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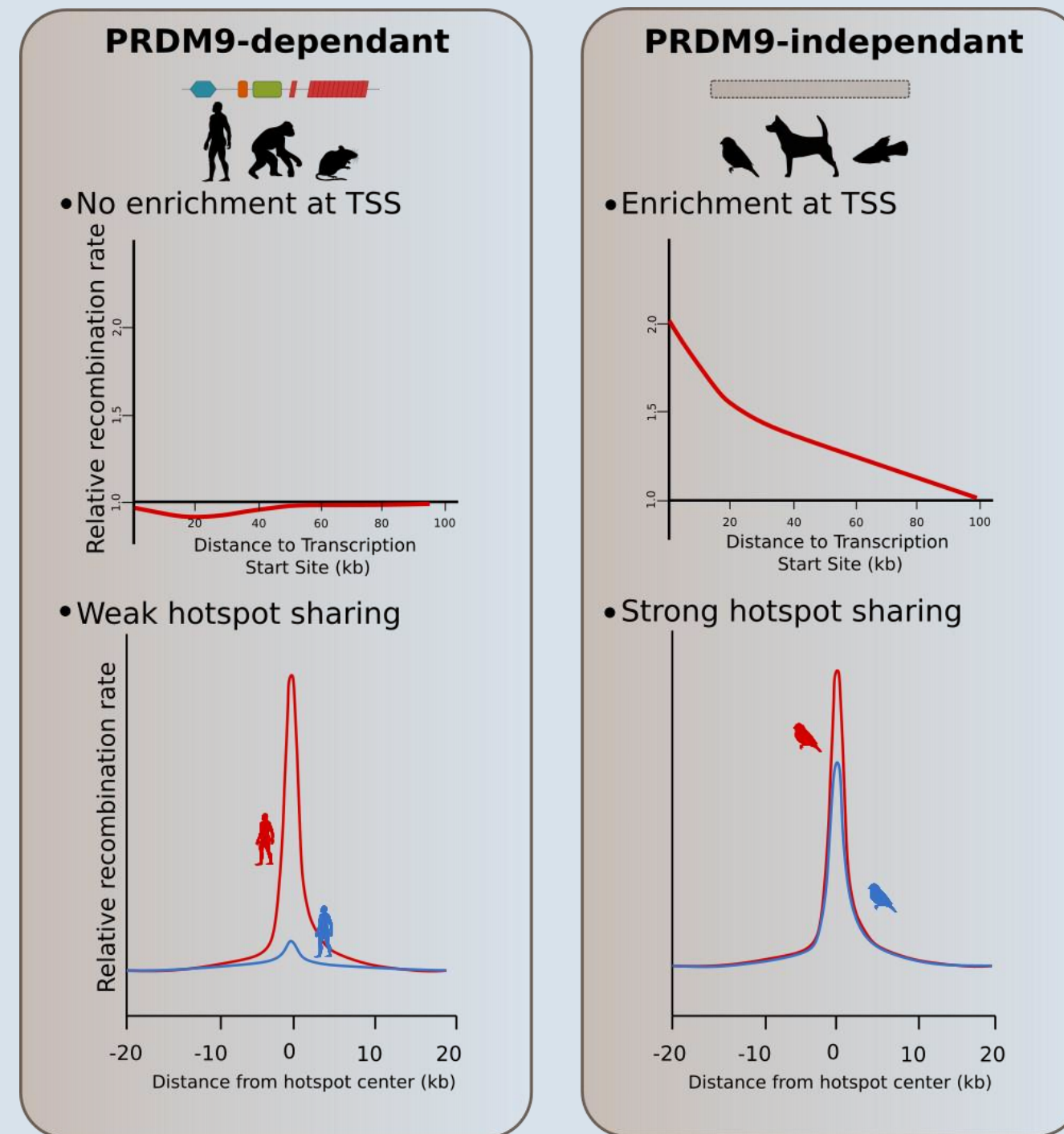
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# Fast evolving recombination landscapes support a role of PRDM9 in directing hotspot location in *Microvelia longipes* genome

