

Supplementary Material

Figure S1. (A) Position of the domain conserved Ubiquitin Family in the ubiquitin sequences of *B. glabrata*, *C. elegans* and *D. melanogaster*. **(B)** Amino acid residues involved in the formation of the active site and ubiquitin chain.

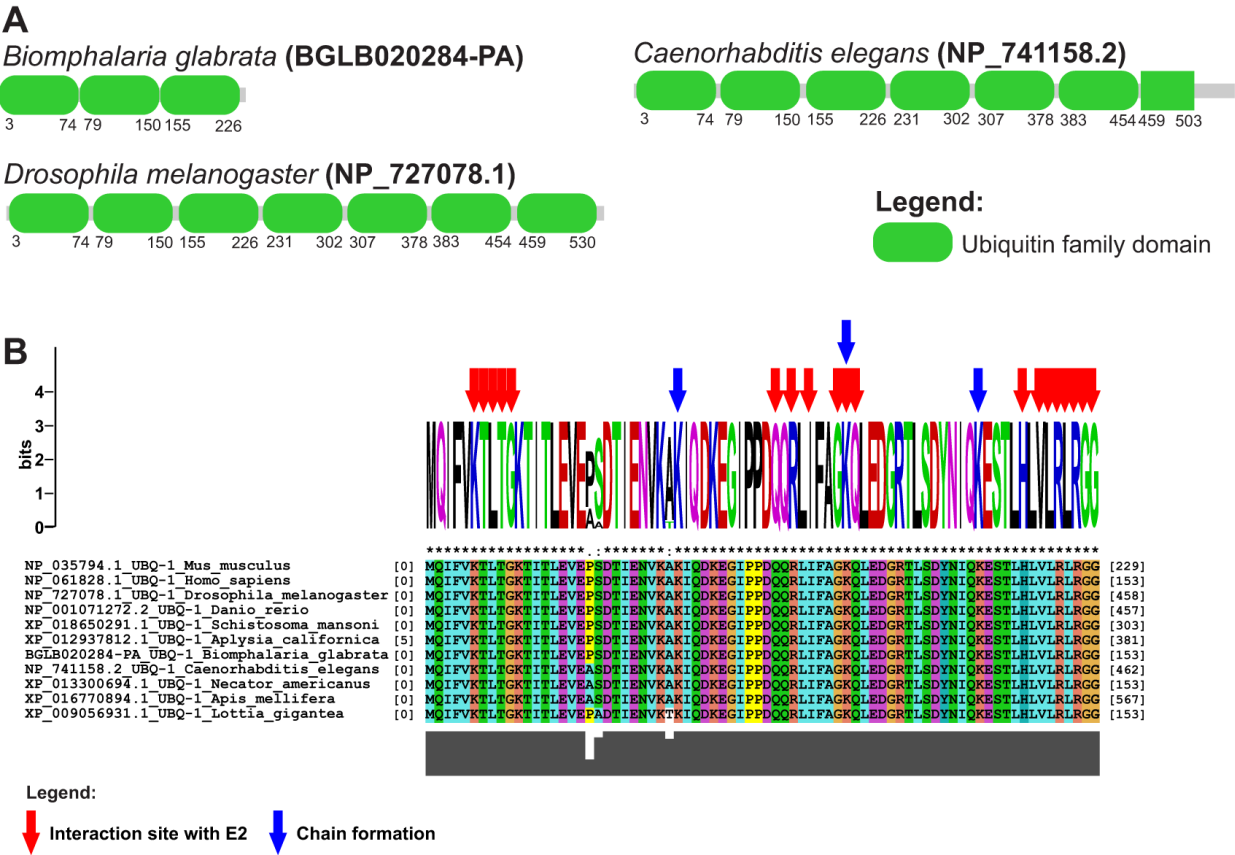


Figure S2. (A) Distribution of the domain conserved UQ_con in the sequences of *B. glabrata* identified as E2. **(B)** Formation of the active site and the interaction with E3 in evidence by arrows in the amino acid residues.

