

## Supplementary information

### additional plots for $d_N$ and $d_S$

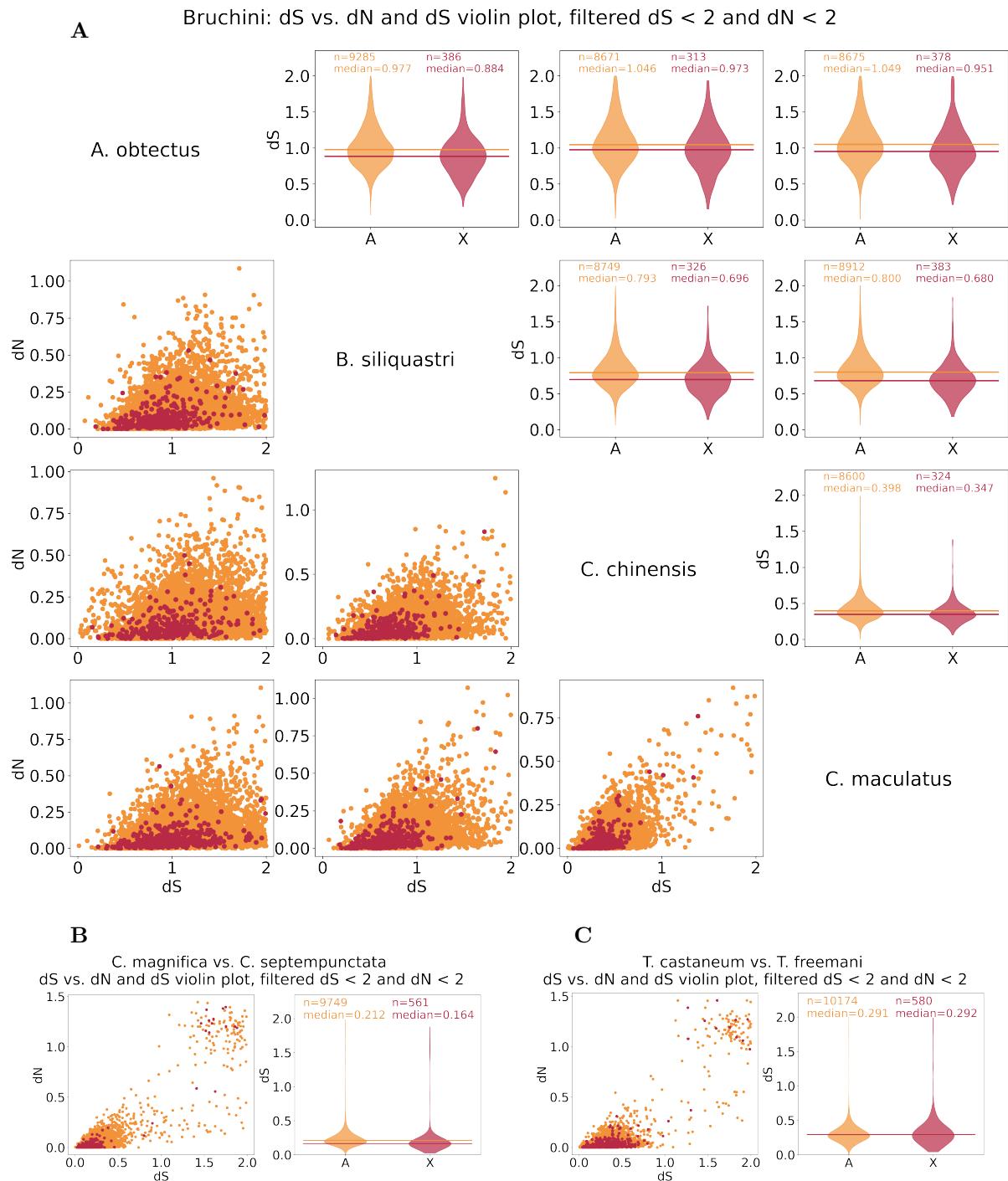
