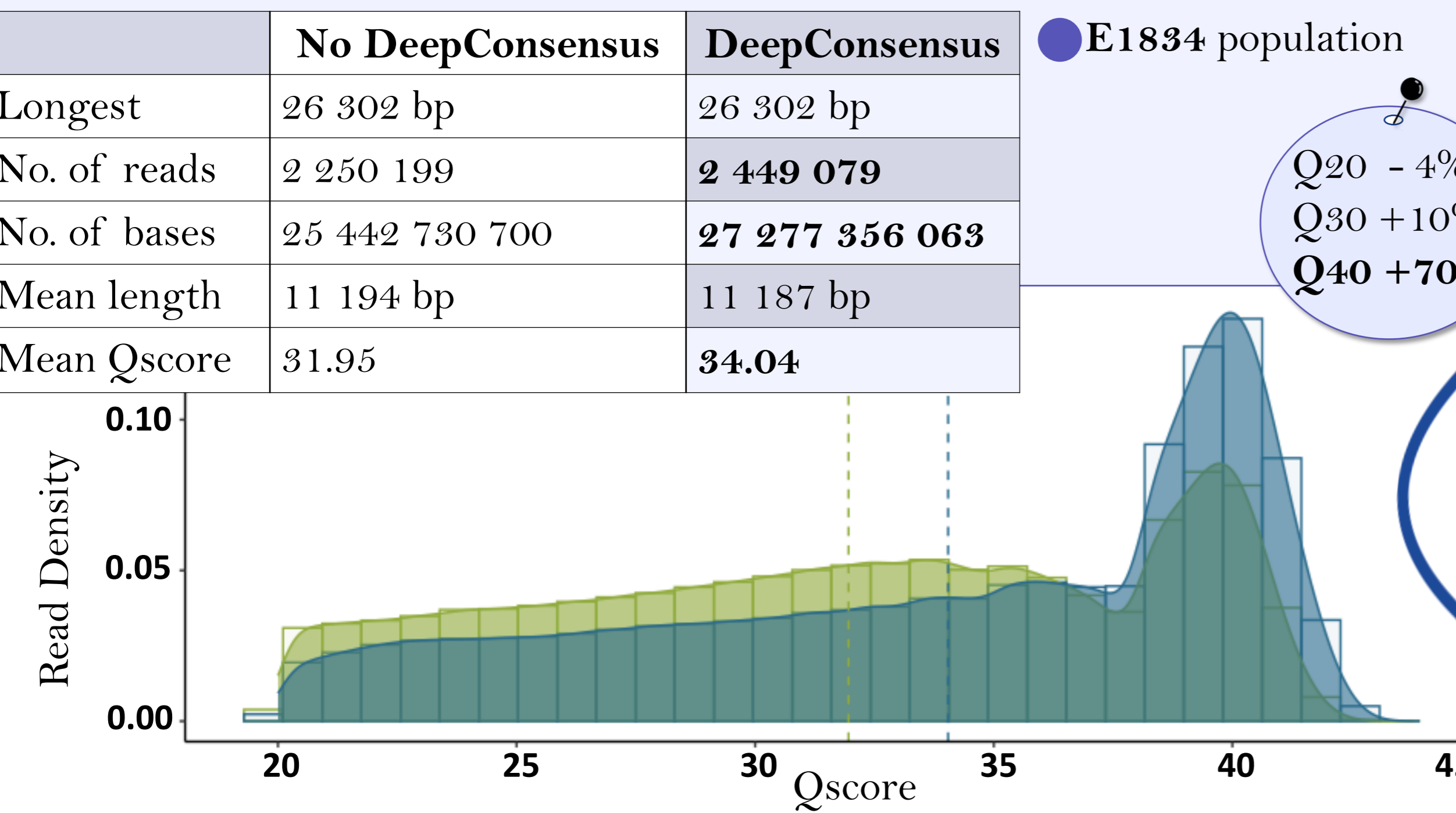
76.7% of these genes are present in three copies.