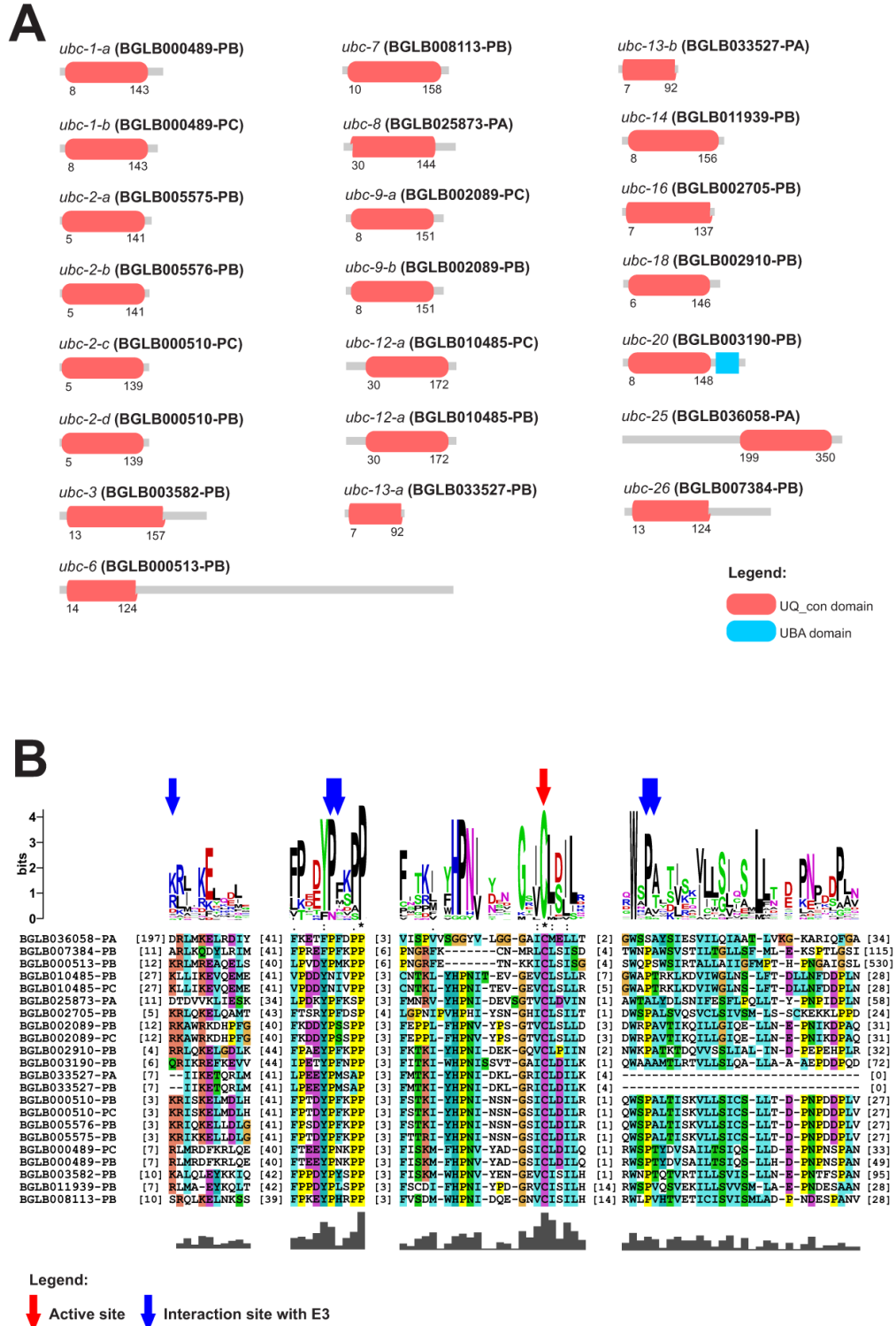


Figure S3. (A) Presence and distribution of the domains conserved found in the sequences of *B. glabrata* identified as E3-HECT. **(B)** Catalytic cleft indicated by arrows on the amino acid residues involved in its formation.