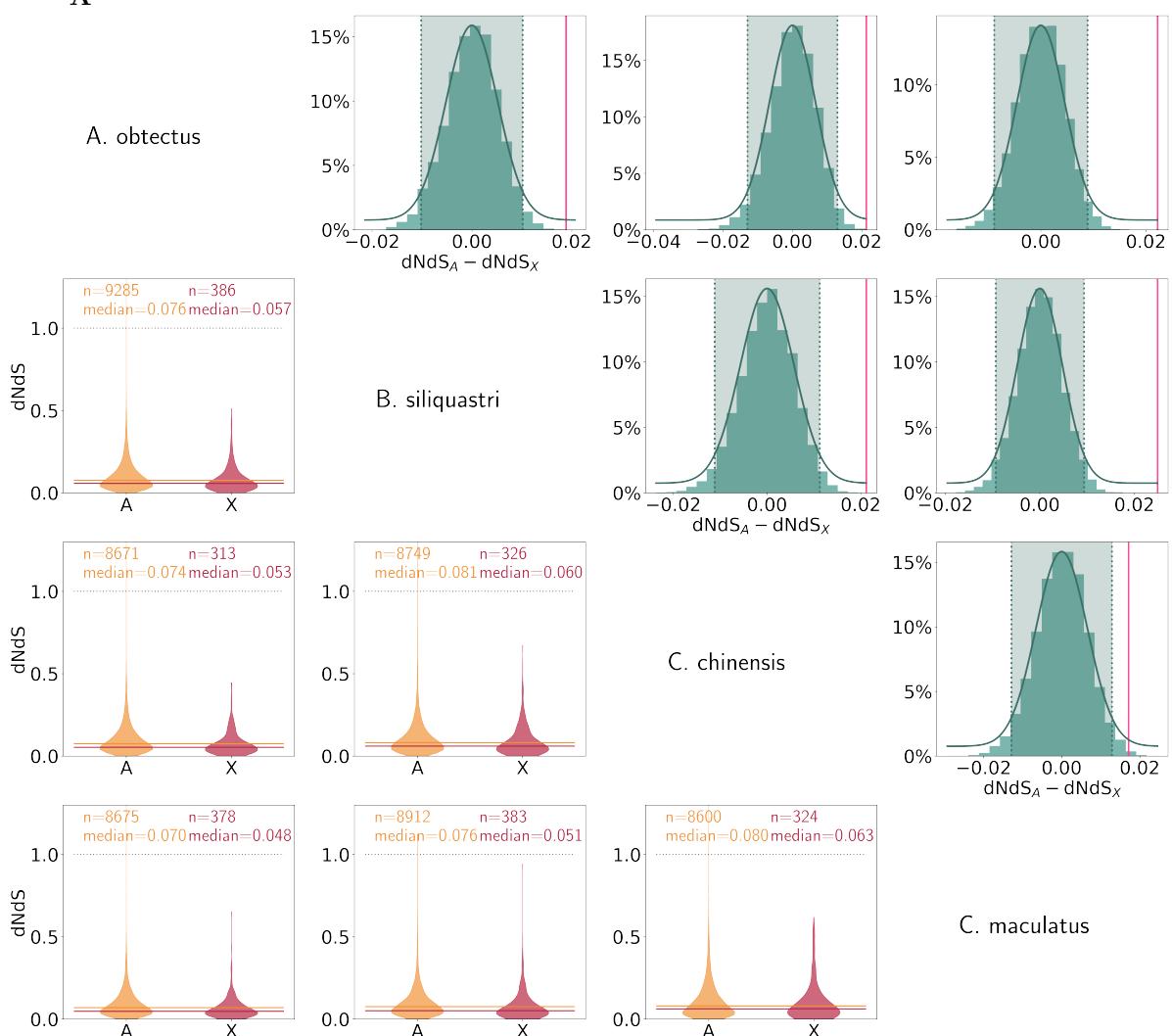
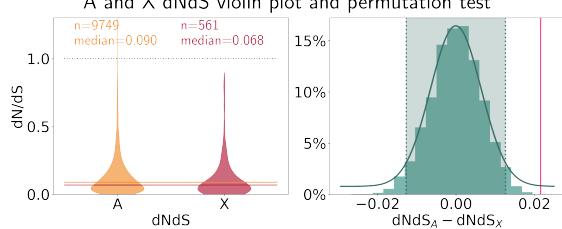
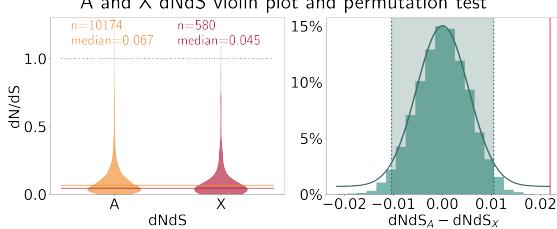


