

Supplementary information

Synteny

B. siliquastri vs. *A. obtectus*

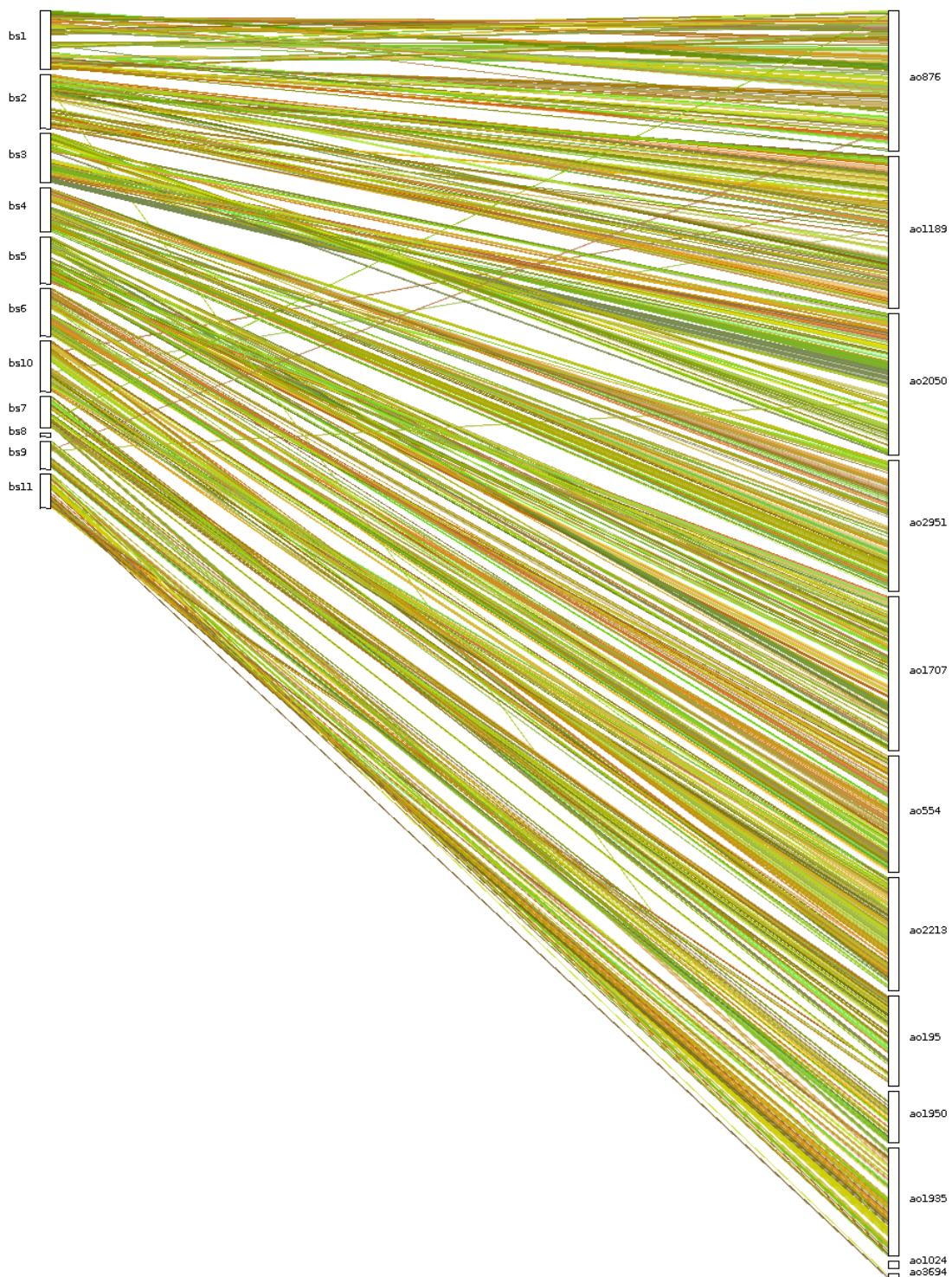


Figure S1: Synteny plot of *B. siliquastri* (left) and *A. obtectus* (right), the X-chromosomes are bs9 for *B. siliquastri* and ao1950 for *A. obtectus* (second from the bottom).