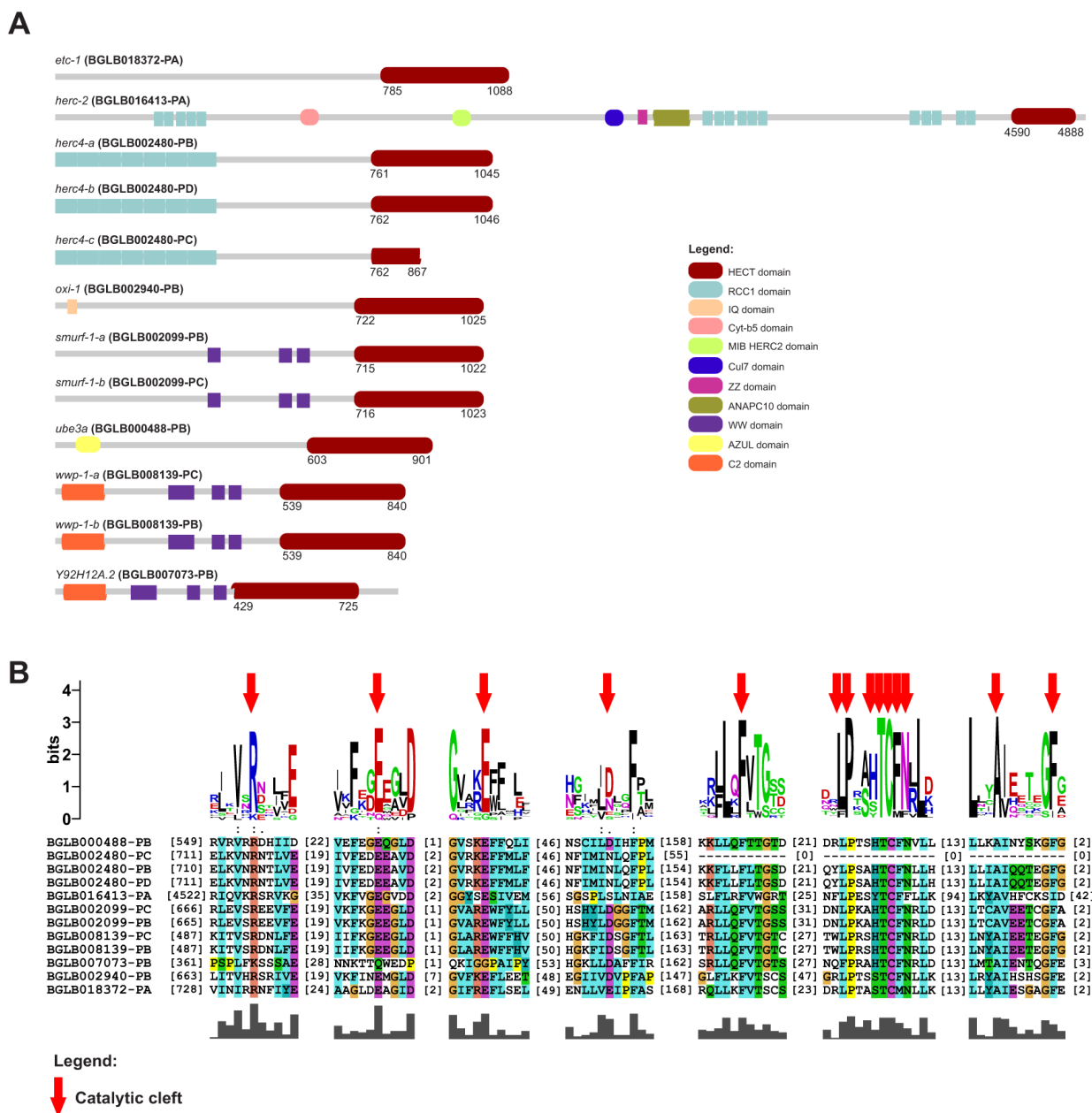


Figure S4. (A) Domains homologous to RING finger represented in their positions and distributions in the E3-RING finger sequences of *B. glabrata*. **(B)** Amino acid residues and their positions related to the formation of the structural motif found in these sequences.