Figure S1:  **$d_S$  vs.  $d_N$  scatterplots and violin plots of  $d_S$  values from X-linked and autosomal orthologs.** Pairwise comparisons between members of three species groups with violin plots of  $d_S$  values for X-linked and autosomal 1-to-1 orthologs, and scatterplots of  $d_S$  vs.  $d_N$ . 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).

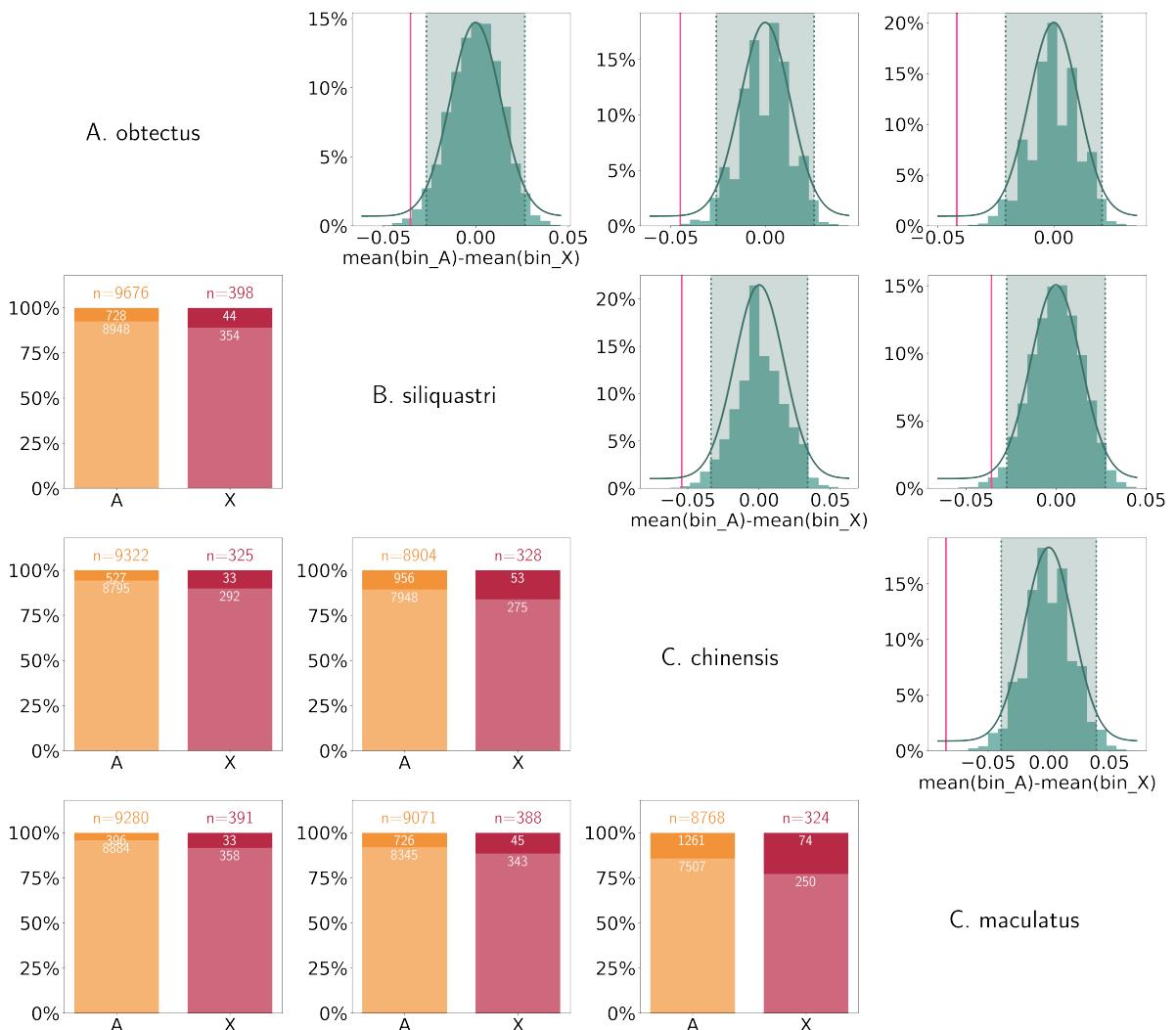
**A**

## Bruchini: A and X dNdS violin plot and permutation test

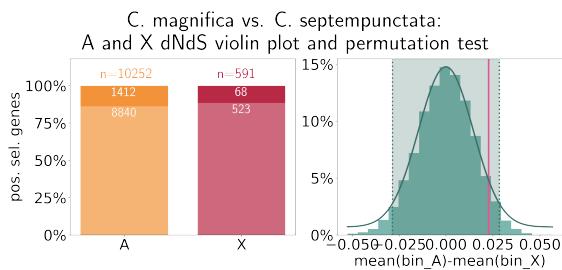
**B**C. magnifica vs. C. septempunctata:  
A and X dNdS violin plot and permutation test**C**T. castaneum vs. T. freemani:  
A and X dNdS violin plot and permutation test