C. maculatus vs. *A. obtectus*

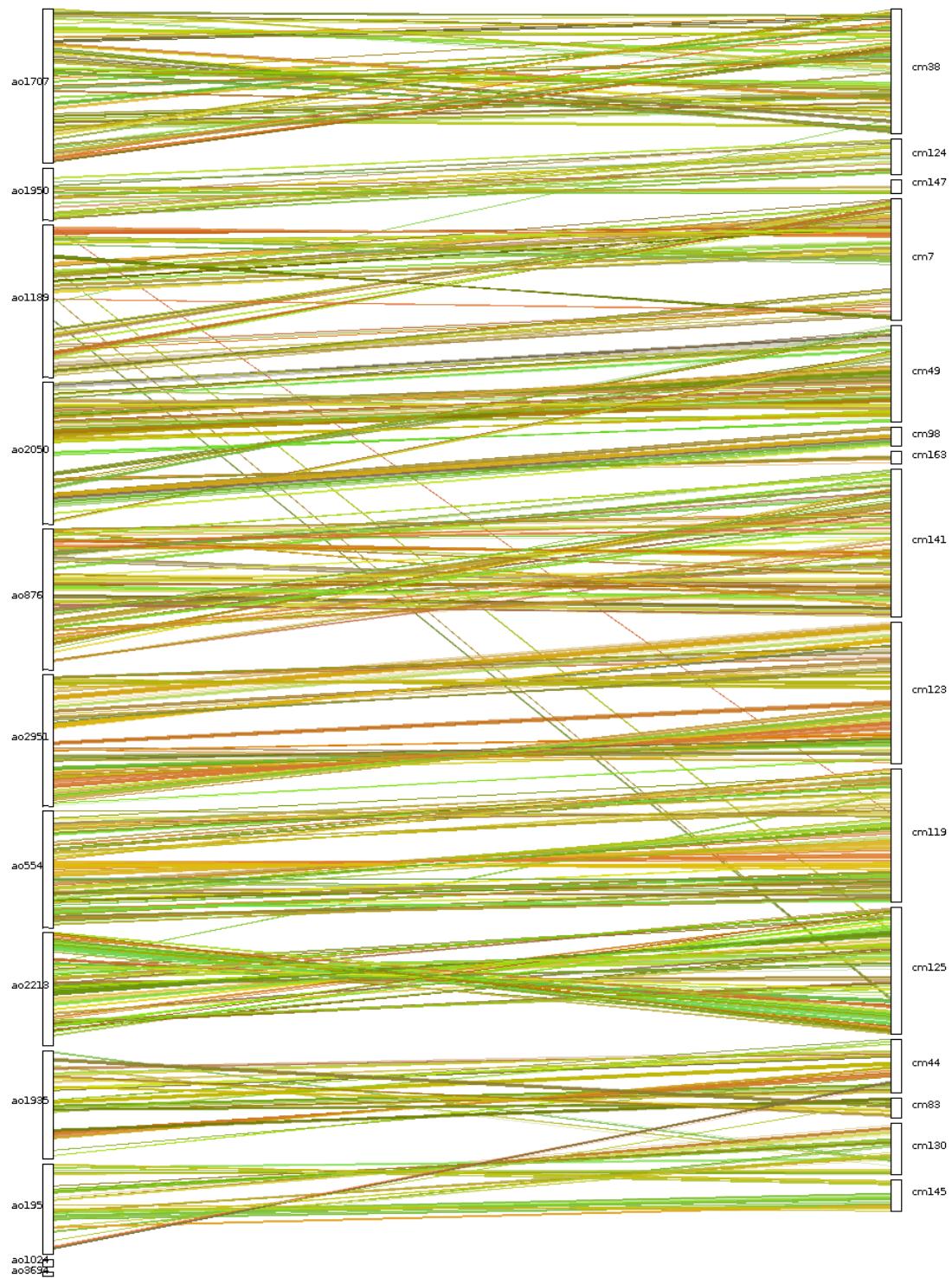


Figure S2: Synteny plot of *A. obtectus* (left) and *C. maculatus* (right), the X-chromosomes are cm124 for *C. maculatus* and ao1950 for *A. obtectus* (second from the top).

