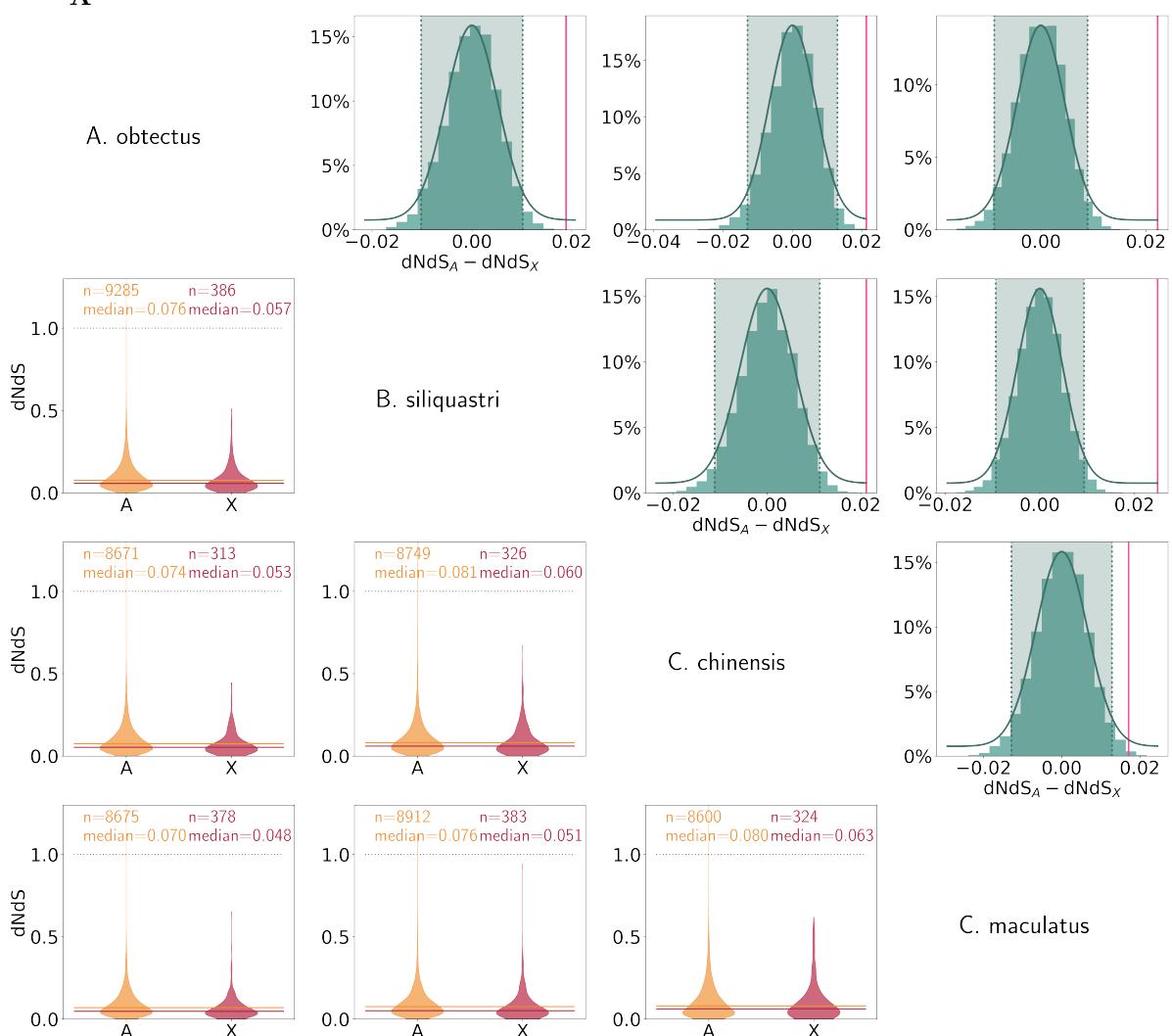
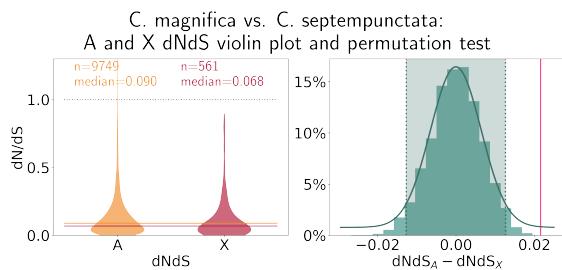
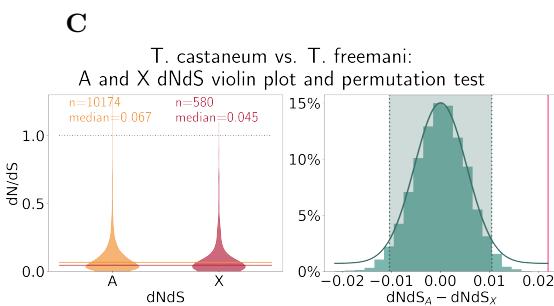