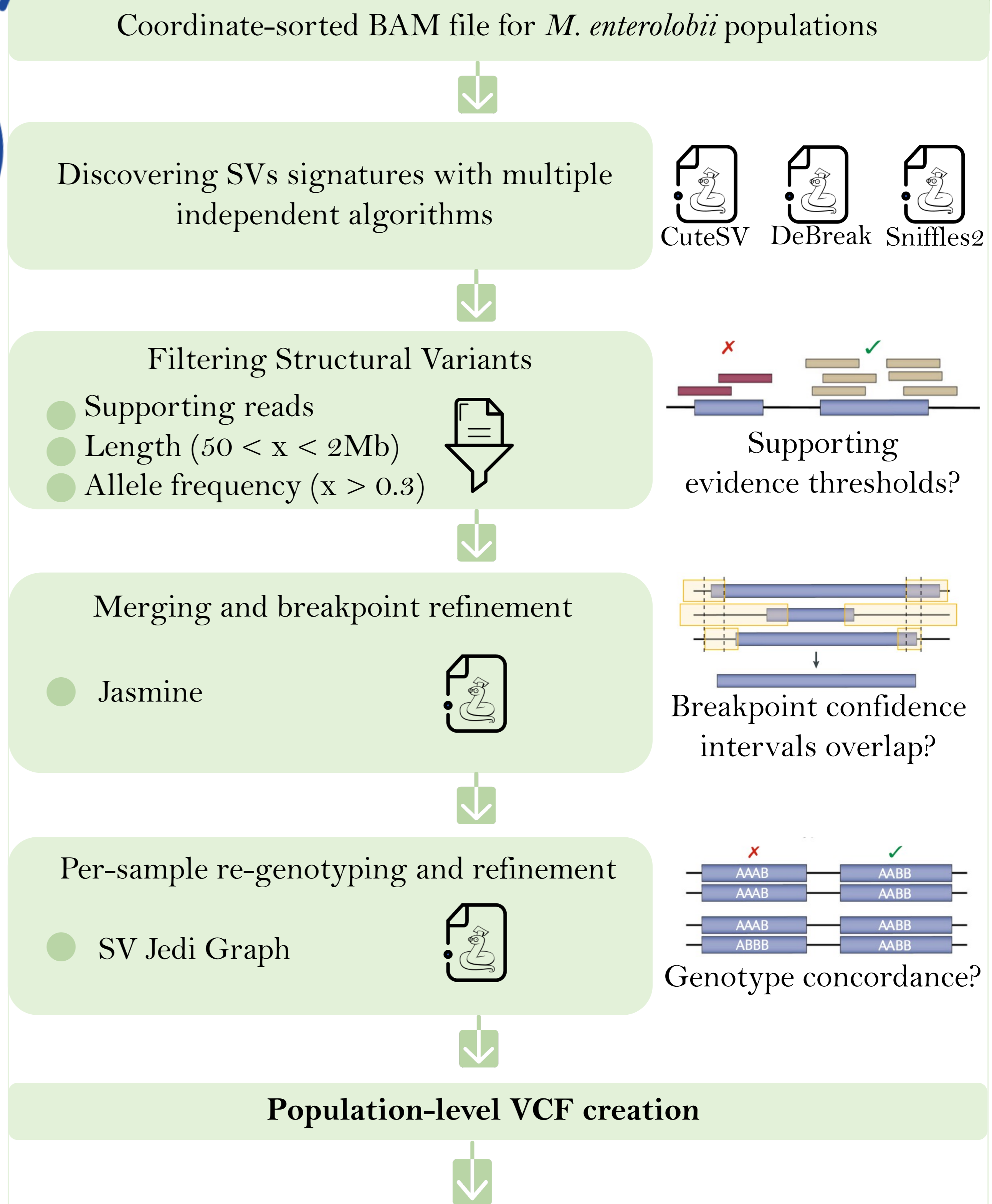
## Data available for the study

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



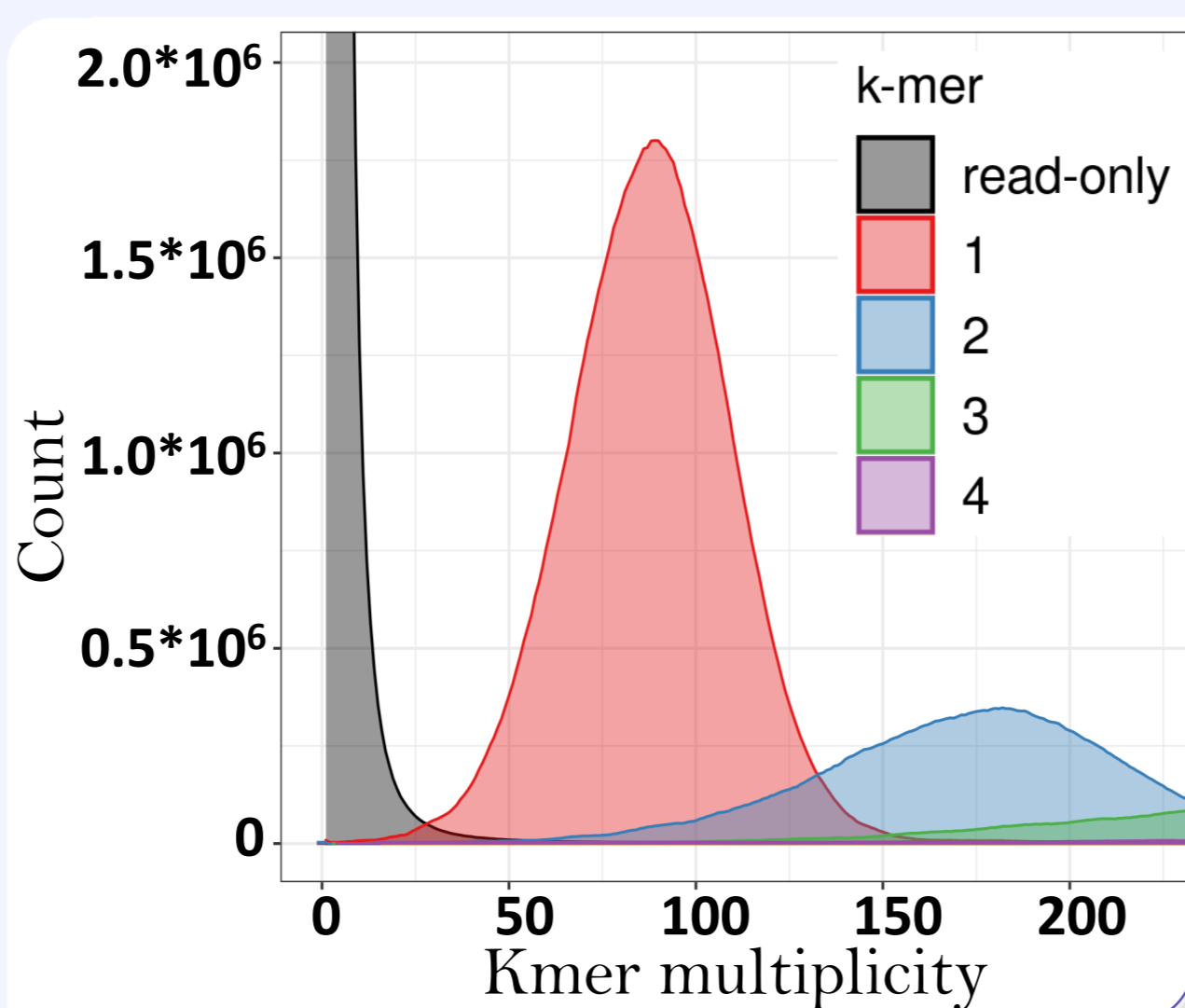
## Workflow strategies for variant calling