C. magnifica vs. *C. septempunctata*

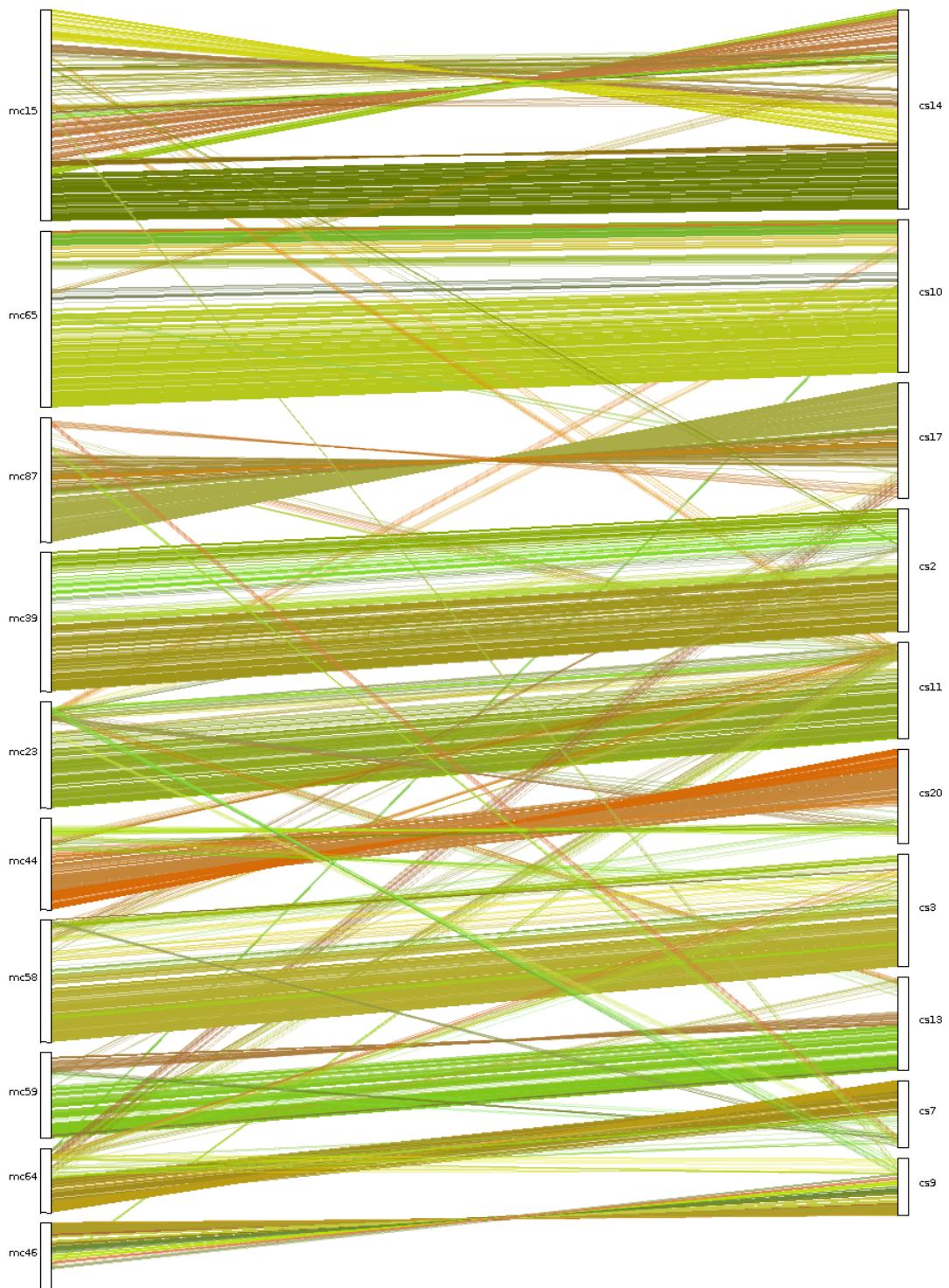


Figure S3: Synteny plot of *C. magnifica* (left) and *C. septempunctata* (right), the X-chromosomes are mc64 for *C. magnifica* and cs7 for *C. septempunctata* (second from the bottom).

T. castaneum vs. *T. freemani*

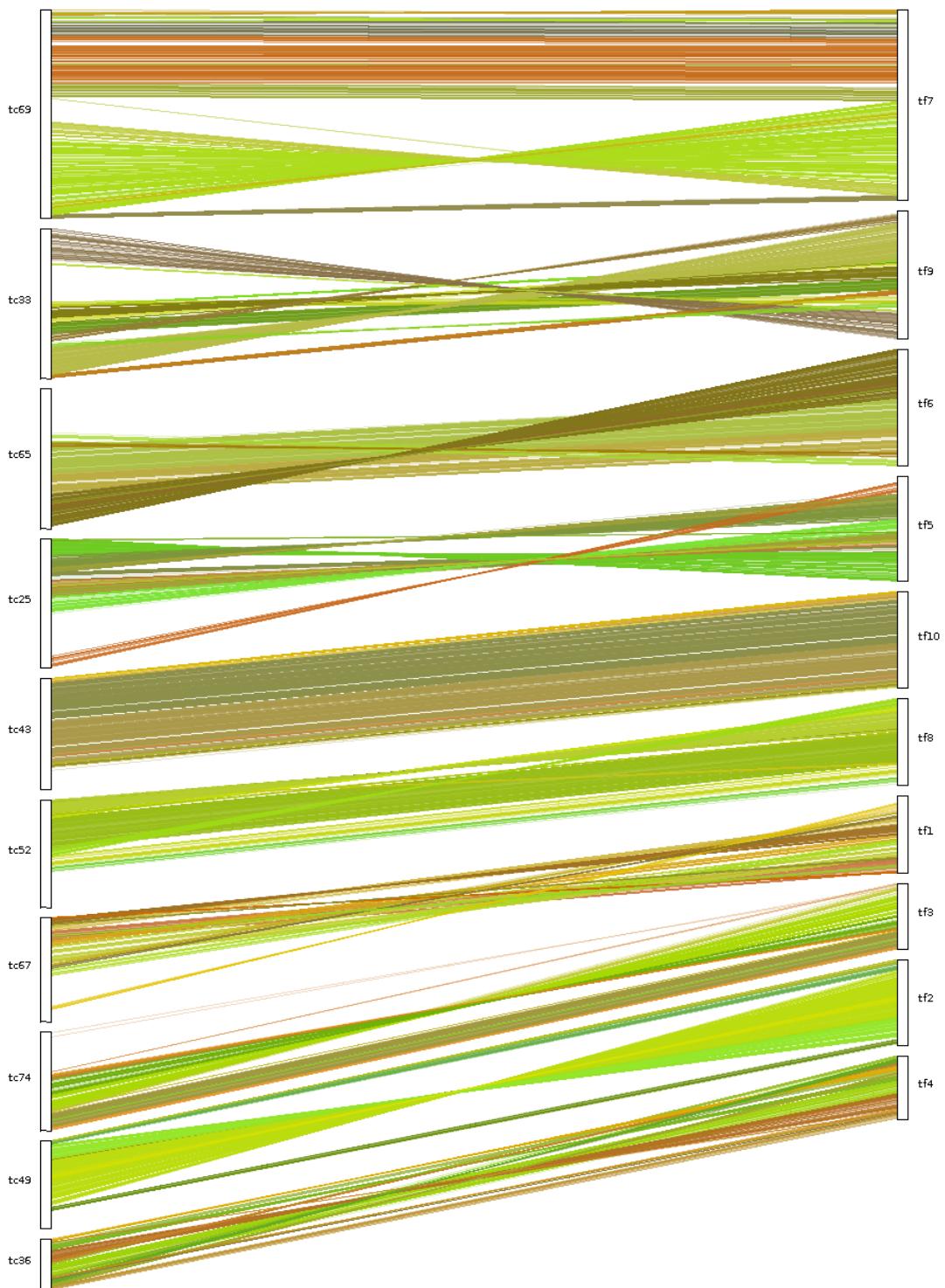


Figure S4: Synteny plot of *T. castaneum* (left) and *T. freemani* (right), the X-chromosomes are tc36 for *T. castaneum* and tf4 for *T. freemani* (first from the bottom).