**Figure S2:  $d_N/d_S$  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**).

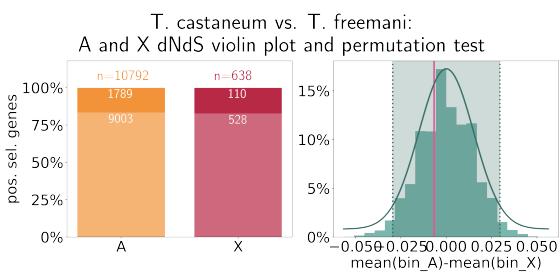
### Bruchini: A and X dNdS violin plot and permutation test



**B**



**C**



**Figure S3: 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.

## 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

## Synteny

*B. siliquastri* vs. *A. obtectus*

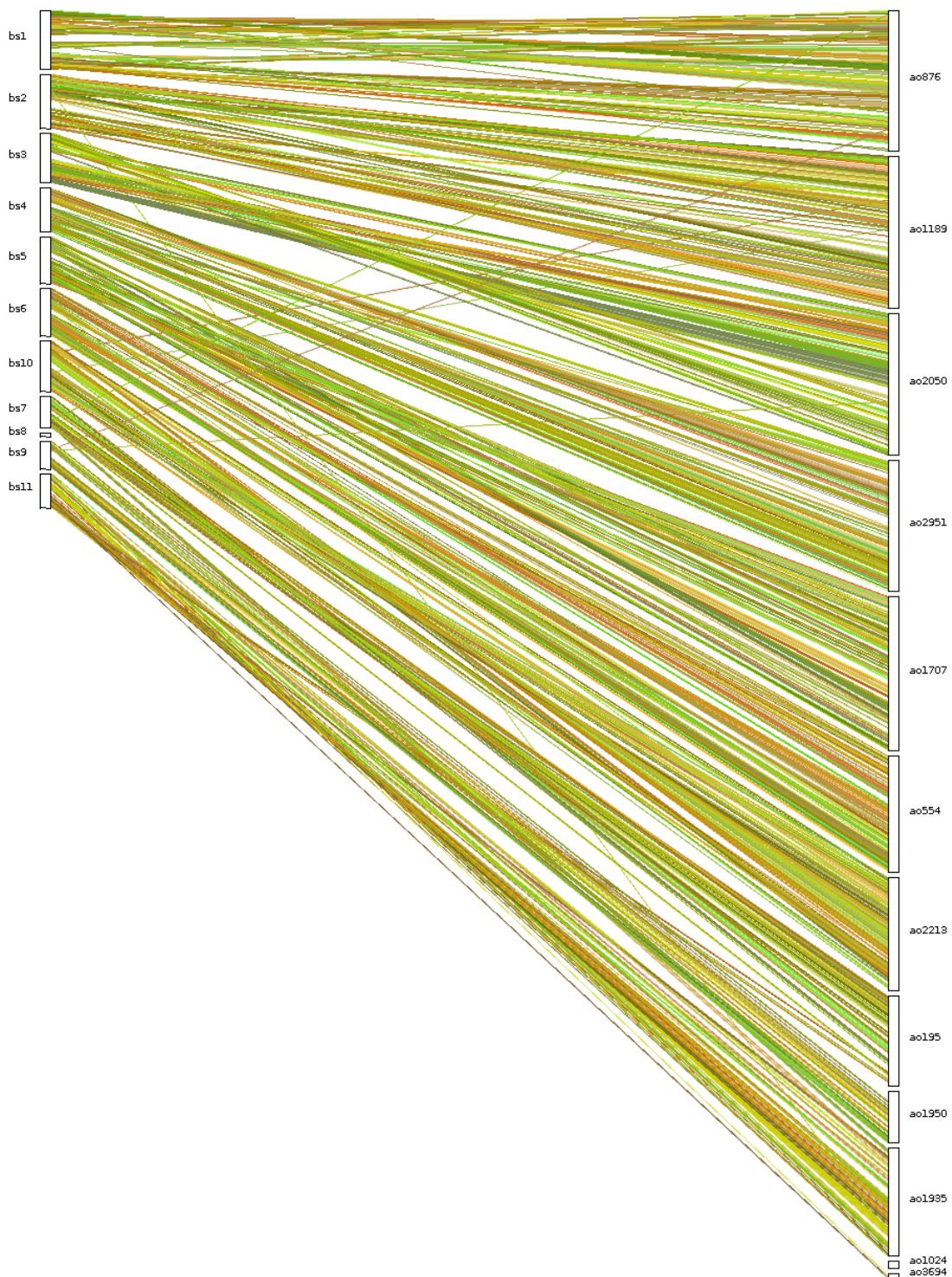


Figure S4: Synteny plot of *B. siliquastri* (left) and *A. obtectus* (right), the X-chromosomes are bs9 for *B. siliquastri* and ao1950 for *A. obtectus* (second from the bottom).

