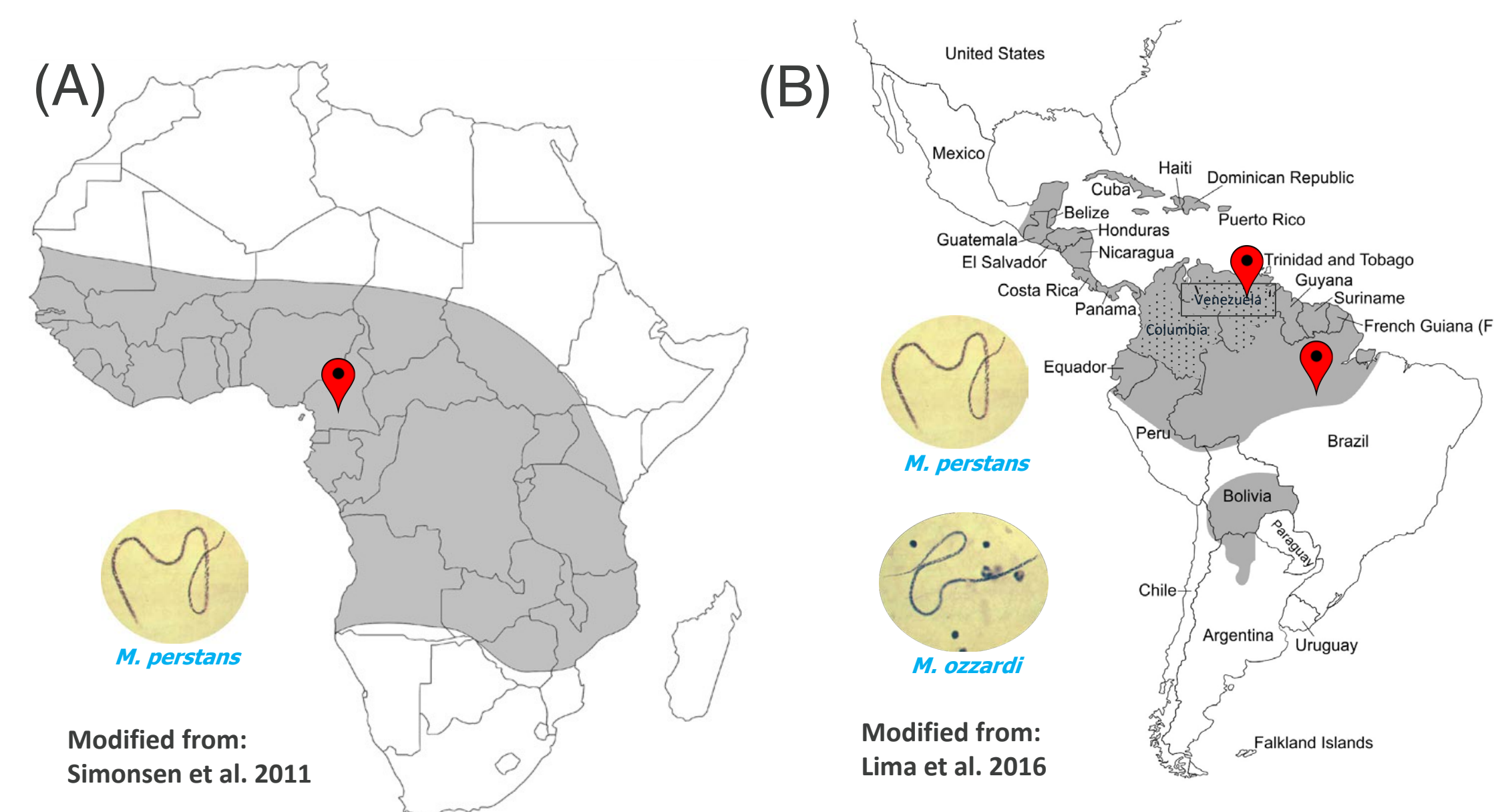


Genome sequences of the human filarial parasites *Mansonella perstans* and *Mansonella ozzardi*