B. siliquastrum vs. *T. castaneum*

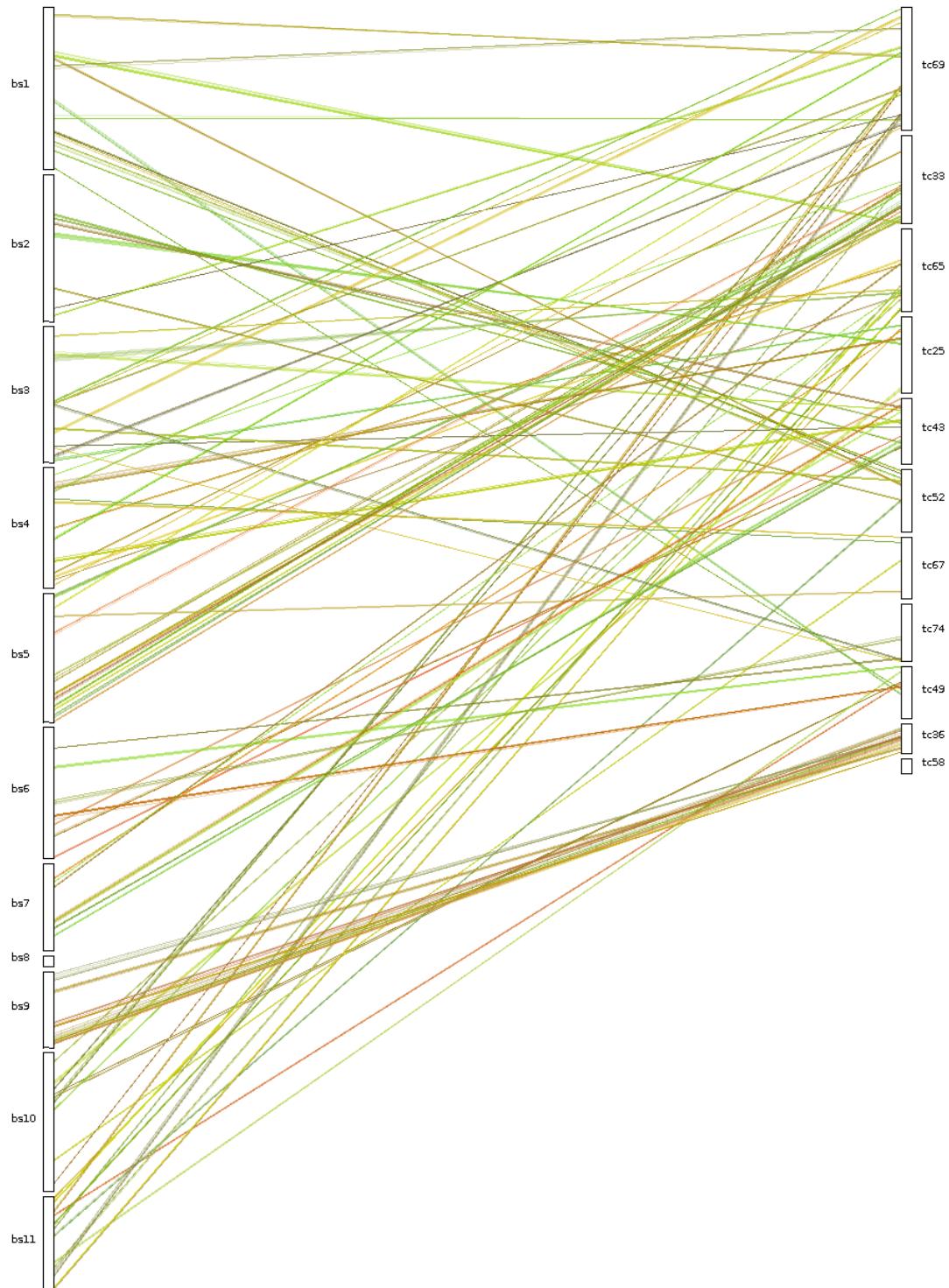


Figure S5: Synteny plot of *B. siliquastrum* (right) and *T. castaneum* (right), the X-chromosomes are bs9 for *B. siliquastrum* and tc36 for *T. castaneum* (third and second from the bottom).