*C. maculatus* vs. *A. obtectus*

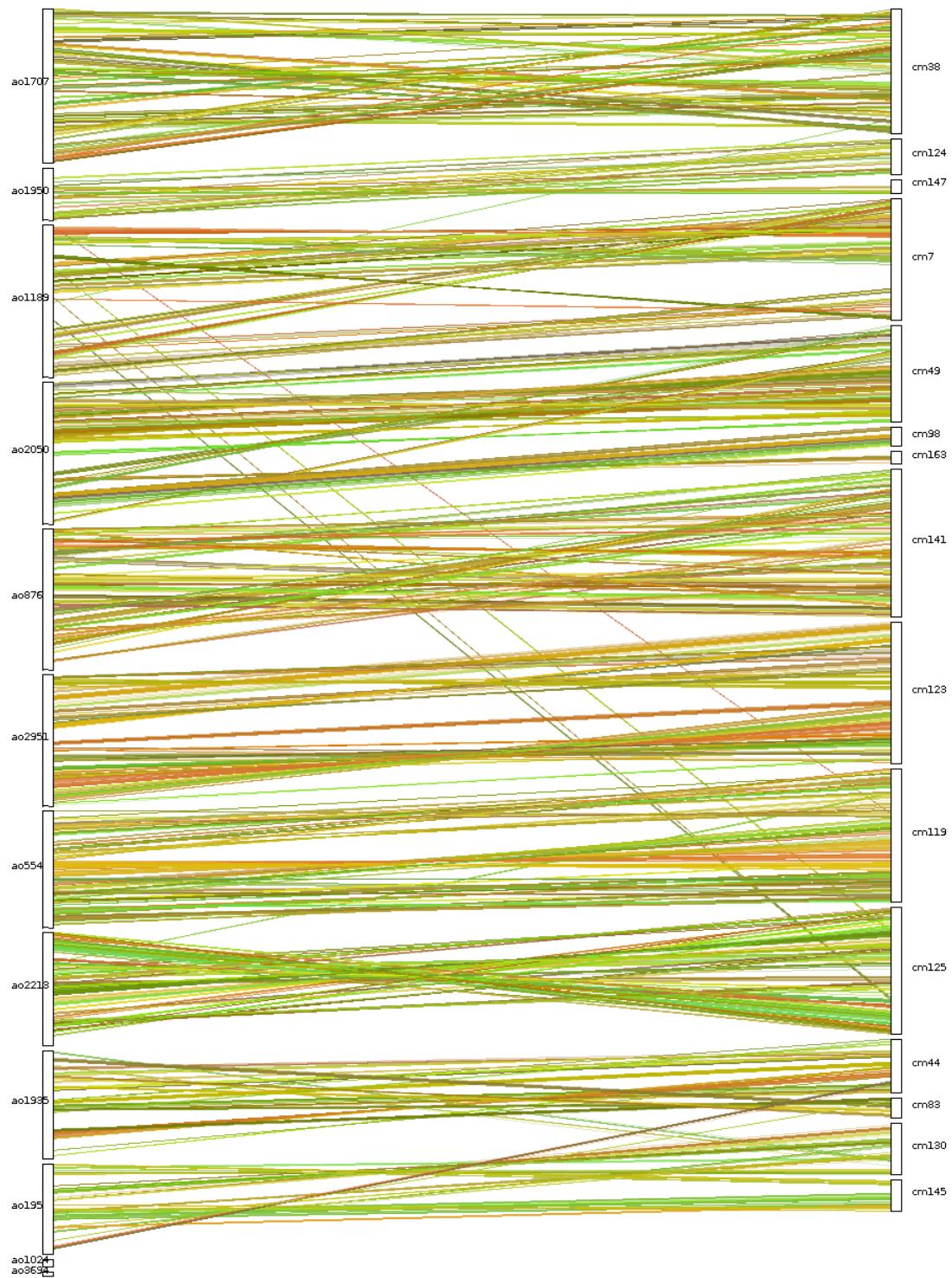


Figure S5: Synteny plot of *A. obtectus* (left) and *C. maculatus* (right), the X-chromosomes are cm124 for *C. maculatus* and ao1950 for *A. obtectus* (second from the top).