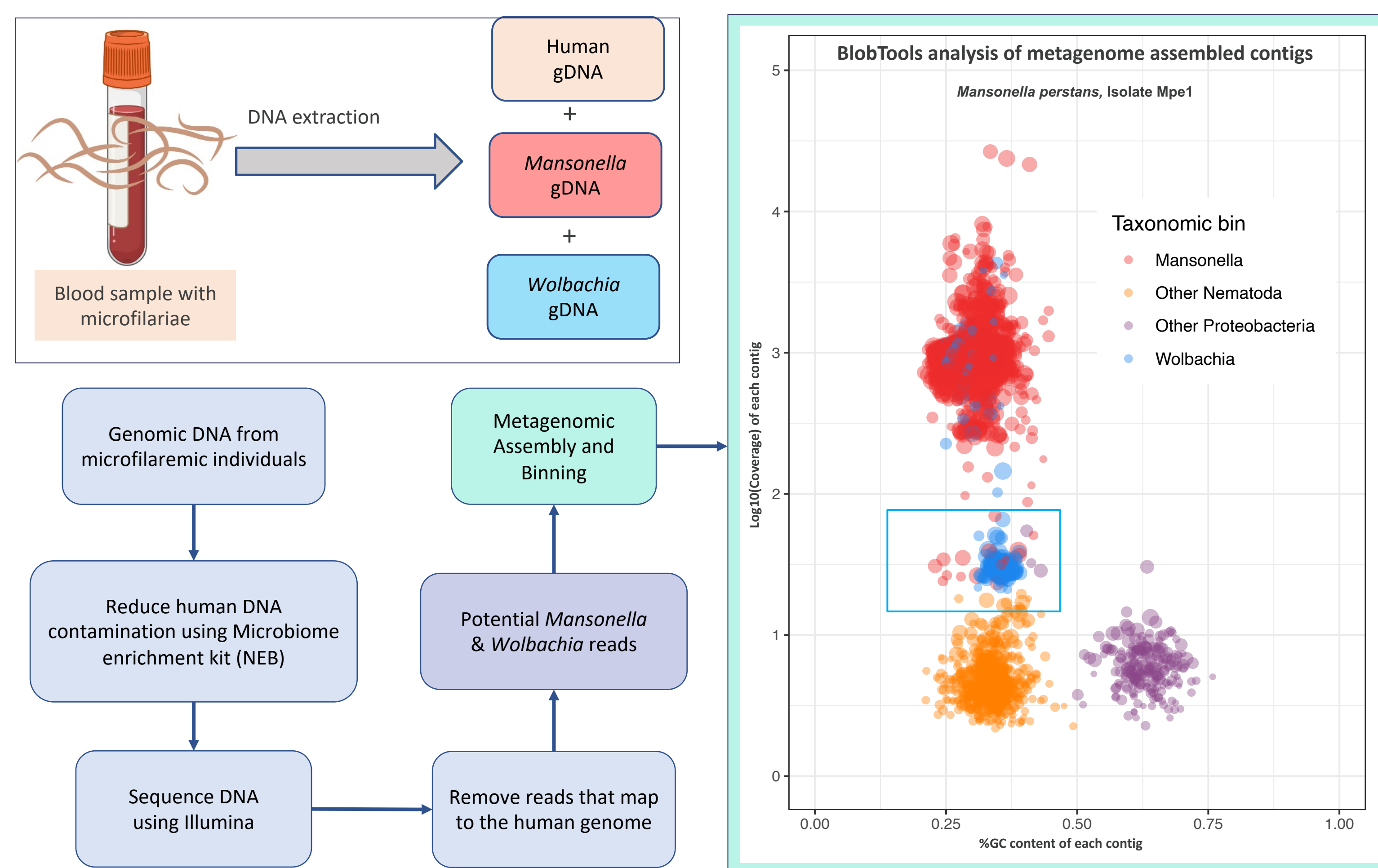
Mansonelliasis : A neglected filarial infection

