

Figure S1. The alignments of tesNAC-β and the orthologous gNAC-β-like proteins. The region with S/T phosphosites is underlined by a red line and markers: crosses indicate the conservative Ser positions in *D. melanogaster* and *D. willistoni* IDR sequences; circles indicate conservative S positions between *D. willistoni* and *D. buskii* IDR sequences.

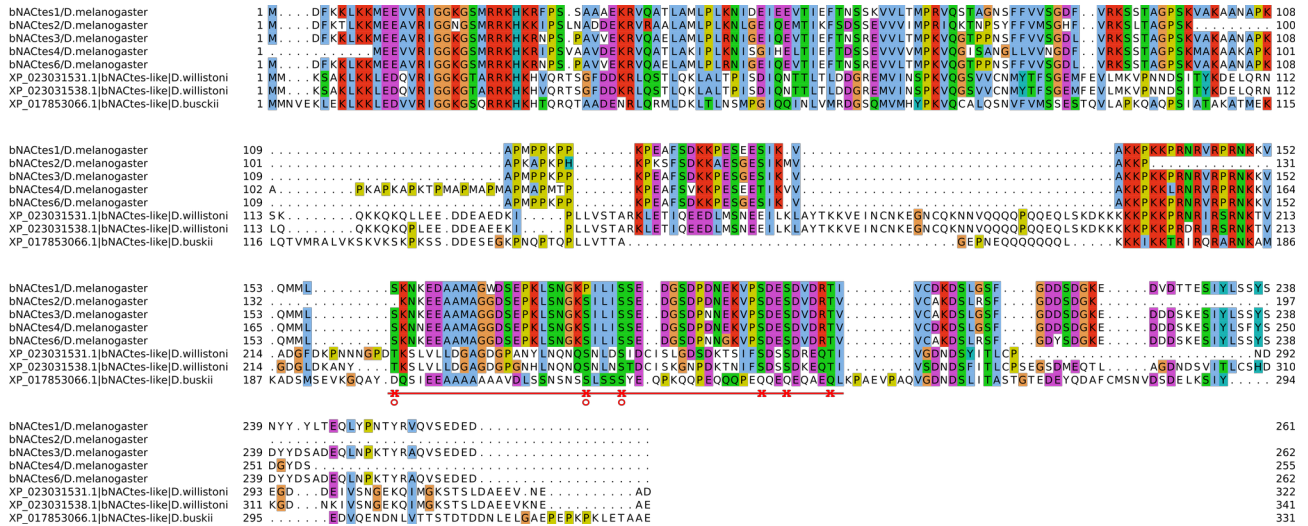


Figure S2. Conserved potential P-dependent clustered phosphosites at the orthologous IDR enriched C-ends of uncNAC- β proteins. The region with S/T phosphosites is underlined by a red line and markers: crosses indicate the conservative Ser positions.



Figure S3. The phylogenetic trees for the NAC- α (**A**) and NAC- β (**B**) proteins of the Drosophilidae genomes. The species, accession number of protein and genomic coordinates of the gene are shown. The identified protein is marked as a “novel” if its accession number is non-available at the non-annotated genome. The blue integers indicate the bootstrap values (only values greater than 0.5 are shown).

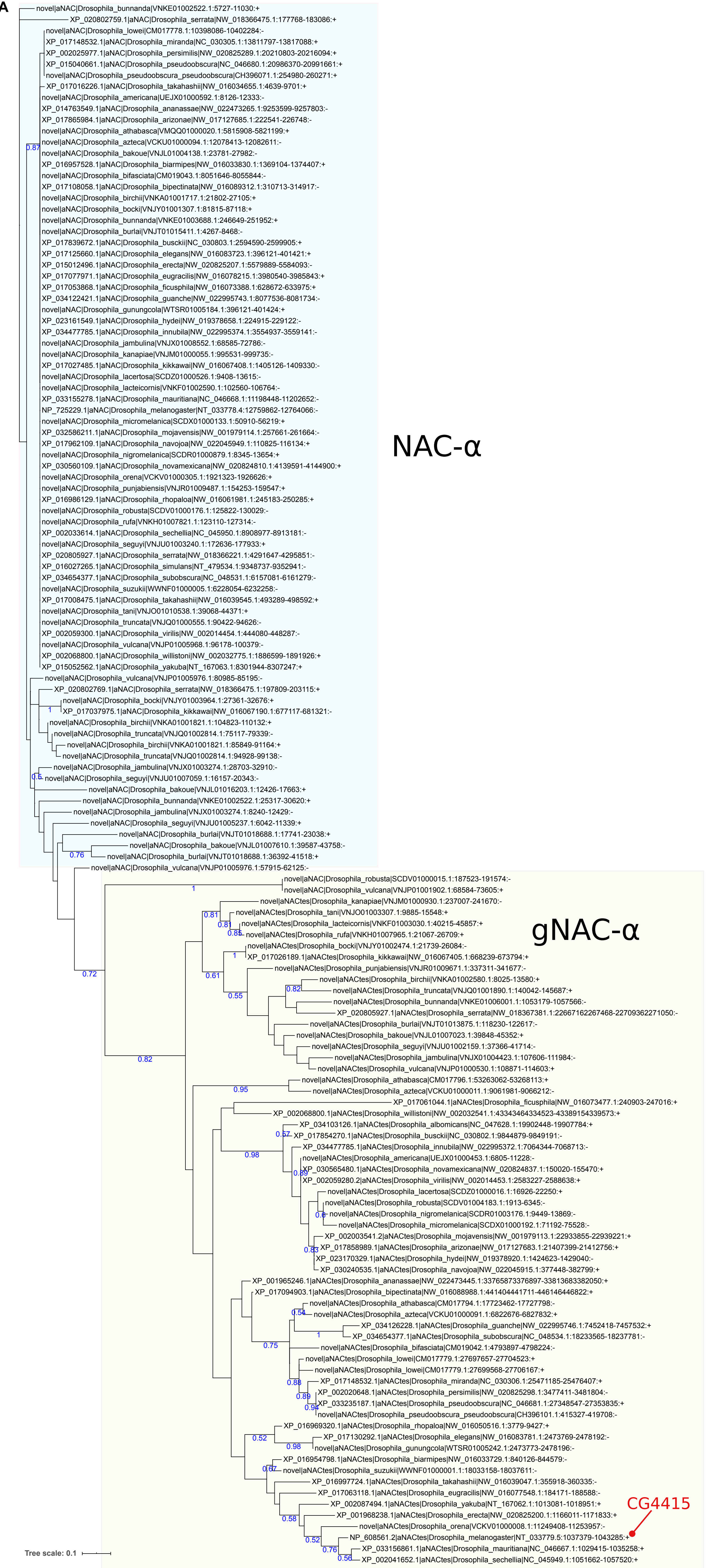


Figure S3

B