**A**

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

**B****C**

**Figure 1:  $d_N/d_S$  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. 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: dS vs. dNdS and dS violin plot, filtered dS < 2 and dNdS < 2

**A**

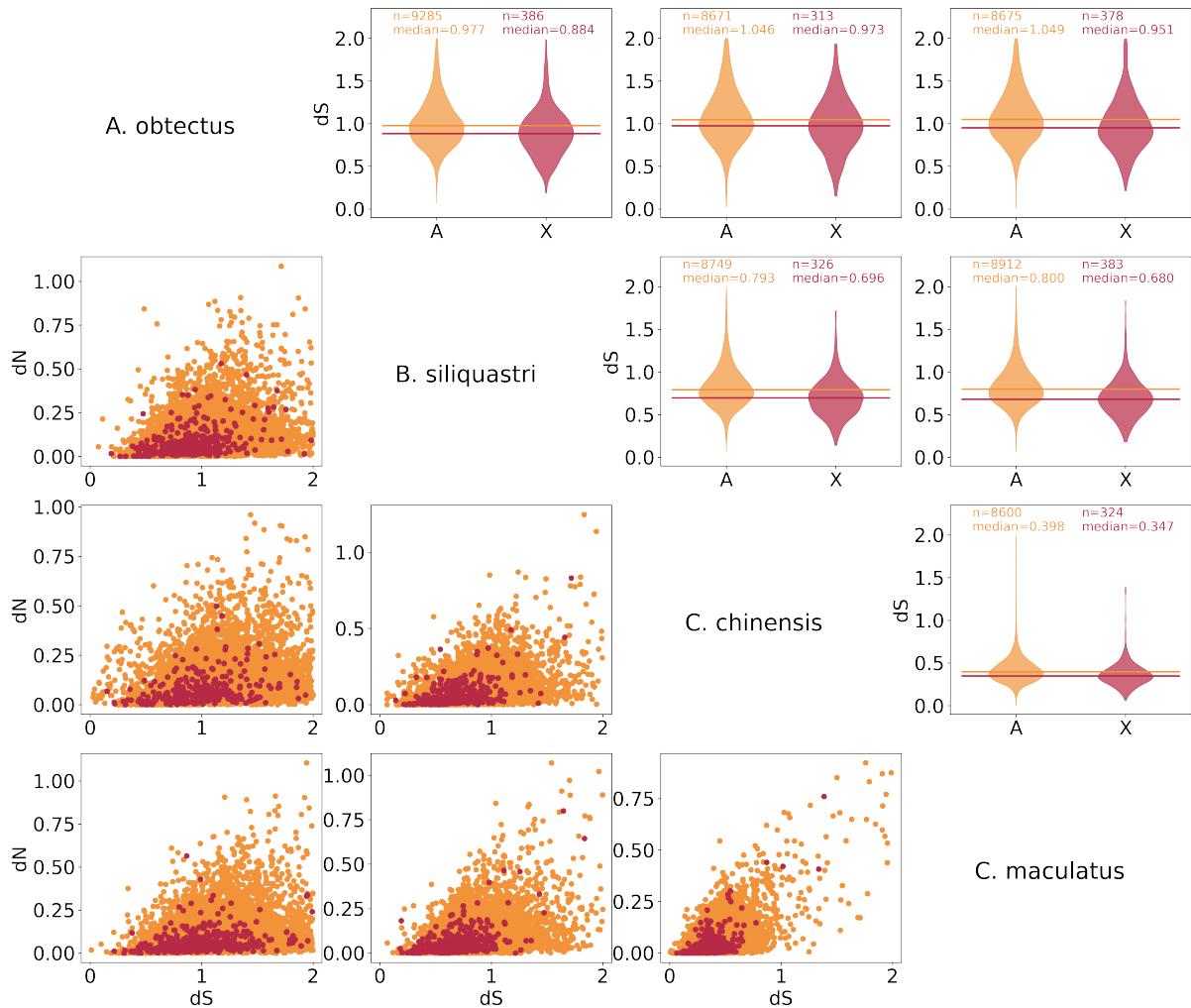


Figure 2: **d<sub>S</sub> vs. d<sub>N</sub> scatterplots and violin plots of d<sub>S</sub> values from X-linked and autosomal orthologs.** Pairwise comparisons between members of three species groups with violin plots of d<sub>S</sub> values for X-linked and autosomal 1-to-1 orthologs, and scatterplots of d<sub>S</sub> vs. d<sub>N</sub>. d<sub>S</sub> is lower for X-linked orthologs in all comparisons except *Tribolium*, where it is almost equal. 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

