

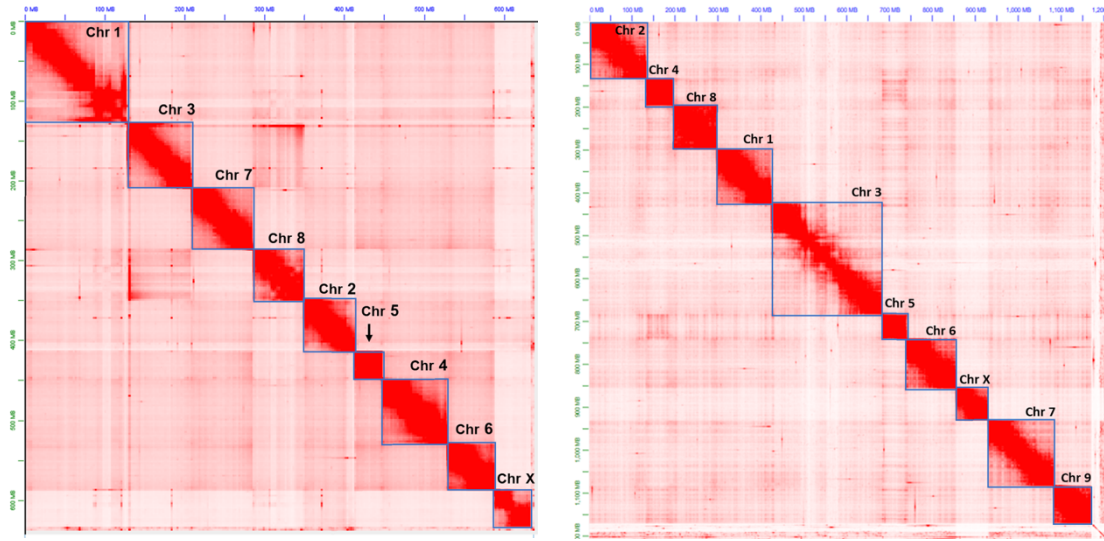


Figure S1. Juicebox Hi-C contact heatmaps. Left panel: *L. splendidula*. Right panel: *L. italica*.