*C. magnifica* vs. *C. septempunctata*

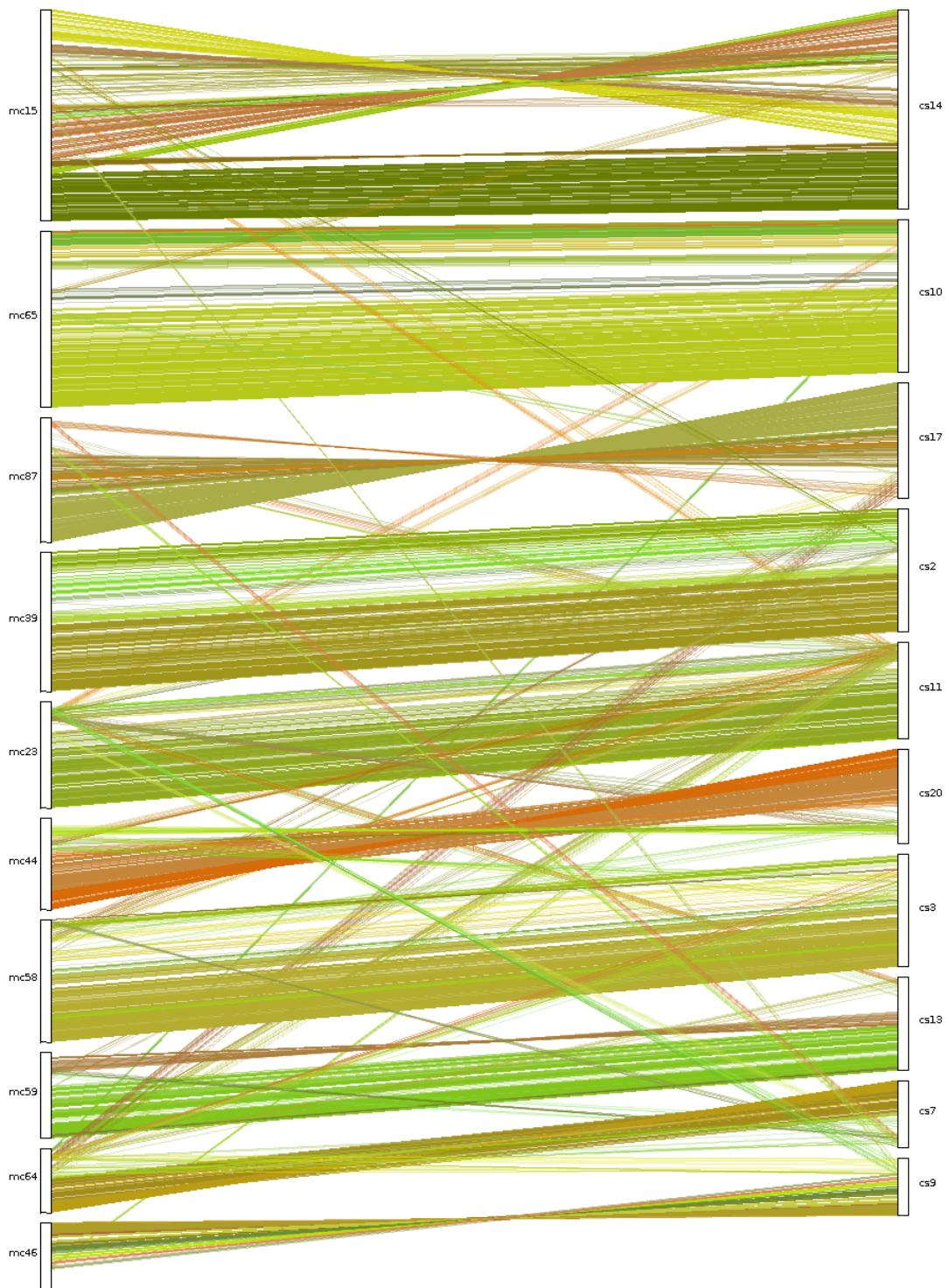


Figure S6: Synteny plot of *C. magnifica* (left) and *C. septempunctata* (right), the X-chromosomes are mc64 for *C. magnifica* and cs7 for *C. septempunctata* (second from the bottom).