additional plots for d_N and d_S

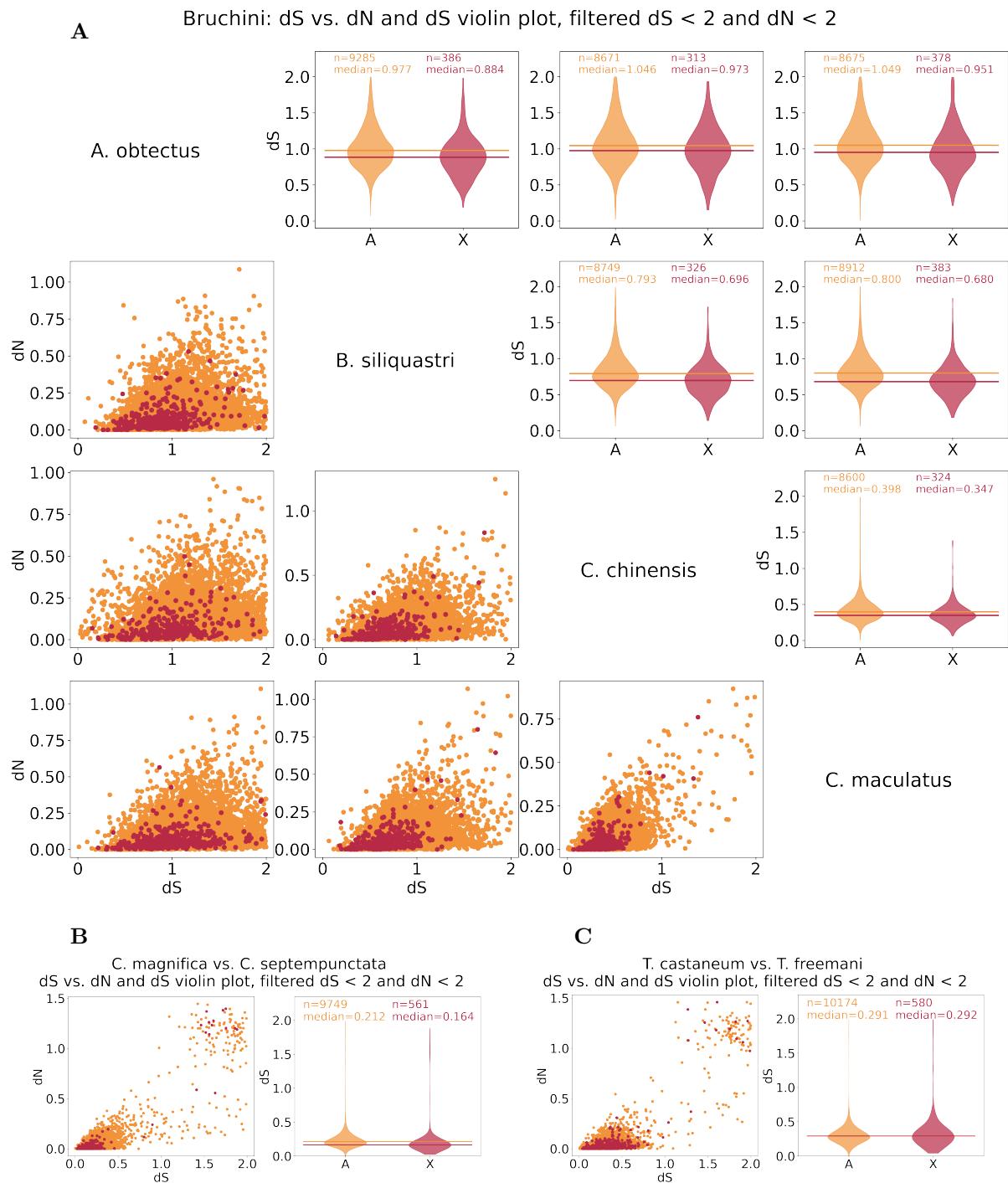


Figure S6: **d_S vs. d_N scatterplots and violin plots of d_S values from X-linked and autosomal orthologs.** Pairwise comparisons between members of three species groups with violin plots of d_S values for X-linked and autosomal 1-to-1 orthologs, and scatterplots of d_S vs. d_N . Permutation tests ($n=10000$) show that d_S is significantly lower for X-linked orthologs in all comparisons within *Bruchini* (**A**) and *Coccinella* (**B**), but not *Tribolium* (**C**).

A

Bruchini: A and X dNdS violin plot and permutation test

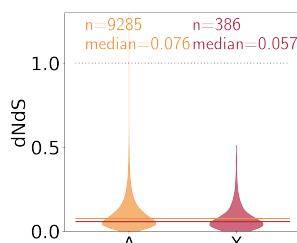
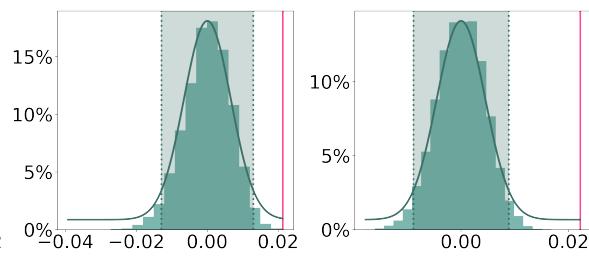
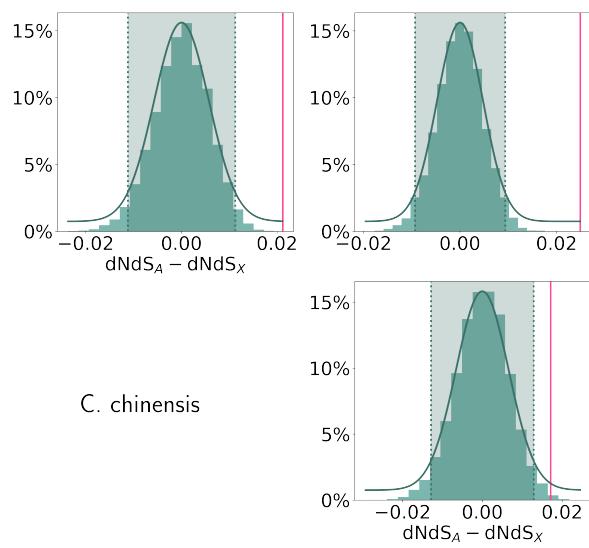
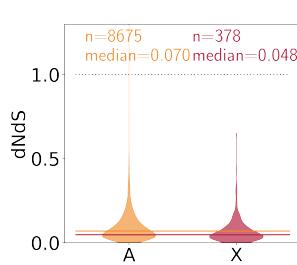
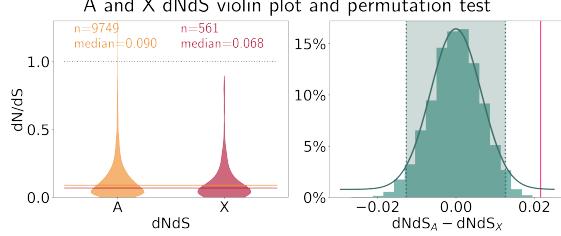
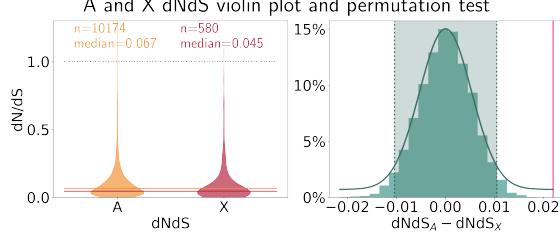
A. obtectus*B. siliquastri**C. chinensis**C. maculatus***B***C. magnifica* vs. *C. septempunctata*:
A and X dNdS violin plot and permutation test**C***T. castaneum* vs. *T. freemani*:
A and X dNdS violin plot and permutation test