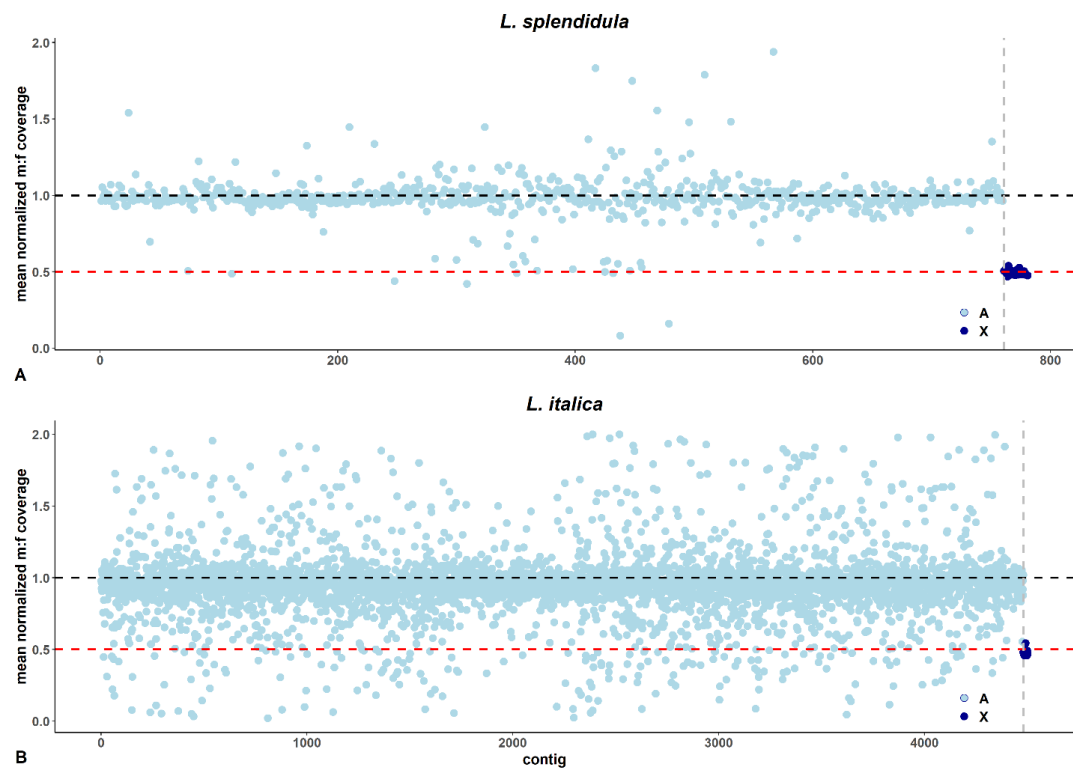


Figure S3. Identification of the X chromosome. Mean normalized male to female coverage ratio per genomic contig. A) *L. splendidula* B) *L. italica*. Shown are only contigs larger than 30kb and used a Wilcoxon Sum Test to identify coverage not deviating from $m:f = 0.5$. X-linked contigs are colored in dark blue and autosomal-linked contigs are colored in light blue.

