

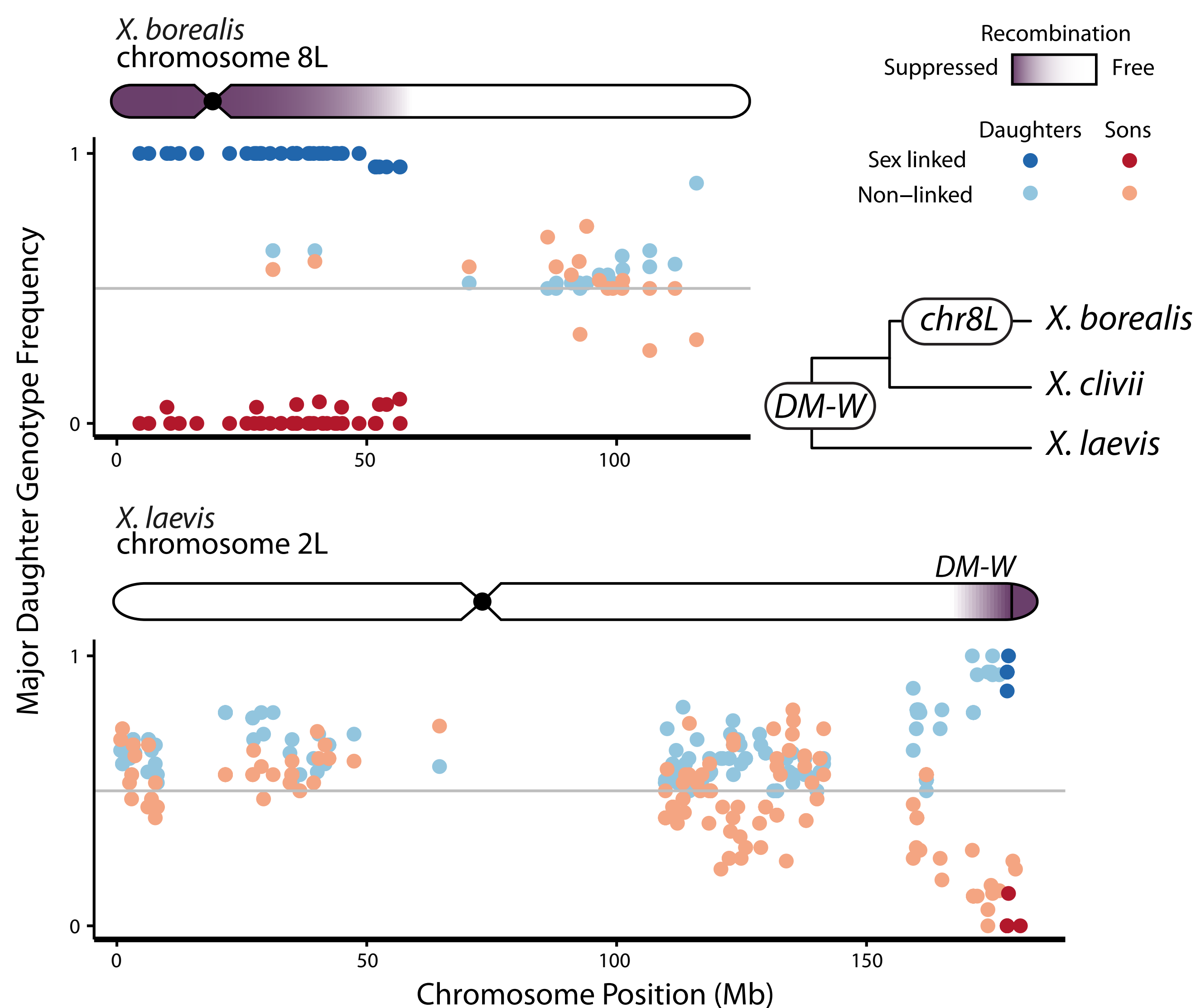
Divergent evolutionary trajectories of two derived homomorphic sex chromosome systems¹