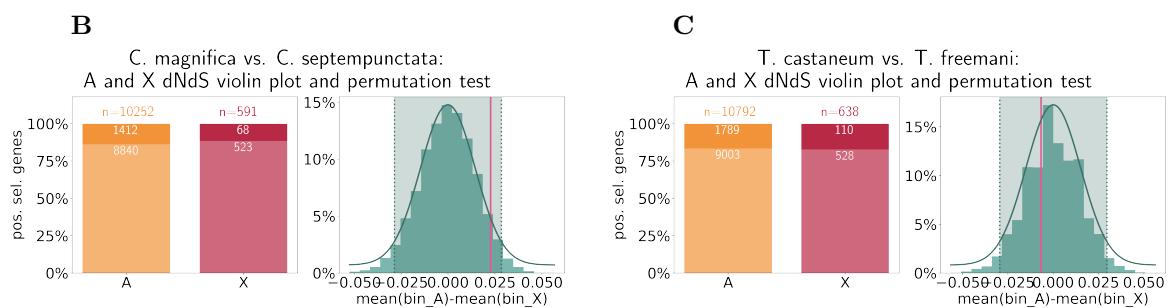
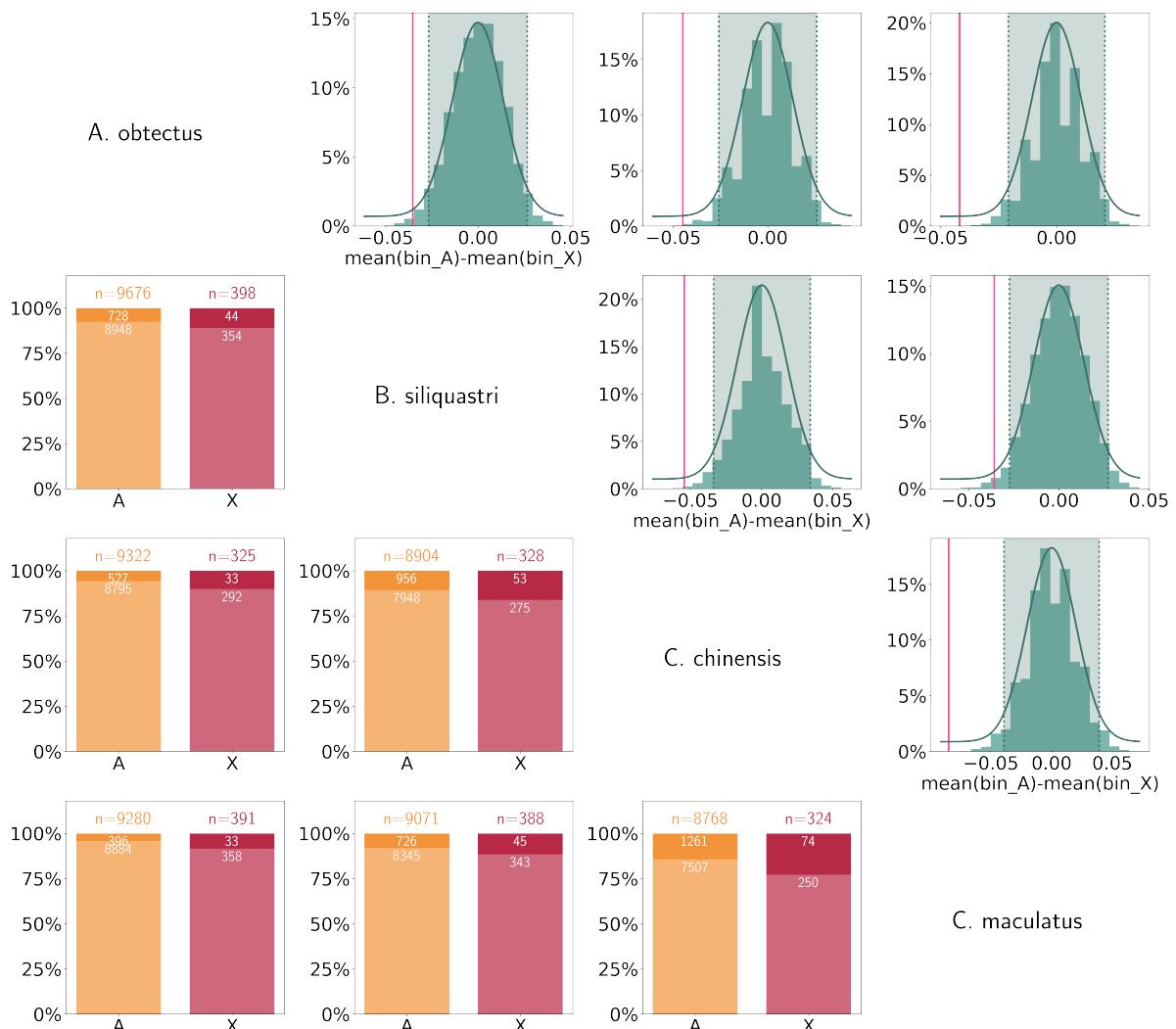
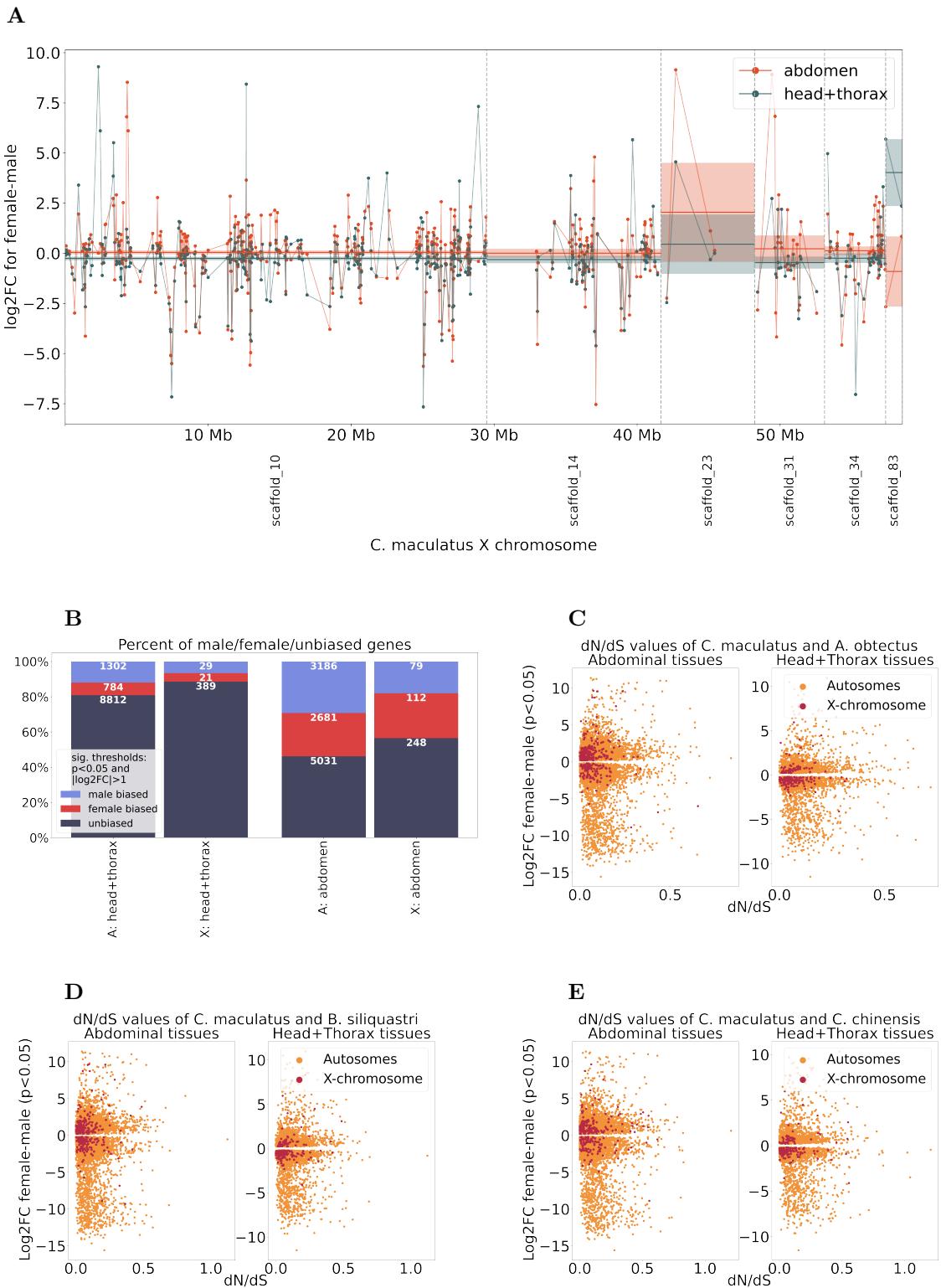


Figure 3: **positively selected orthologs split into autosomal or X-linked.** Positively selected genes are determined via likelihood ratio test comparison between paml site models M1a and M2a. The within-family comparisons are performed for three species groups: *Bruchini* (**A**), *Coccinella* (**B**) and *Tribolium* (**C**).



**Figure 4: Differential expression analysis.** We are utilizing the log<sub>2</sub> fold change (og2LFC) information from genes in *C. maculatus* and combining it with  $d_N/d_S$  between these genes and their 1-to-1 orthologs in other bruchids. The log<sub>2</sub>FC contrast is always female-male, therefore positive values indicate female-bias and negative values indicate male-bias. **A:** log<sub>2</sub>FC of all genes on X-linked contigs in somatic (head+thorax) and reproductive (abdominal) tissues. **B:** number of sex biased genes in abdominal (reproductive) tissues and head and thorax (somatic) tissues. **C-E:** Scatterplot of significantly differentially expressed genes showing  $d_N/d_S$  of *A. obtectus* (**C**), *B. siliquastri* (**D**) and *C. chinensis* (**E**) respectively.