Figure S7: d_N/d_S ratio and permutation tests for significance. Pairwise comparisons between members of three species groups with violin plots of d_N/d_S values for X-linked and autosomal 1-to-1 orthologs, and permutation tests (10000 permutations) to assess significance. The permutation test show frequency histograms of median differences between autosomal and X-linked d_N/d_S , with the shaded area showing the 95% confidence interval according to a normal distribution. The vertical pink line shows the true observed difference in mean between autosomal and X-linked d_N/d_S . All pairwise comparisons show significantly lower d_N/d_S values on X-linked orthologs. The within-family comparisons are performed for three species groups: *Bruchini* (**A**), *Coccinella* (**B**) and *Tribolium* (**C**).

Bruchini: A and X dNdS violin plot and permutation test

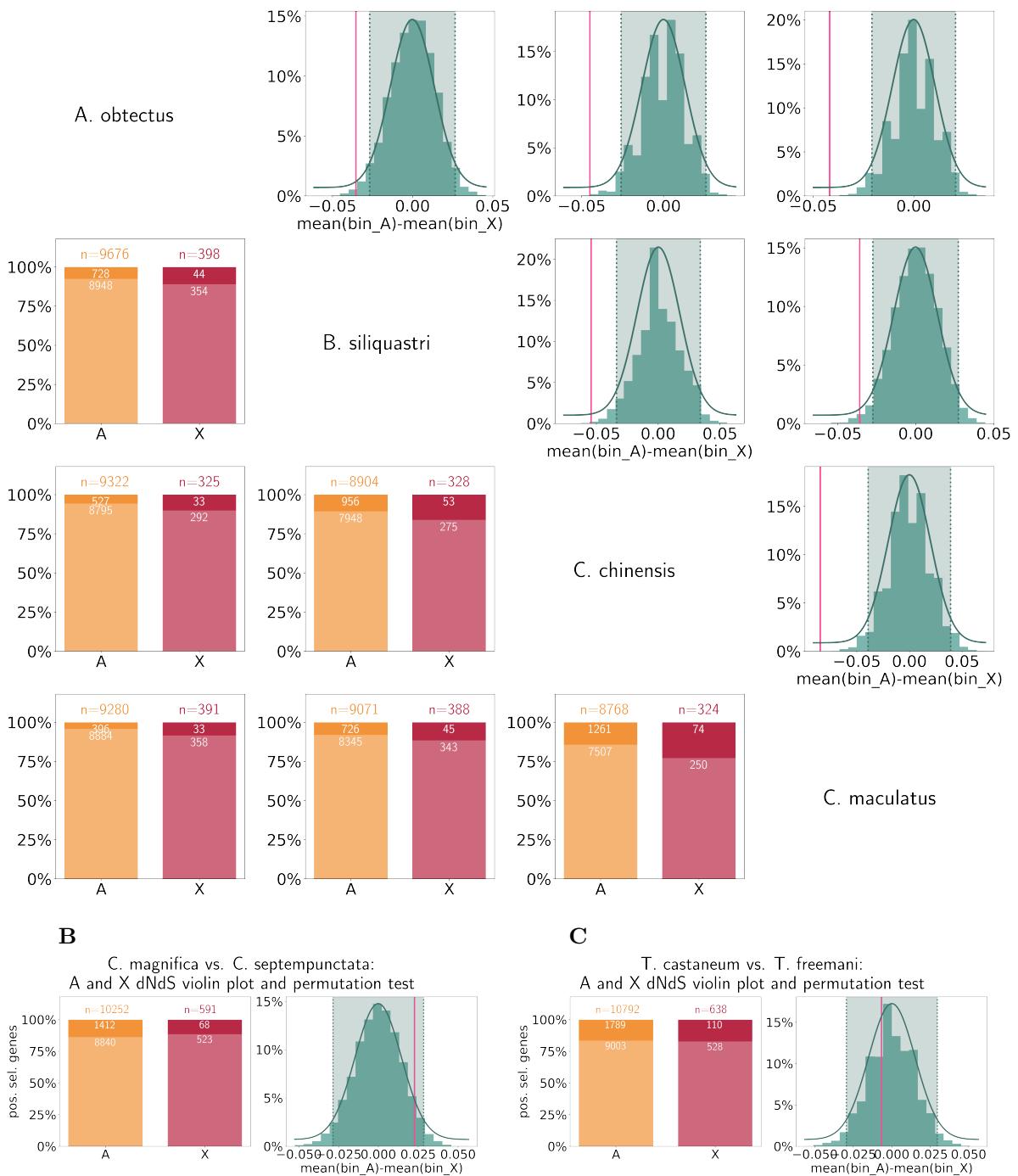


Figure S8: positively selected orthologs split into autosomal or X-linked. Positively selected genes are determined via likelihood ratio test comparison between paml site models M1a and M2a. The permutation tests show frequency histograms of median differences between the percentage of orthologs for 10000 permutations with positively selected codons between autosomal and X-linked orthologs, with the shaded area showing the 95% confidence interval according to a normal distribution. The vertical pink line shows the true observed difference in percentage of orthologs with positively selected codons between autosomal and X-linked orthologs. *Bruchini* (**A**), show an enrichment of positively selected X-linked orthologs in all pairwise comparisons, while *Coccinella* (**B**) and *Tribolium* (**C**) show no significant difference.