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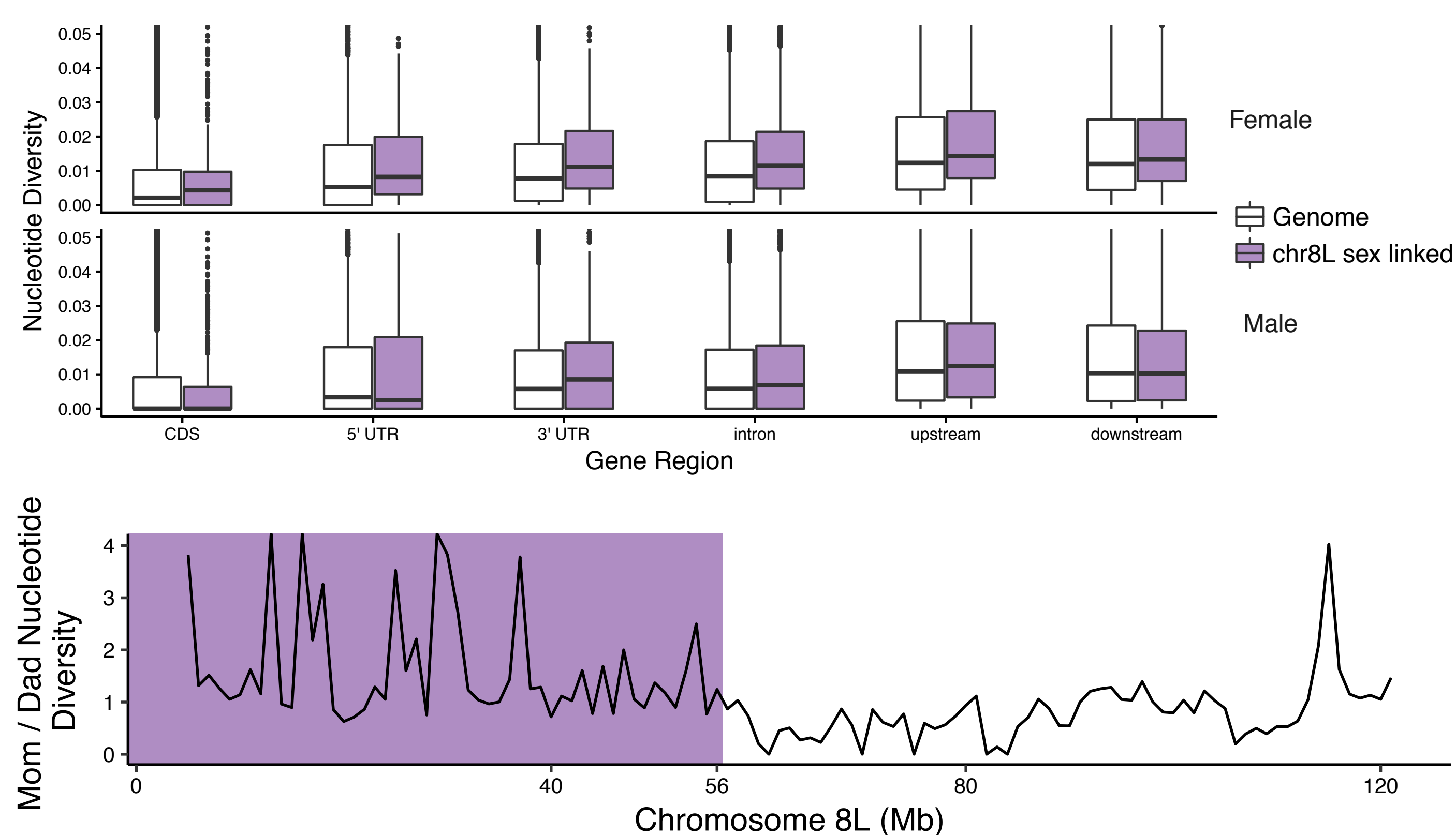
Introduction

Turnover of sex chromosomes is commonplace, but the fate after establishment is variable, and time is not always a factor². Recombination suppression often spreads along a chromosome over time, with nuclear divergence following³. Here, we compare the fates of homomorphic sex chromosomes in closely related African clawed frogs (*Xenopus*), where multiple sex chromosome turnover events have occurred⁴ using reduced and whole genome sequencing on lab-reared families.