- Mansonelliasis** is a widespread yet neglected filariasis of humans, caused by infection with any of the three filarial species: *Mansonella perstans*, *M. ozzardi* and *M. streptocerca*.
- M. perstans*** infections are endemic in Central and West Africa (Figure 1A), and in a few areas of South America (stippled region in Figure 1B).
- M. ozzardi*** infections are highly prevalent in South America and the Caribbean islands (Figure 1B).
- Transmission to humans is via insect vectors
 - Biting midges of *Culicoides* spp. for *M. perstans*
 - Culicoides* midges as well as black flies of *Simulium* spp. for *M. ozzardi*



The goal of the current study was to obtain whole genome sequences of *M. perstans* and *M. ozzardi*

Mansonella Genomes: Challenges and Solutions

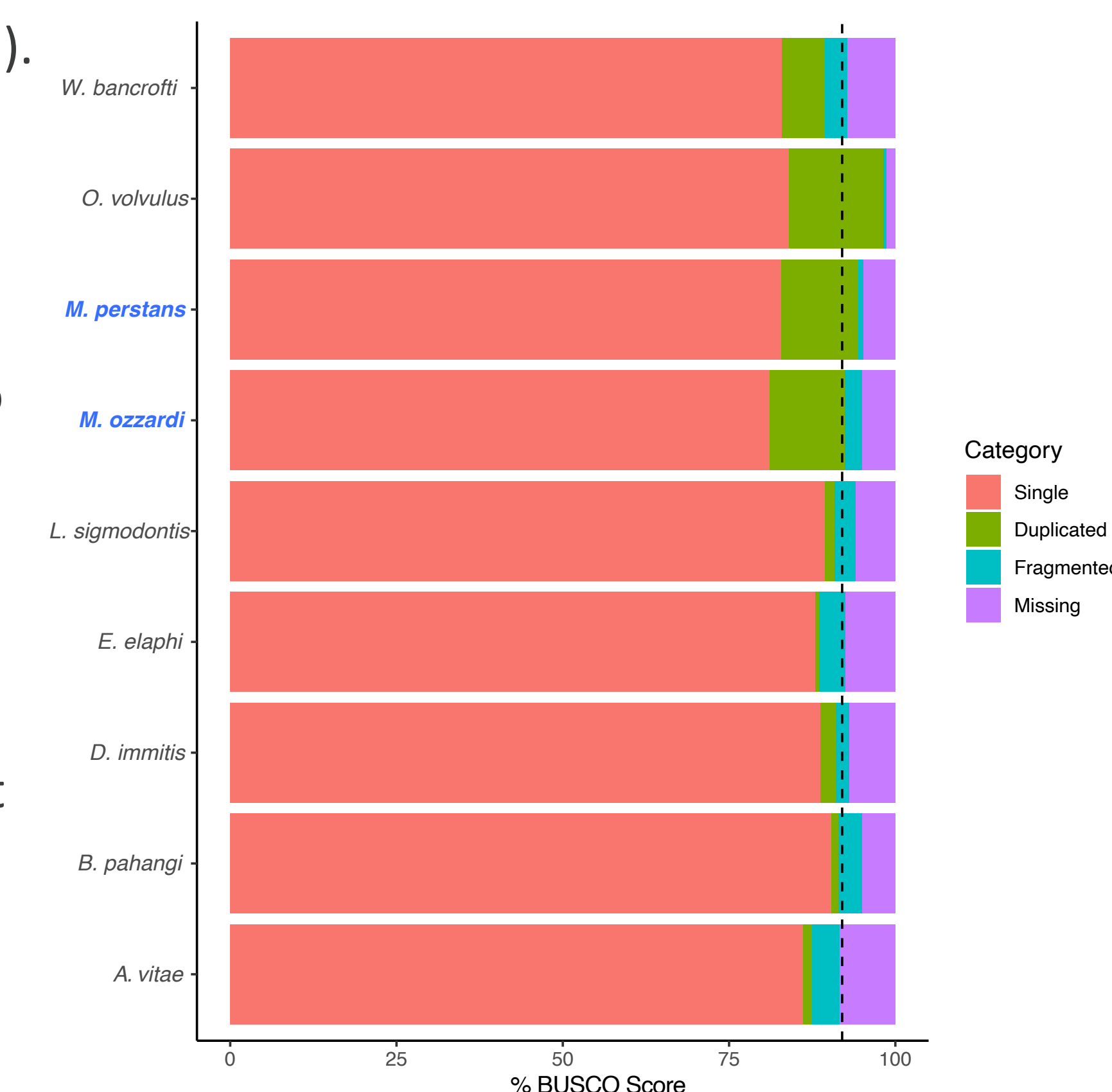


Mansonella Genome : Draft Assemblies

| | <i>M. perstans</i> | <i>M. perstans</i> | <i>M. ozzardi</i> | <i>M. ozzardi</i> |
|-----------------------|--------------------|--------------------|-------------------|-------------------|
| Sample Name | Mp2 | Mp1 | Moz1 | Mo2 |
| Sampling site | Cameroon | Cameroon | Brazil | Venezuela |
| Sequencing Platform | PacBio | Illumina | Illumina | Illumina |
| Assembled genome size | 79 Mb | 75.15 Mb | 76.32 Mb | 75.53 Mb |
| Number of scaffolds | 818 | 7,302 | 5,143 | 5,075 |
| Largest scaffold | 1.25 Mb | 217.3 kb | 294 kb | 258 kb |
| Scaffold N50 size | 259 kb | 27.7 kb | 36.79 kb | 38.25 kb |
| %GC | 30.34 | 30.07 | 29.65 | 29.67 |
| Predicted genes | 12,576 | 16,482 | 11,532 | 12,137 |