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## Introduction

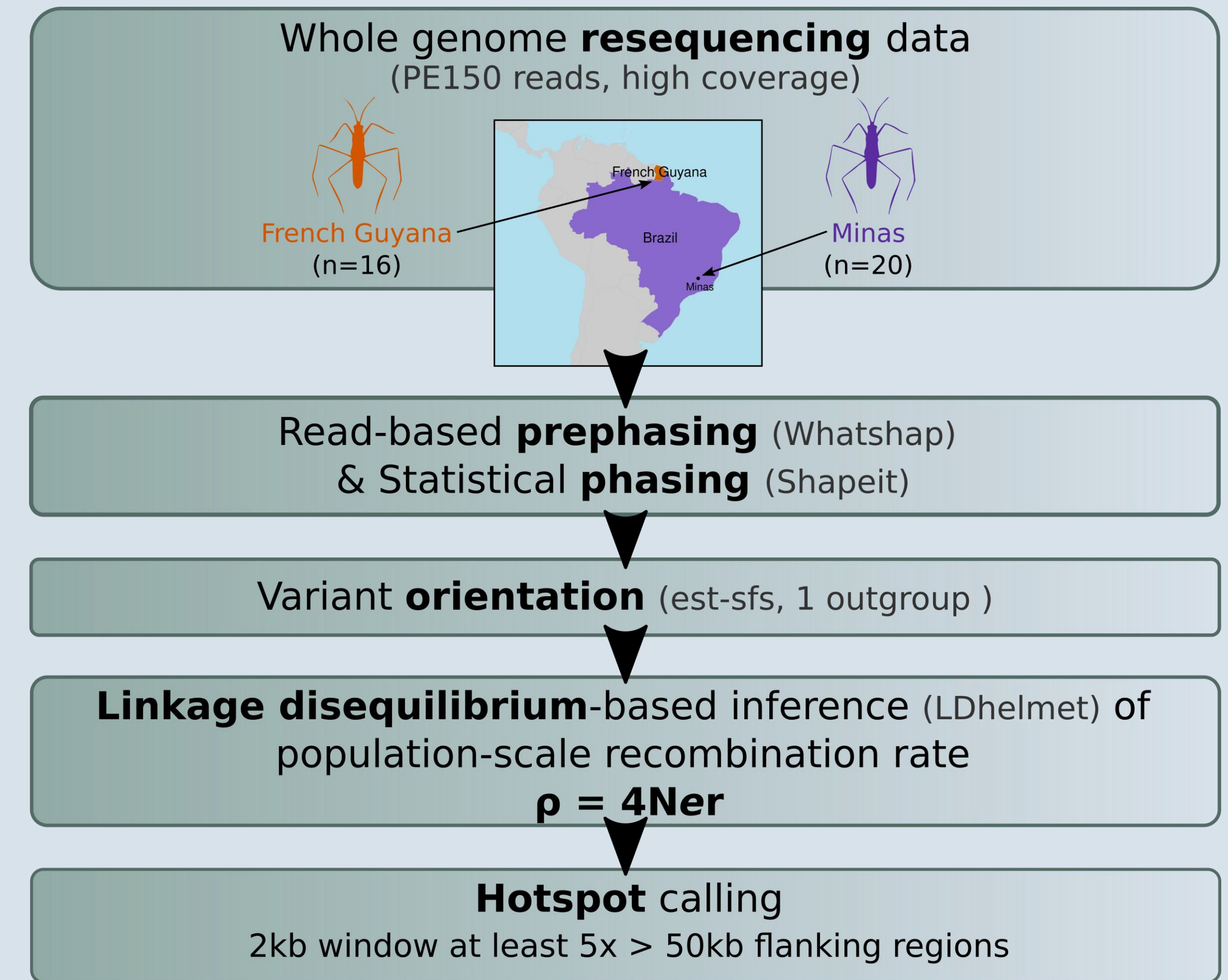
- Recombination has a major role in shaping genome evolution.
- Recombination events tend to concentrate at hotspot positions in a wide range of species.
- PRDM9 protein determines recombination events in mammals and leads to rapid evolution of their recombination landscapes (Myers et al., 2010, Auton et al., 2012). By contrast, it has been lost in other taxa which show conserved hotspots (e.g. birds, dogs, teleosts; Singhal et al., 2015, Auton et al., 2013, Baker et al., 2017).
- Full-length copies of PRDM9 have been found in other animal species, but their function is still unknown.



Is the regulation of recombination by PRDM9 ancestral in the animal kingdom ?