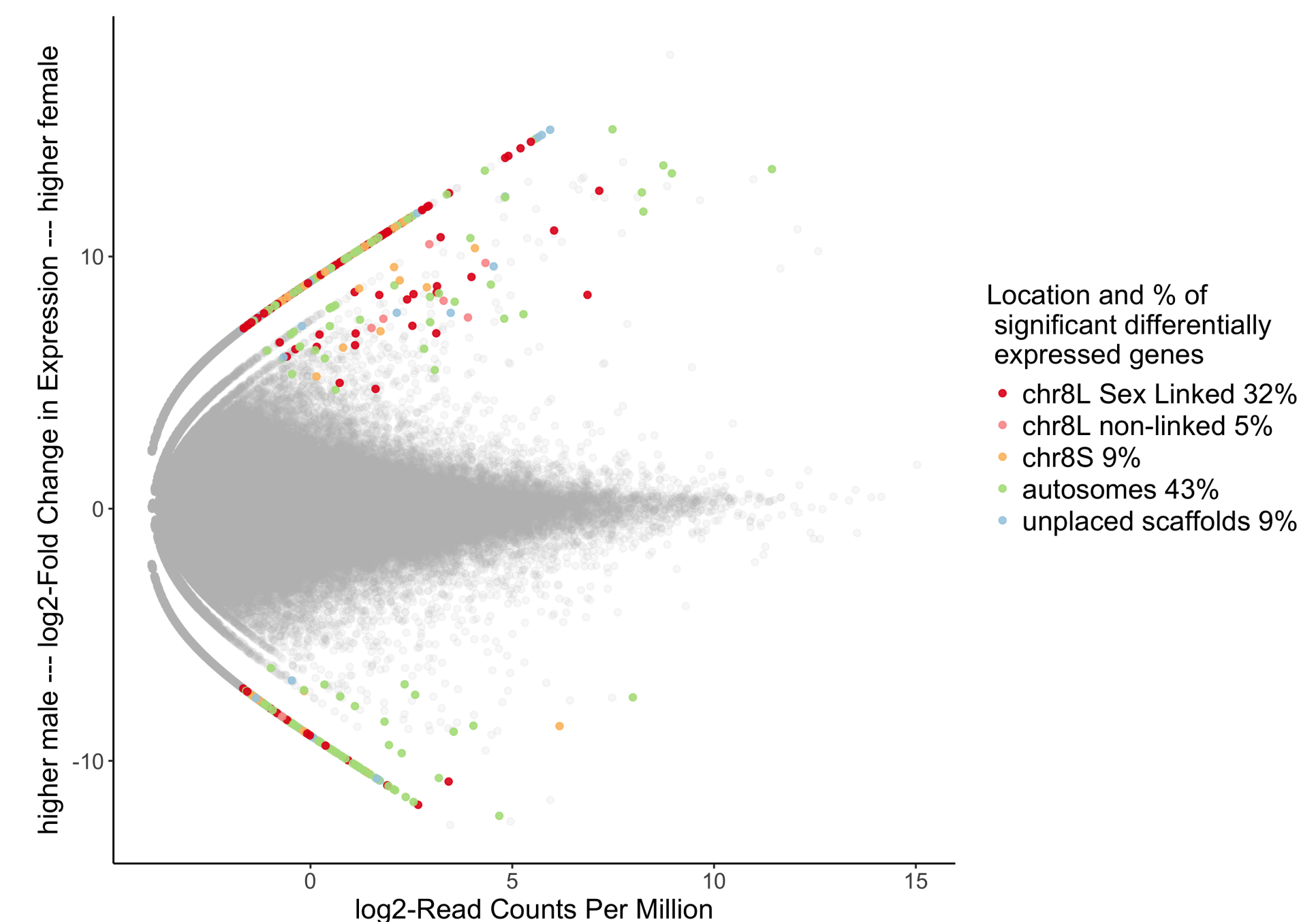
Expansive recombination suppression for sex chromosomes of one species, minimal in the other

The sex chromosomes of *X. laevis* have retained a small sex linked region, whereas in *X. borealis* suppressed recombination spans ~50% of the chromosomes. A single recombination event is evident in the daughters at the end of the region, defining the boundary of strongly suppressed recombination (less clear is a similar event in sons). Phylogenetic analyses support the *X. borealis* as derived with respect to *X. laevis*.