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

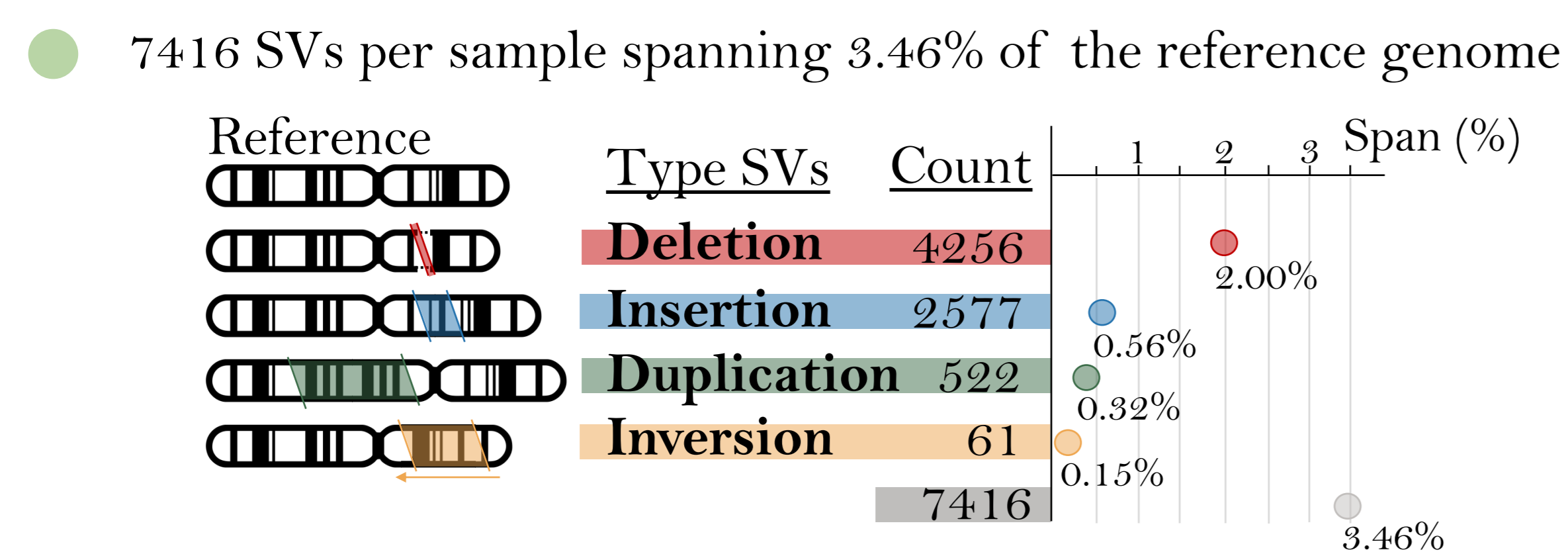
Assembly Size (Mb)	273
No. Contigs	556
Minimum (bp)	14 620
Maximum (bp)	8 284 238
N50 (bp)	<b>2 114 331</b>

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



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



## Acknowledgements