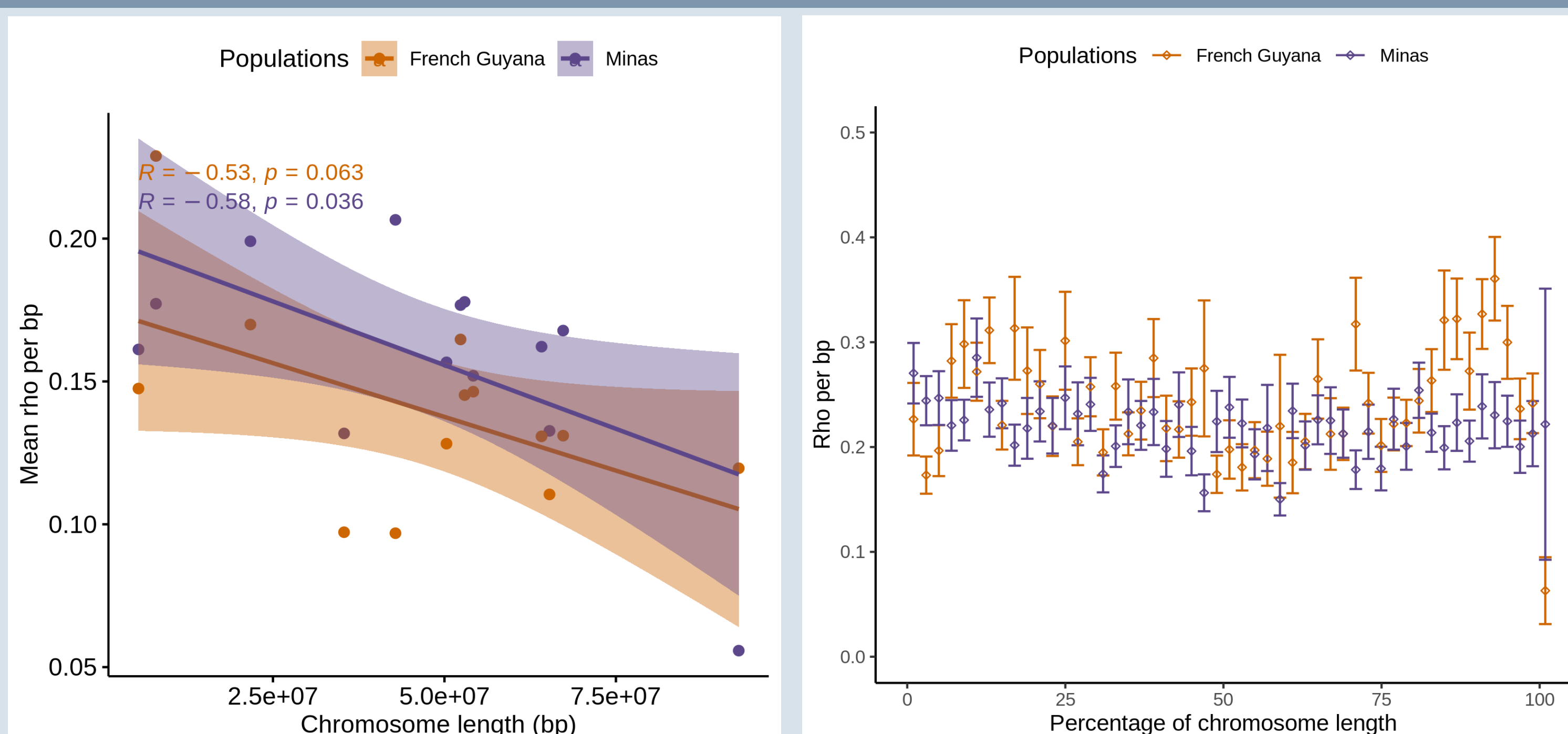
Characterization of the recombination landscapes and their evolution in two populations of the water strider *Microvelia longipes*