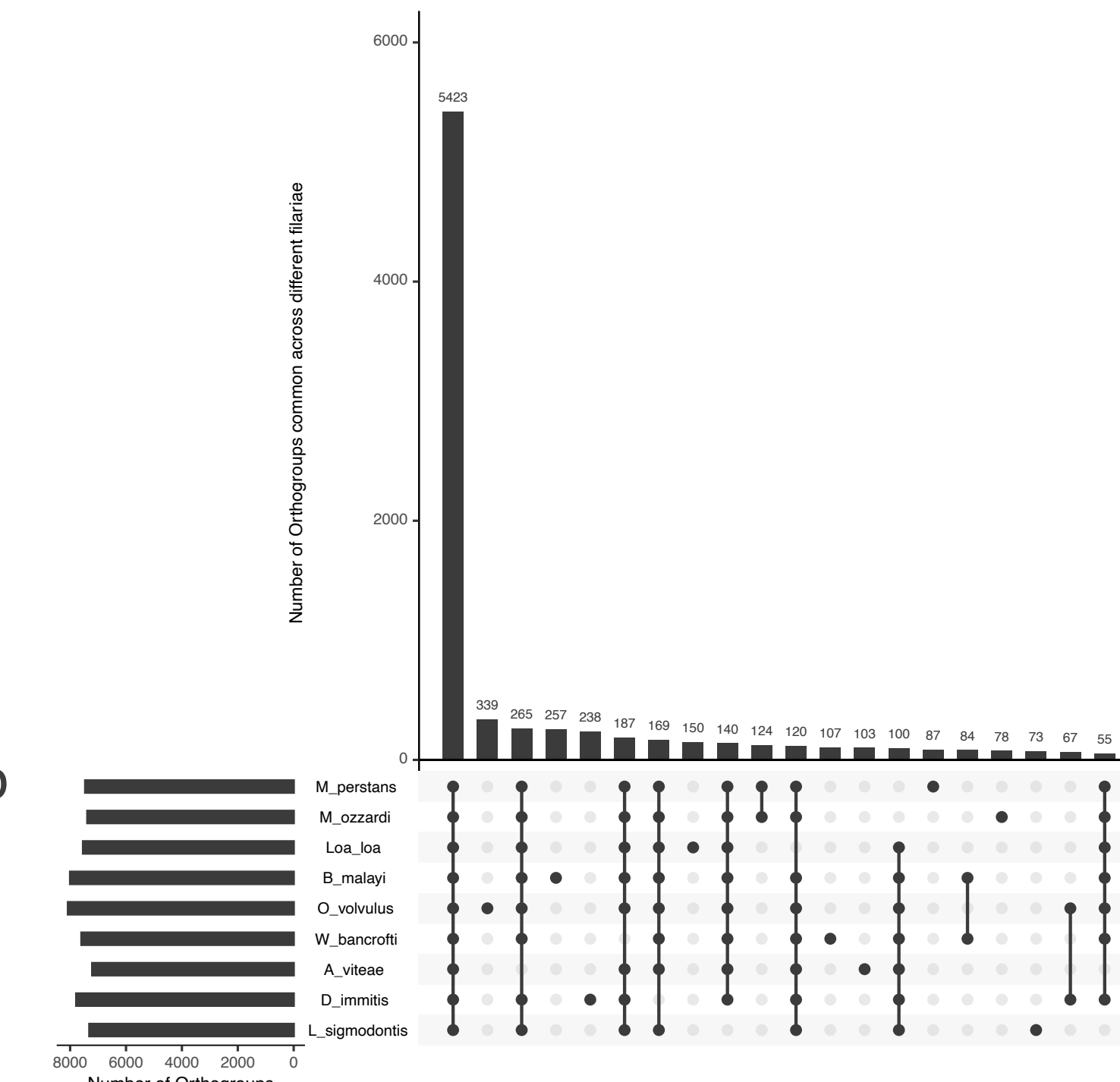
Completeness of Mansonella Genomes

- The completeness of gene content of assembled draft genomes was evaluated using the BUSCO software (Simão et al. 2015).
- The BUSCO score of a genome is calculated as the percentage of universal Single Copy Orthologs (SCOs) encoded by a genome, as compared to a reference set of SCOs known to be highly conserved in a particular taxa.
- M. perstans* and *M. ozzardi* encode more than 90 % of the 3,131 SCOs that are conserved across all nematodes.
- The BUSCO scores of assembled *Mansonella* genomes is similar to that from other sequenced filarial genomes, suggesting that these assemblies contain most of the protein coding genes they are estimated to encode.