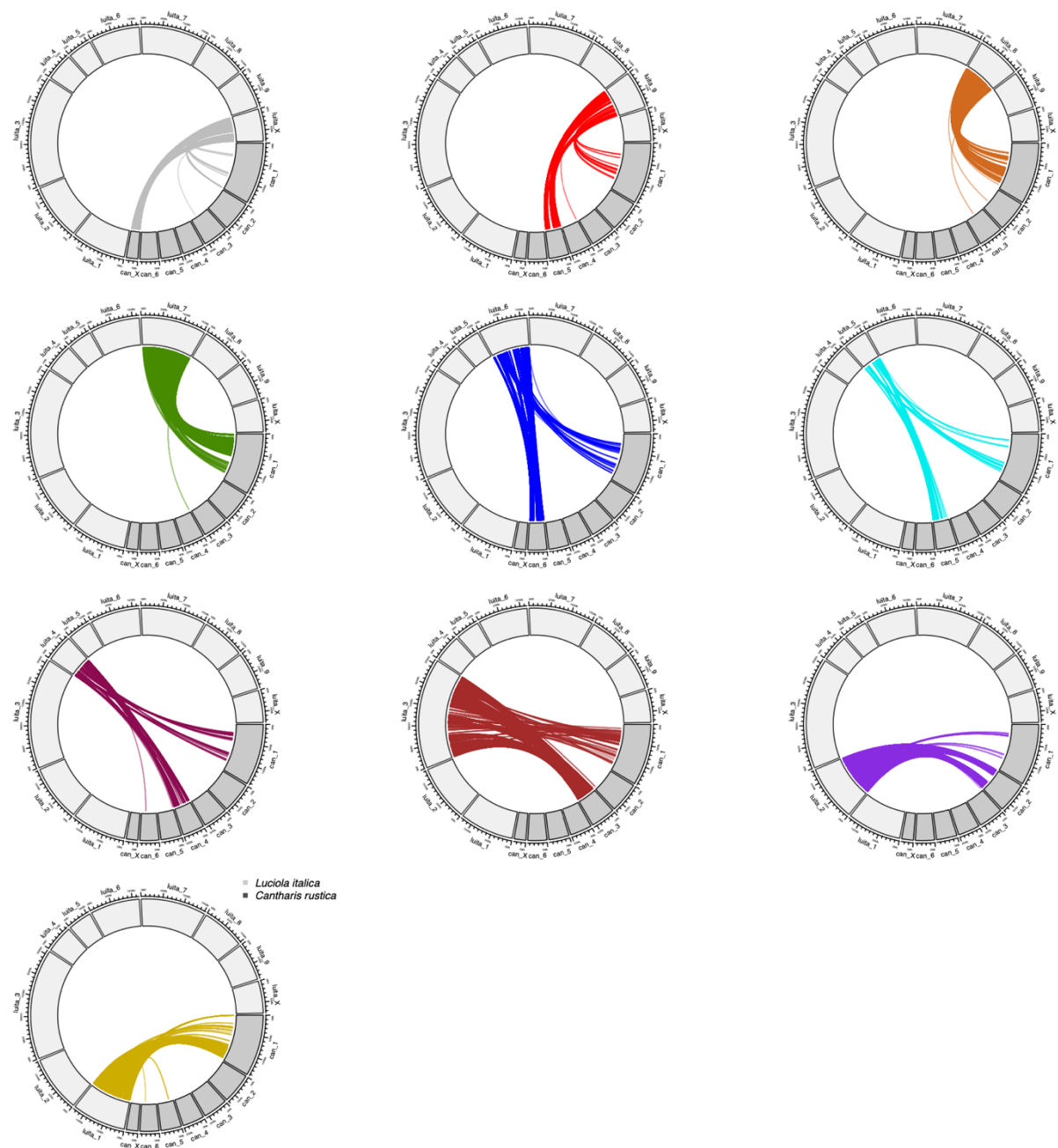


Figure S4. Genome synteny per chromosome of *L. italica* against *Cantharis rustica*.

