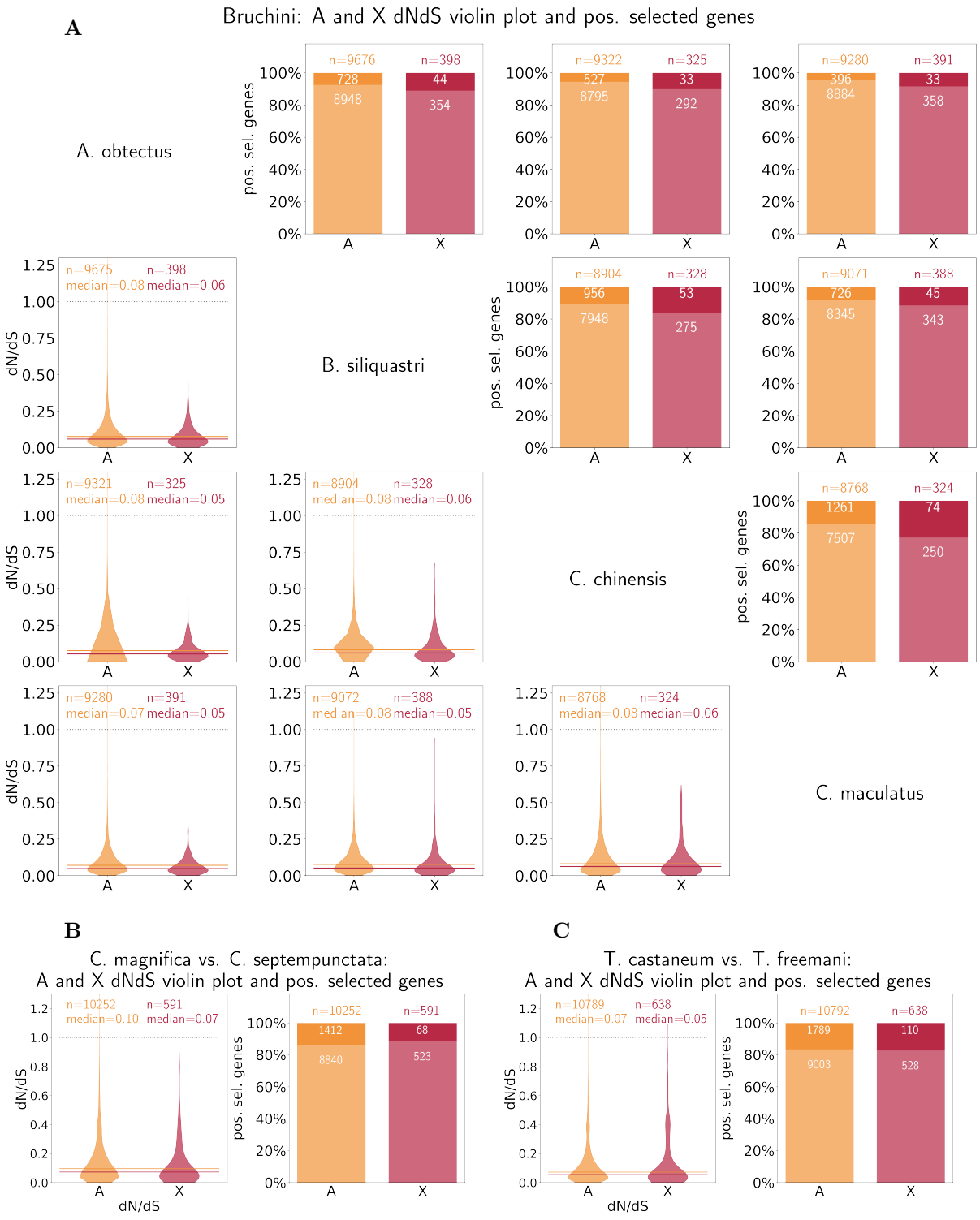

Figure 1: **d_N/d_S and abundance of positively selected genes.** *Bottom left*: Pairwise comparisons between members of three species groups with violin plots of d_N/d_S values for X-linked and autosomal 1-to-1 orthologs, and scatterplots of d_S vs. d_N. Permutation tests (n=10000) show that d_N/d_S is significantly lower for X-linked orthologs in all comparisons within *Bruchini* (**A**) and *Coccinella* (**B**), but not *Tribolium* (**C**). *Top right*: The bar plot show the percentage of genes that contain codons under positive selection according to paml site-model analysis (likelihood ratio test comparison between paml site models M1a and M2a). *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.