*T. castaneum* vs. *T. freemani*

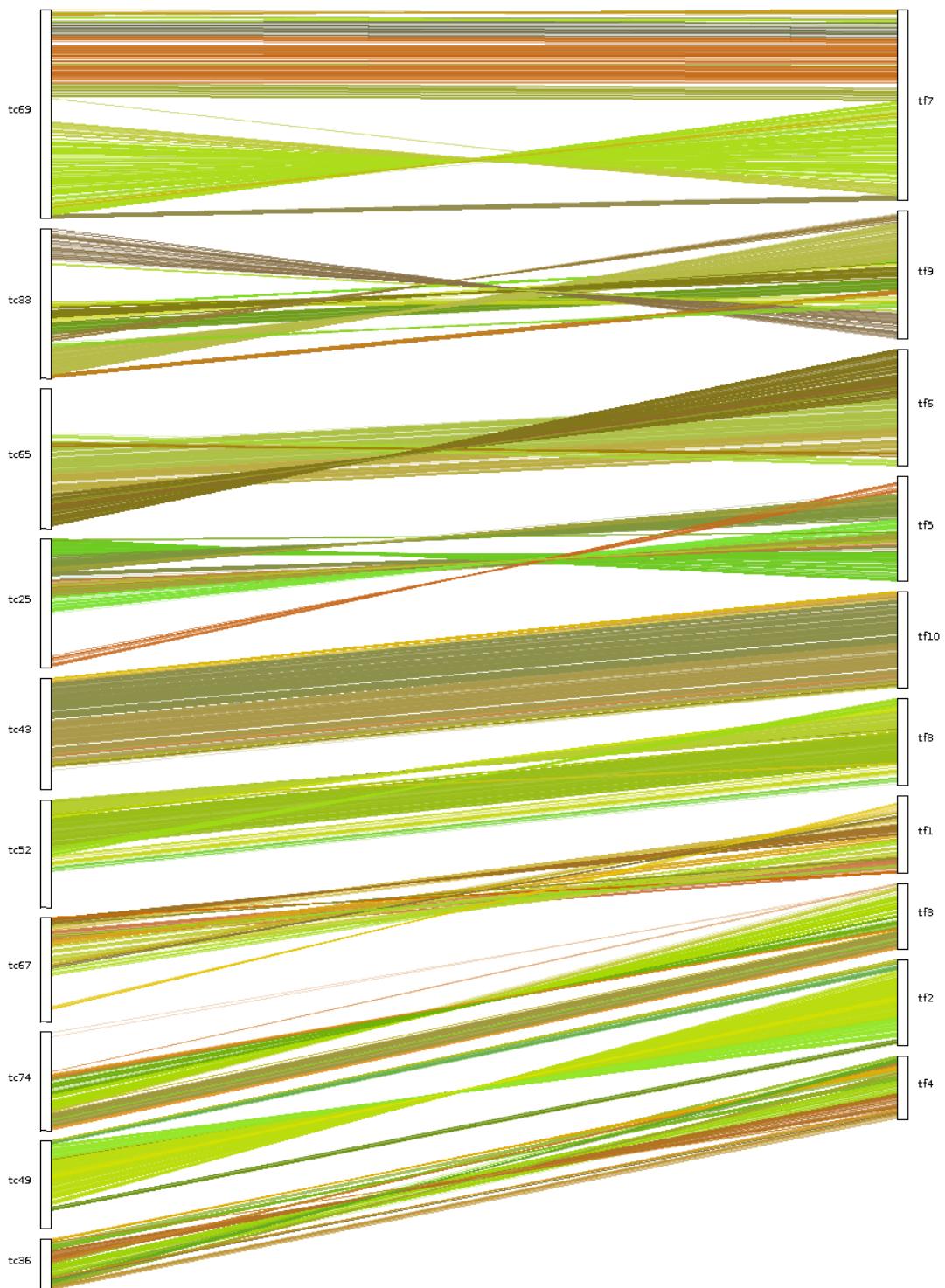


Figure S7: Synteny plot of *T. castaneum* (left) and *T. freemani* (right), the X-chromosomes are tc36 for *T. castaneum* and tf4 for *T. freemani* (first from the bottom).