## Materials and Methods

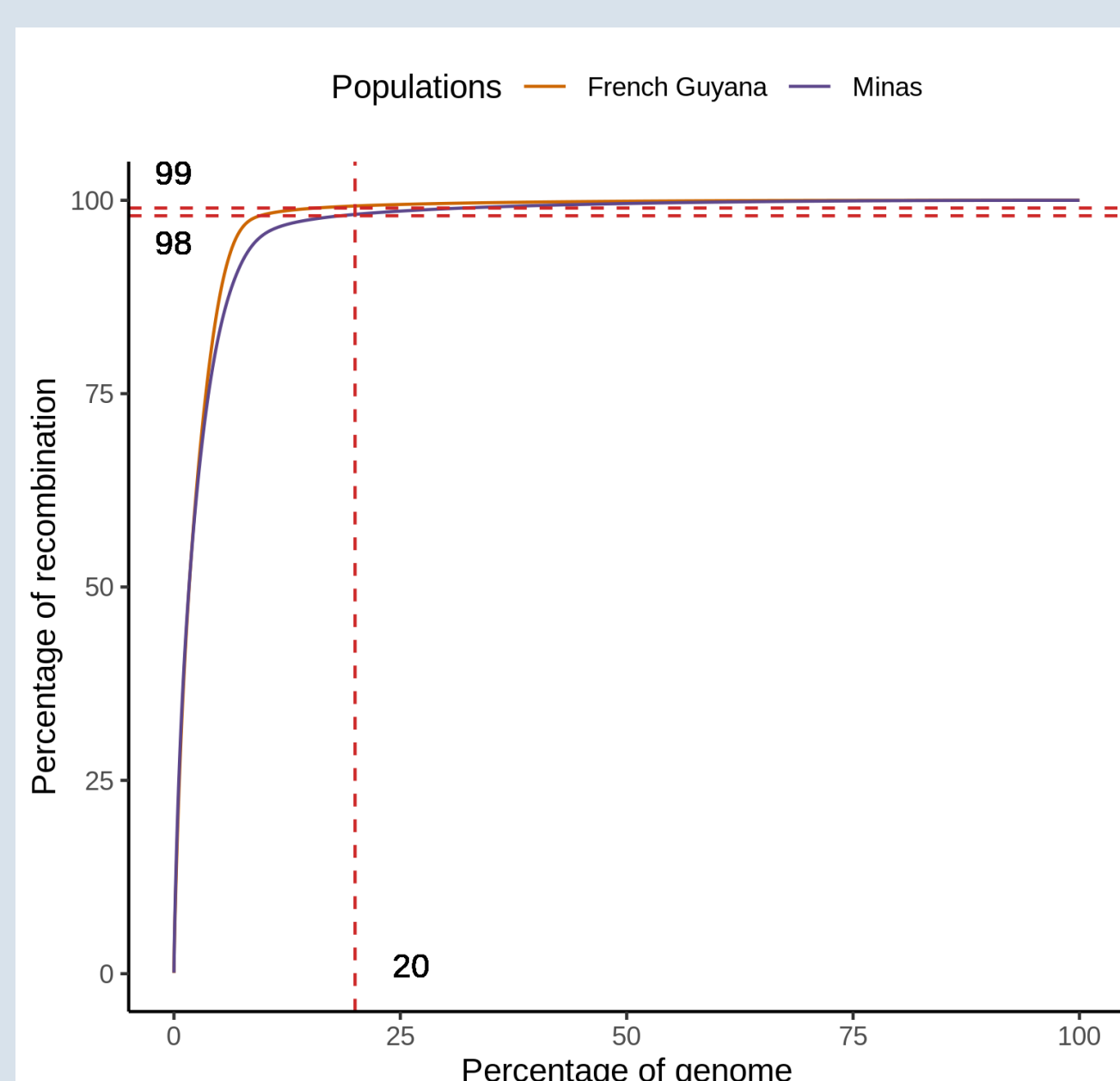


## Results

### *M. longipes* recombination landscapes show inter and intra chromosomal variations in recombination rate

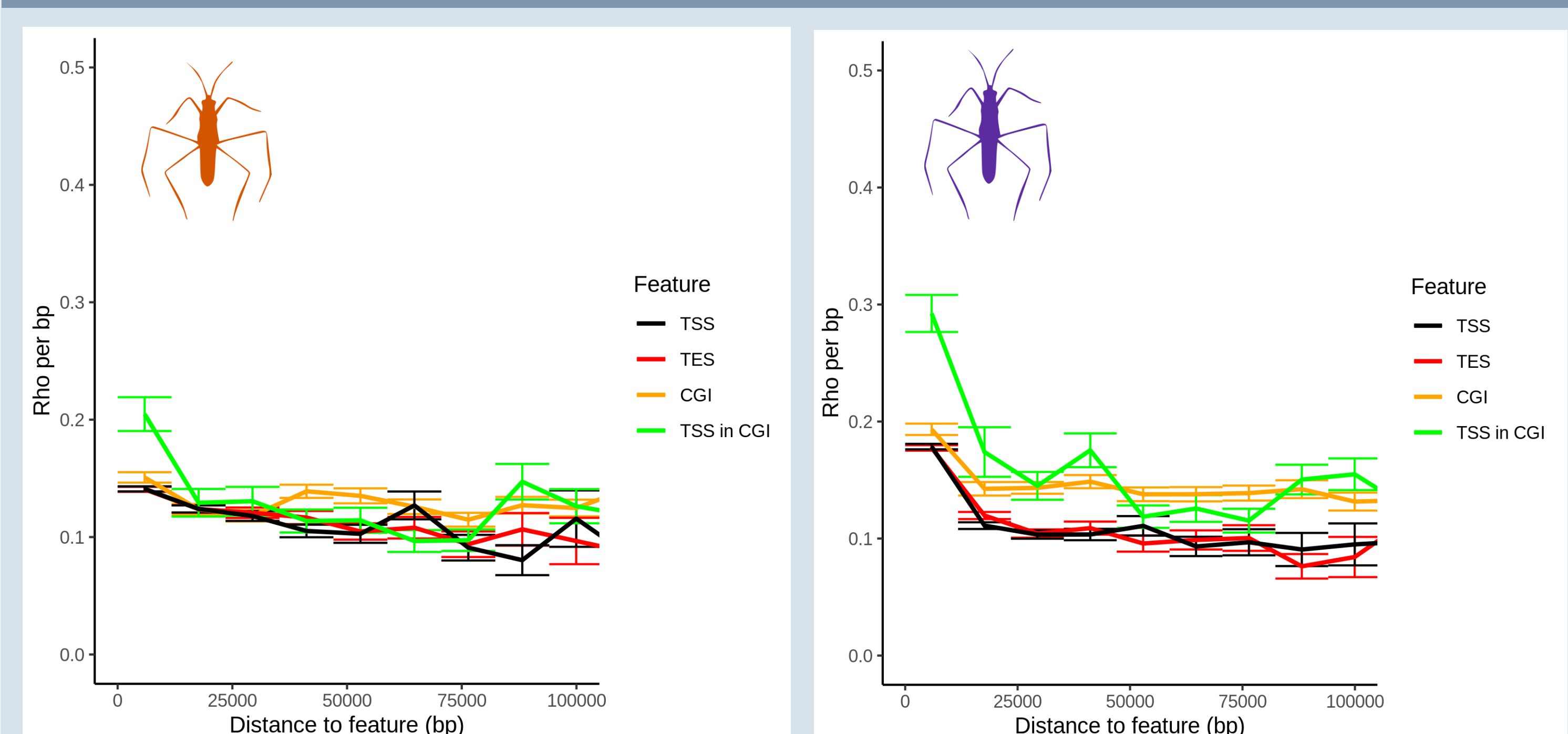


**Averaged recombination rates  $\rho$  decrease with chromosome length and with distance to telomeres.** One crossing-over (CO) per meiosis per chromosome is obligatory to ensure their proper segregation, but more COs usually prevented by chromosomal interference. Thus small chromosomes display higher recombination rates. Heterochiasmy and interference can explain the deficit of recombination in centro-chromosomal regions as compared to telomeres.