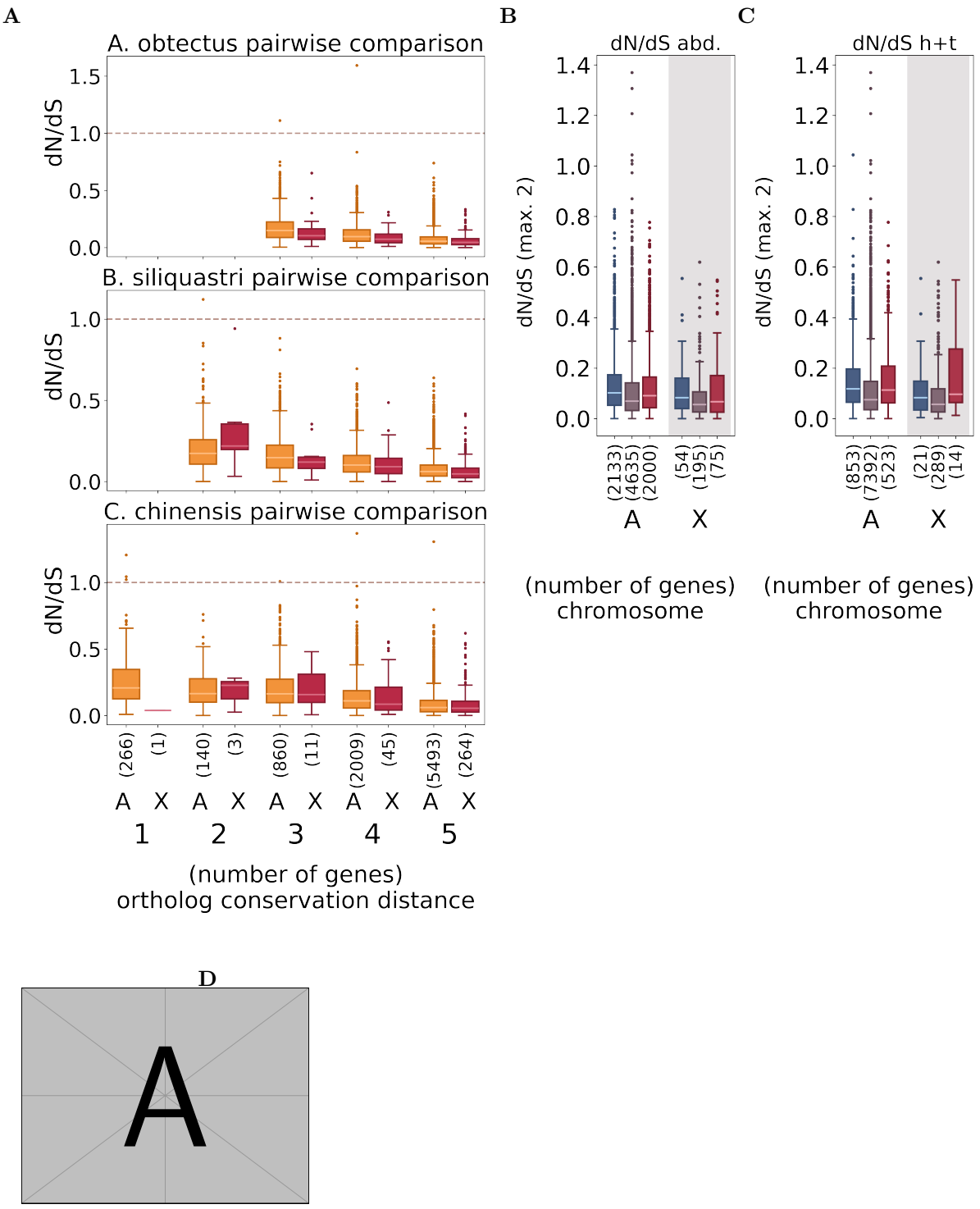

Figure 2: **Differential expression analysis**

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