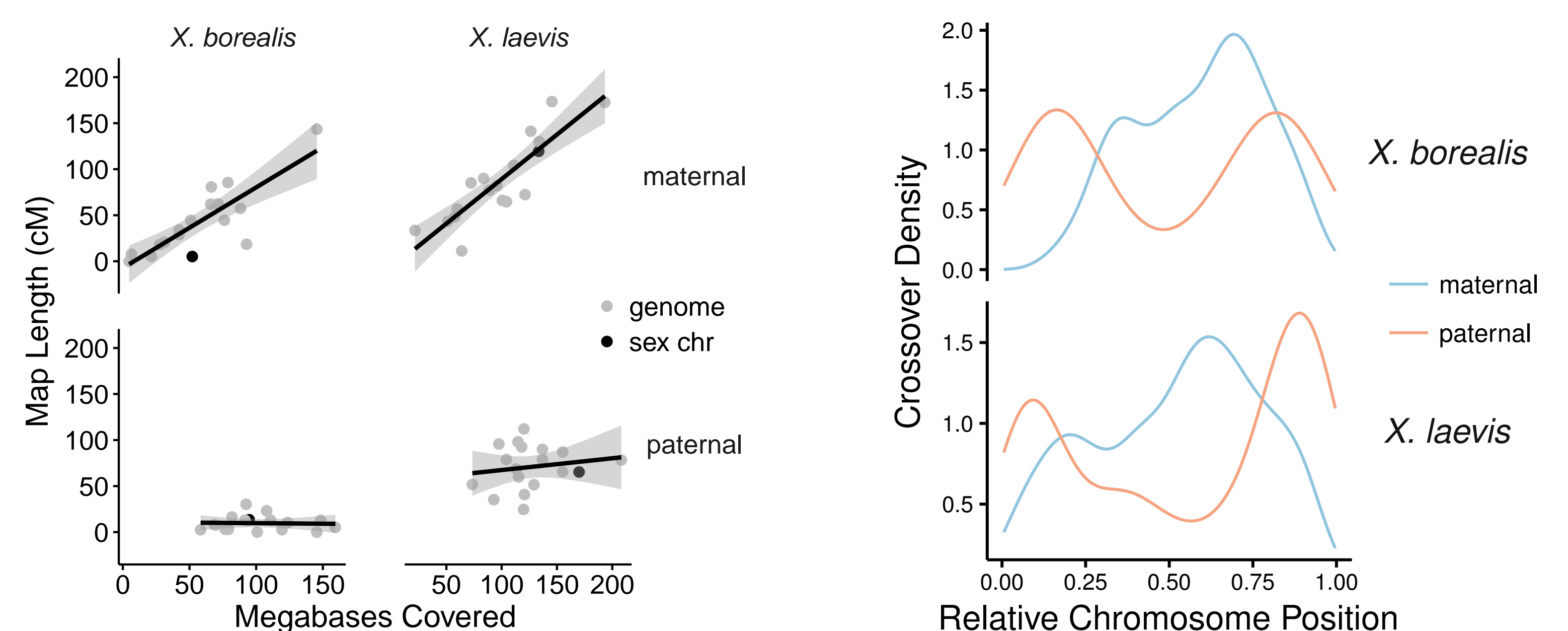
Modest sex chromosome divergence in the large suppressed region

A modest increase in nucleotide diversity between the ZW compared to the ZZ sex chromosomes in *X. borealis* indicates that recombination has been consistently suppressed in the sex linked region, but not for very long (female: autosomes $\pi = 0.003$ – 0.010 , sex chr = 0.011). Attenuation of divergence at the end of the sex linked region may indicate early strata formation. Also, there is no evidence of large deletions (assessing coverage differences between a female and male).



Great accumulation of sexually antagonistic genes (and possible W–Z allele expression differences)

Despite the young age and modest divergence, the sex linked region of *X. borealis* contains 32% of the SA genes in the genome. Comparisons to *X. laevis*, where this region is autosomal, is ongoing. Preliminary analyses of genes present on both the W and Z suggests that the Z allele has higher expression than the W allele, thus, slight degeneration of the sex specific chromosome may affect expression (LMM: higher Z expression = 2.9 , 0.41 – 5.3 95% CI read count data).



More recombination in the heterogametic sex; crossover locations are sex-specific

Female maps were longer than male maps (*X. laevis* = $1572/1275$ cM; *X. borealis* $719/165$ cM), despite spanning less of the genome overall, with *X. laevis* maps spanning ~2x more of the genome. As seen for many other species, crossovers in females were biased to the middle of chromosomes and in males towards the ends, likely resulting in female maps positively scaling with Mb covered, unlike male maps.

Conclusion

These results highlight that sex chromosomes can rapidly accumulate “mature” features of large recombination suppression and sexually antagonistic genes, despite an overall modest differentiation (*X. borealis*). As well, whether or not these features form may be unpredictable, and even sex chromosomes of closely related species can evolve quite differently.

References and Acknowledgements

1. B. L. S. Furman, B. J. Evans, *Genome Biology and Evolution* **10**, 742–755 (2018).
2. A. E. Wright, R. Dean, F. Zimmer, J. E. Mank, *Nature Communications* **7** (2016).
3. B. Charlesworth, *Science* **251**, 1030–1033 (1991).
4. B. L. S. Furman, B. J. Evans, *G3: Genes/Genomes/Genetics* **6**, 3625–3633 (2016).

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