additional differential expression analyses

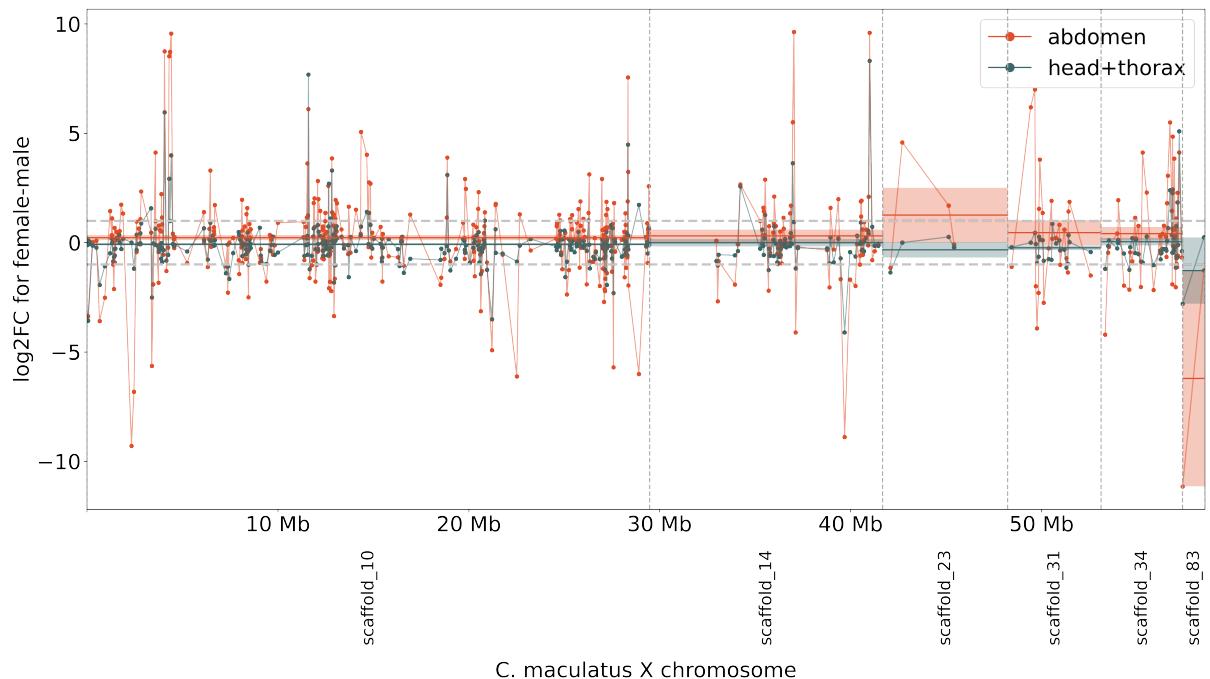


Figure S9: dosage compensation

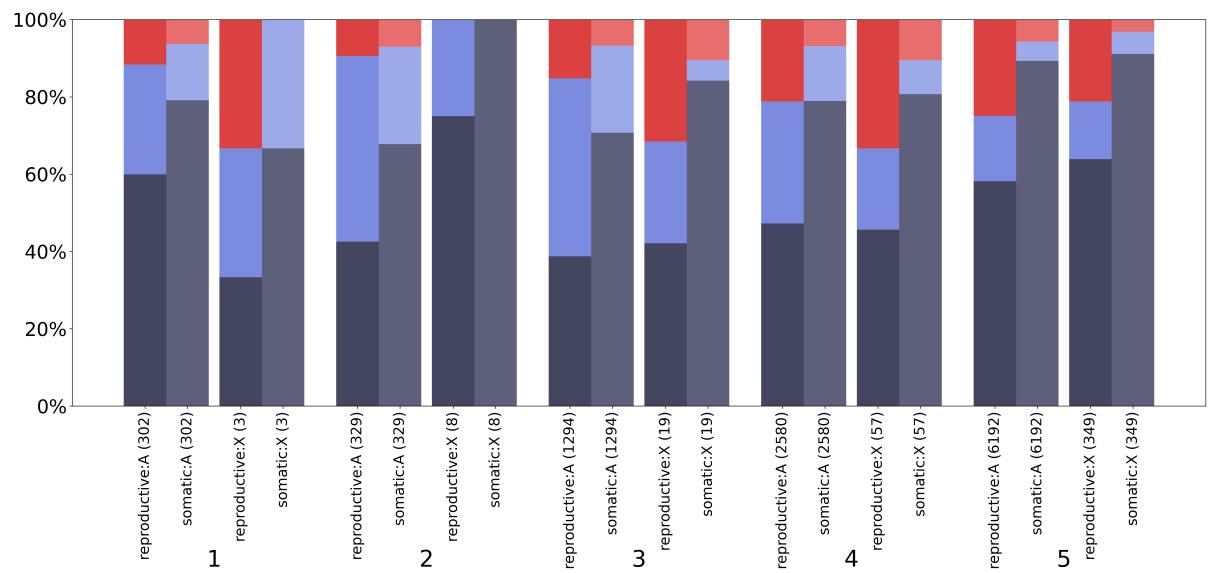


Figure S10: sex bias proportion by chromosome and conservation distance

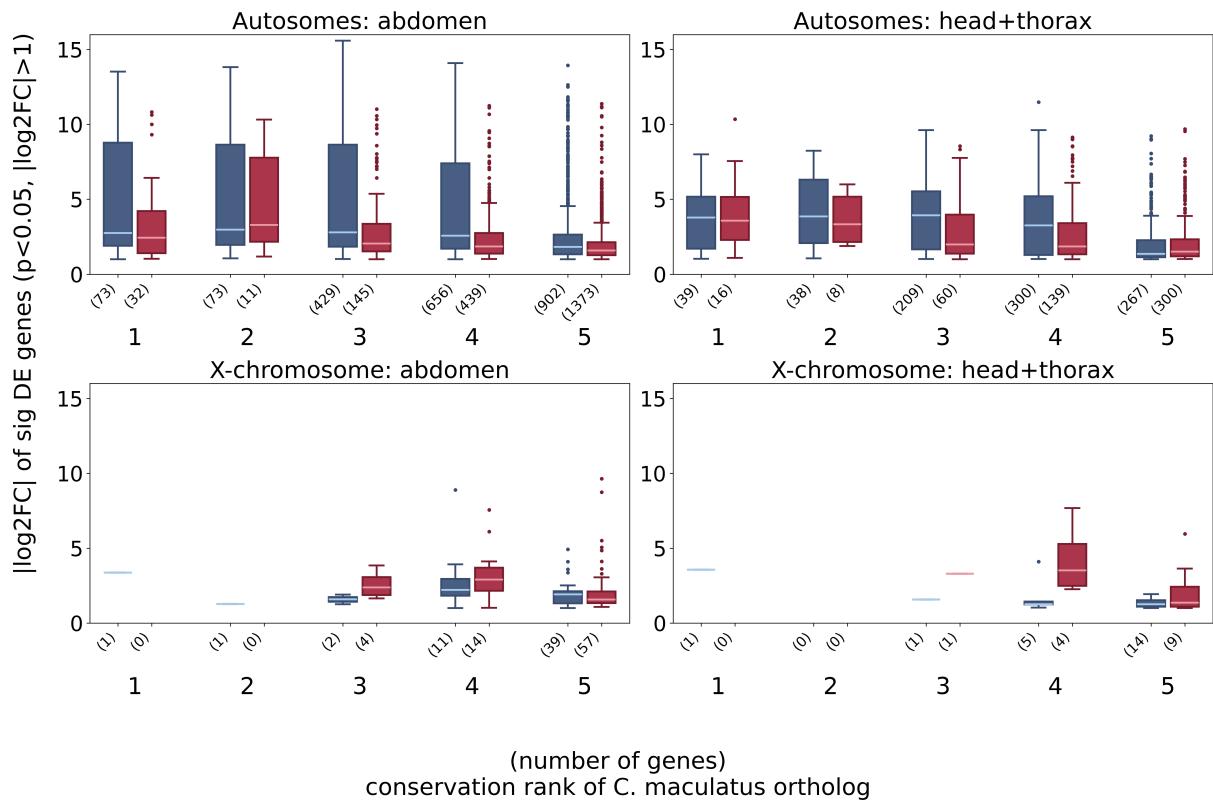


Figure S11: sex bias proportion by chromosome and conservation distance

Genome annotation

Table S1: BUSCO scores for *C. magnifica*, *T. freemani* and *C. maculatus* genome annotations

BUSCO category	<i>C. magnifica</i>	<i>T. freemani</i>	<i>C. maculatus</i>
Complete BUSCOs	972 (96.0%)	978 (96.6%)	999 (98.7%)
Complete and single-copy BUSCOs	877 (86.6%)	896 (88.5%)	731 (72.2%)
Complete and duplicated BUSCOs	95 (9.4%)	82 (8.1%)	268 (26.5%)
Fragmented BUSCOs	9 (0.9%)	14 (1.4%)	6 (0.6%)
Missing BUSCOs	32 (3.1%)	21 (2.0%)	8 (0.7%)
Total BUSCO groups searched	1013	1013	1013
total number of genes	18978	18028	14861