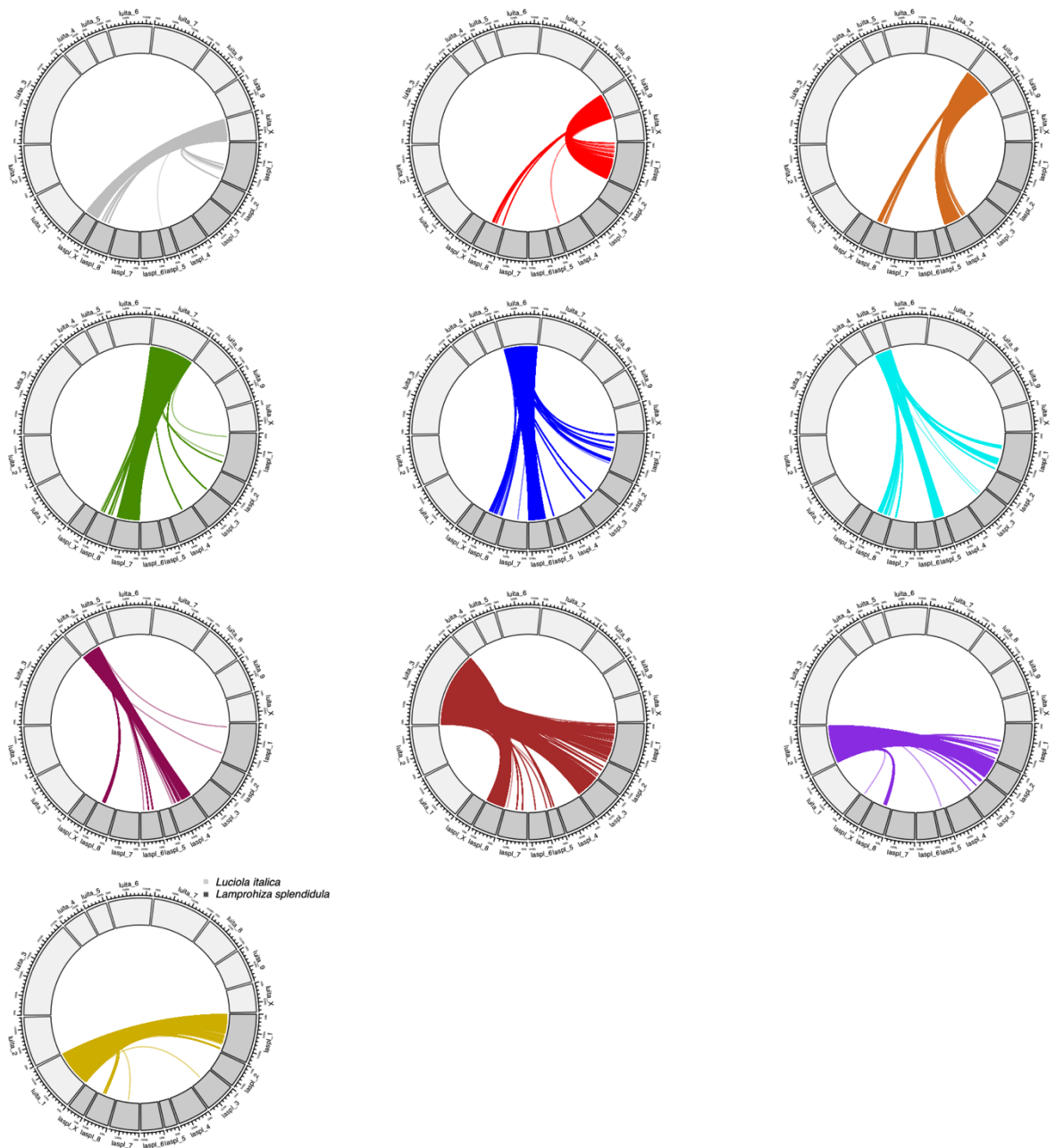


Figure S5. Genome synteny per chromosome of *L. italica* against *L. splendidula*.

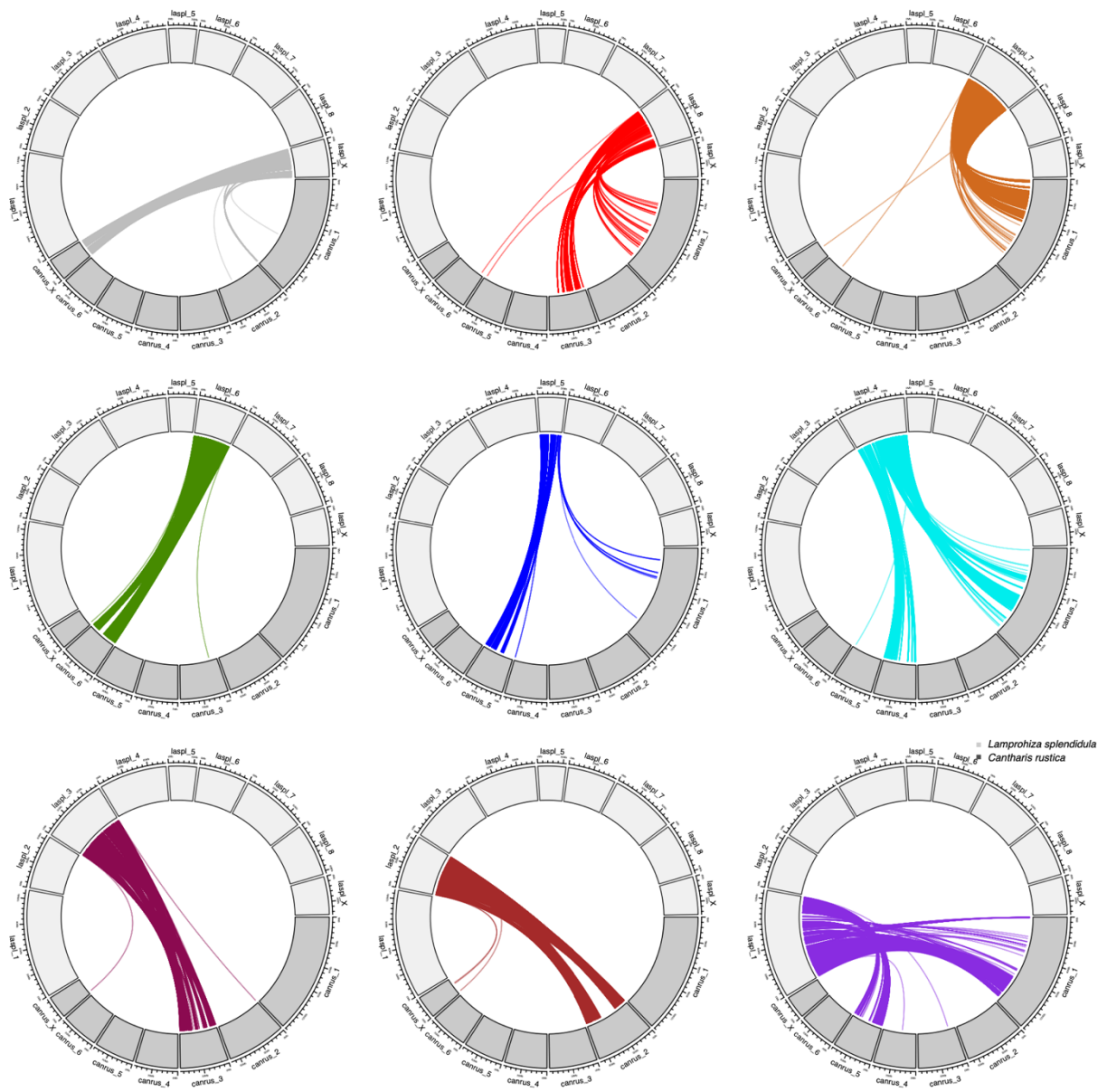


Figure S6. Genome synteny per chromosome of *L. splendidula* against *C. rustica*.