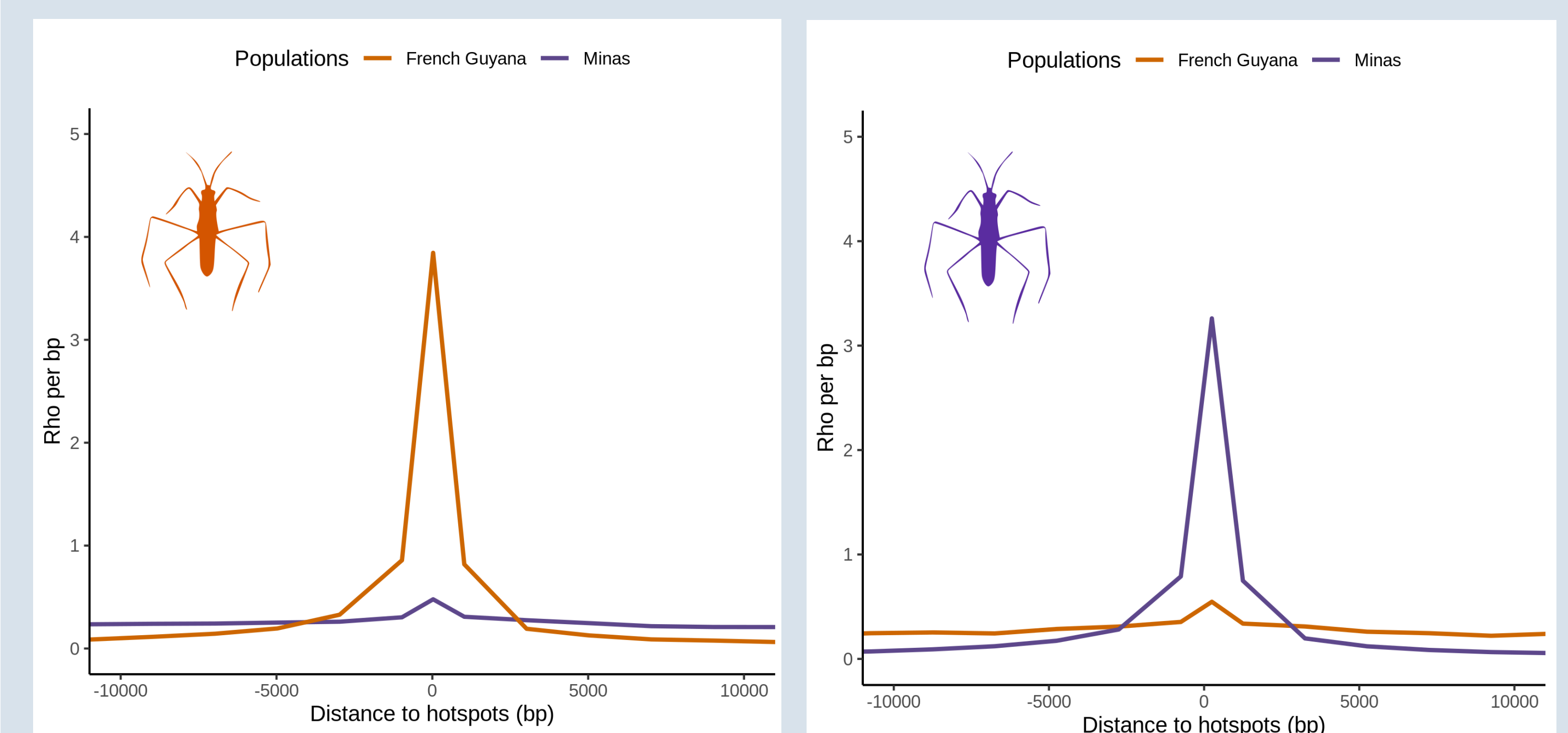


**Recombination rates are concentrated in hotspots.** At fine scale, more than 95% of the recombination events are clustered in only 20% of the genome, revealing the presence of hotspots outside of which recombination is rare. In both populations, 50% of the recombination is restricted in the ~ 10,000 hotspots identified.

### PRDM9 footprints revealed by recombination rates at promotor-like features and highly divergent hotspots



**Limited enrichment of recombination rates at promotor-like features.** Recombination weakly increases at transcription start and end sites (TSS/TES), CpG islands (CGI) and in TSS in CGI, as in humans and mice. On the contrary, the alternative mechanism directing recombination sites in species lacking PRDM9 targets these regions (e.g. in birds, dogs, swordtail fish).



**Fast evolving recombination landscapes between French Guyana and Minas populations.** Despite low differentiation between the two populations ( $F_{st} = 0.14$ ), only ~9% of hotspots are shared between them, revealing divergent and thus unstable recombination landscapes.

## Conclusion

- The low enrichment of recombination events at promotor-like features and the lack of sharing of hotspots over a short evolutionary time scale are signatures of a PRDM9-dependant system and differ from the patterns observed in non-PRDM9 organisms.
- The role of PRDM9 in the regulation of recombination in water striders needs to be validated by looking at DNA motifs enriched at hotspots on which PRDM9 can bind, by assessing the allelic repertory of PRDM9 in this species (i.e. a high number of alleles indicates a fast evolution of the protein), the mapping of double-strand breaks to identify empirically the location of recombination events.
- These PRDM9-like patterns must be determined in other taxa in order to assess its common role in animals.

## Acknowledgments

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