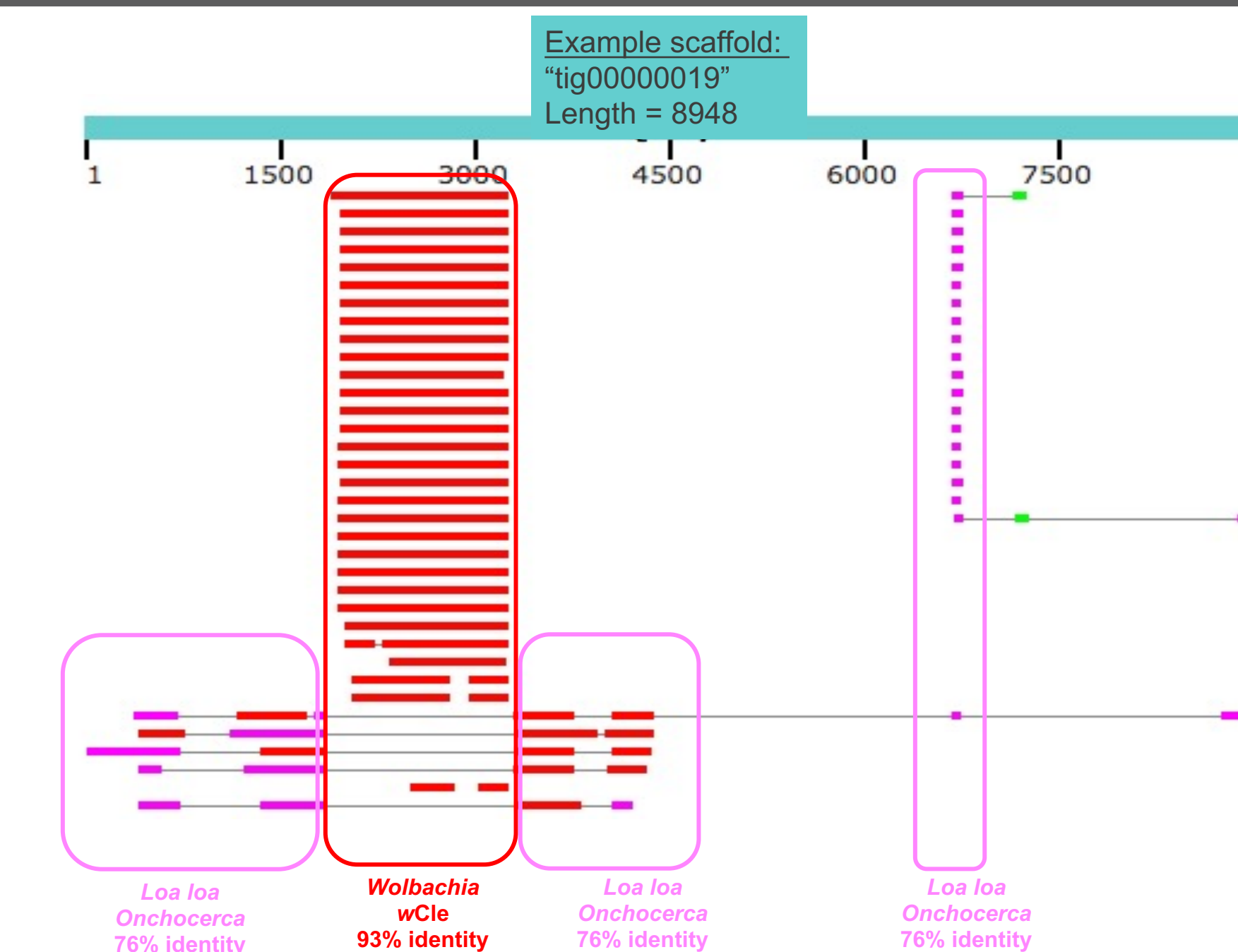
Orthology analysis across Onchocercidae

- Orthologous genes across different filarial nematodes were identified using the OrthoFinder (Emms and Kelly 2019)
- The analysis identified about 5,400 genes conserved across all filarial genomes analyzed
- Around 80 proteins were found to be unique to *M. perstans* and *M. ozzardi*



Horizontal DNA transfer from Wolbachia to Mansonella

- The BlobTools analysis identified many scaffolds with high sequence similarity to *Wolbachia*, but which had a read coverage and %GC overlapping *Mansonella*
- Further analysis of these scaffolds confirmed Horizontal DNA Transfer (HDT) from *Wolbachia* to *Mansonella*.
- Wolbachia*-like regions flanked by regions with high similarity to filarial genomes



Conclusions and Future Directions

- Draft assemblies of *M. perstans* and *M. ozzardi* have been obtained.
- Metagenomic assembly and binning were critical to
 - Disentangle genomes from complex clinical samples
 - Identify regions of Horizontal DNA Transfer (HDT) from the endosymbiont

References:

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- Simão, F. A. et al. (2015) BUSCO: assessing genome assembly and annotation completeness with single-copy orthologs. *Bioinformatics* **31**.
- Emms DM, Kelly S. (2019) OrthoFinder: phylogenetic orthology inference for comparative genomics. *Genome Biology*. **20**: 238.