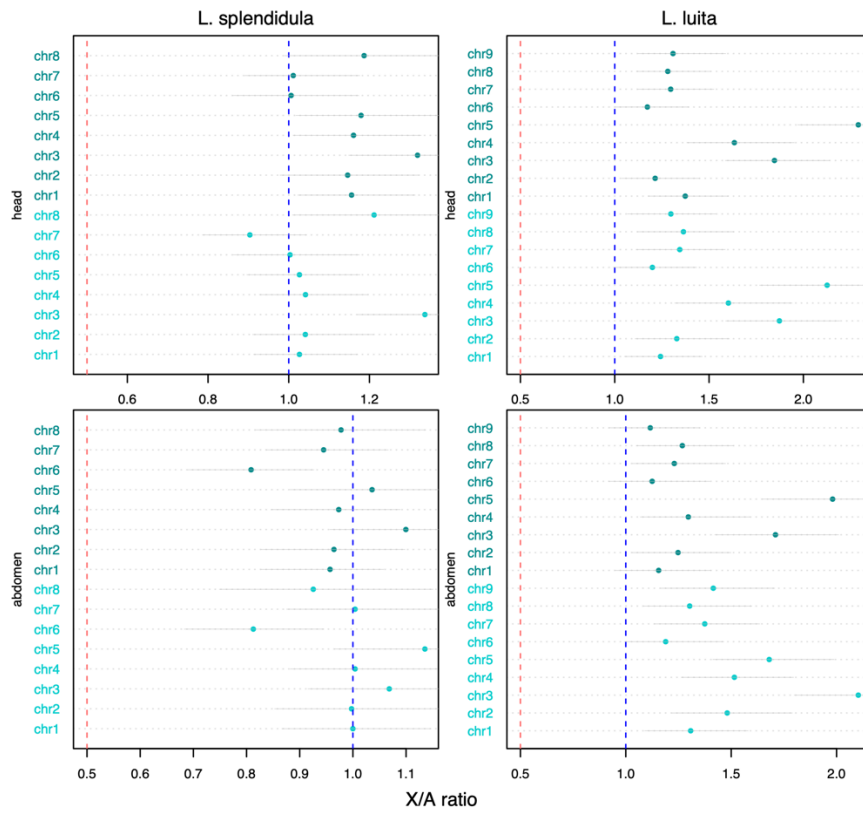


Figure S7. Gene expression ratios between the X and the autosomal (A) chromosomes in head and abdomen tissue of *L. splendidula* and *L. luita*, shown for females (light blue) and males (dark blue).

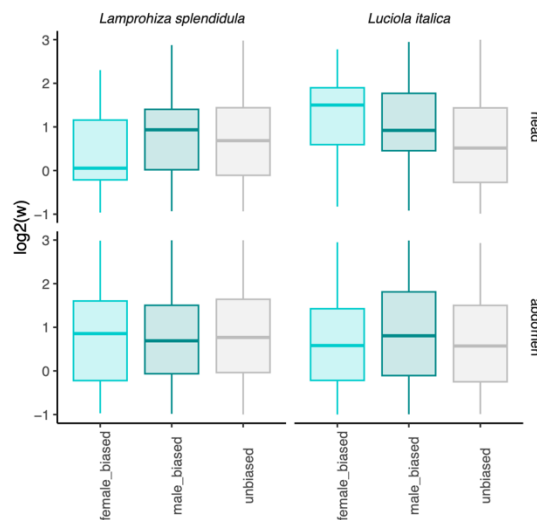


Figure S8. Branch-site model to evaluate differences in protein evolutionary rate between sex- and unbiased genes.