*B. siliquastrum* vs. *T. castaneum*

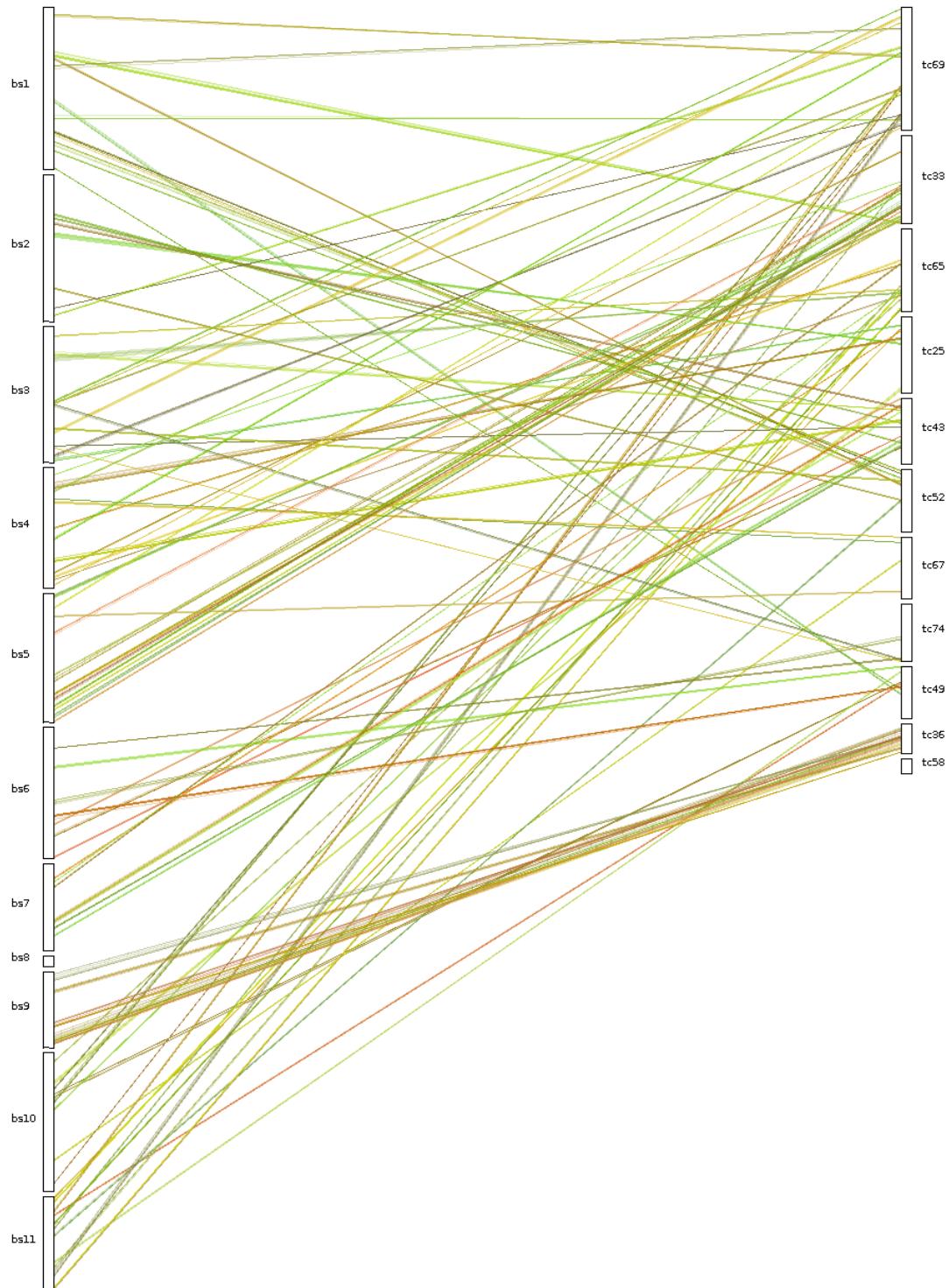


Figure S8: Synteny plot of *B. siliquastrum* (right) and *T. castaneum* (right), the X-chromosomes are bs9 for *B. siliquastrum* and tc36 for *T. castaneum* (third and second from the bottom).

## additional differential expression analyses