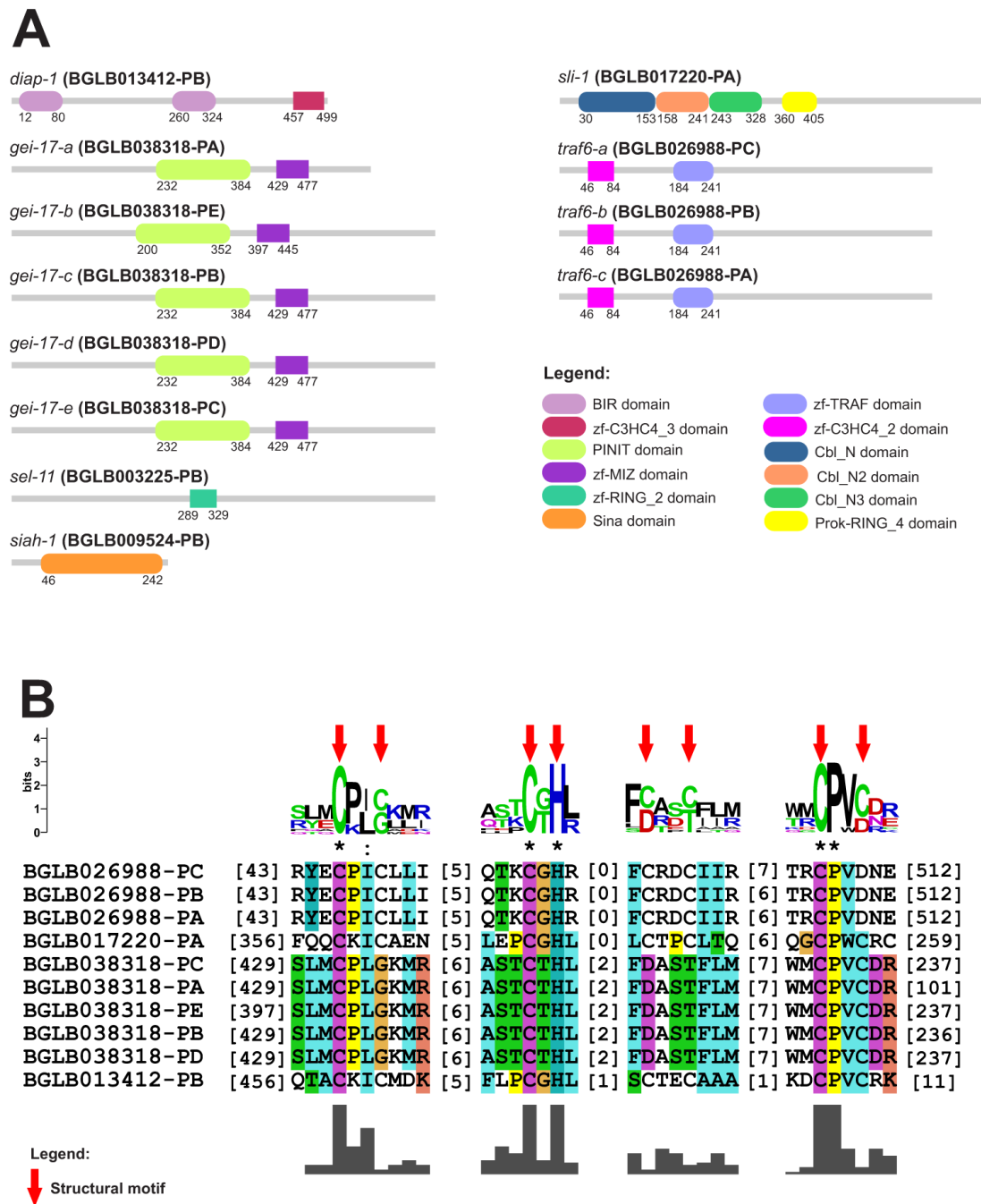


Figure S5. (A) Demonstration of the presence and distribution of the conserved domains present in the *B. glabrata* E3-U-box sequences. **(B)** Amino acid residues and their positions related to the formation of the structural motif.

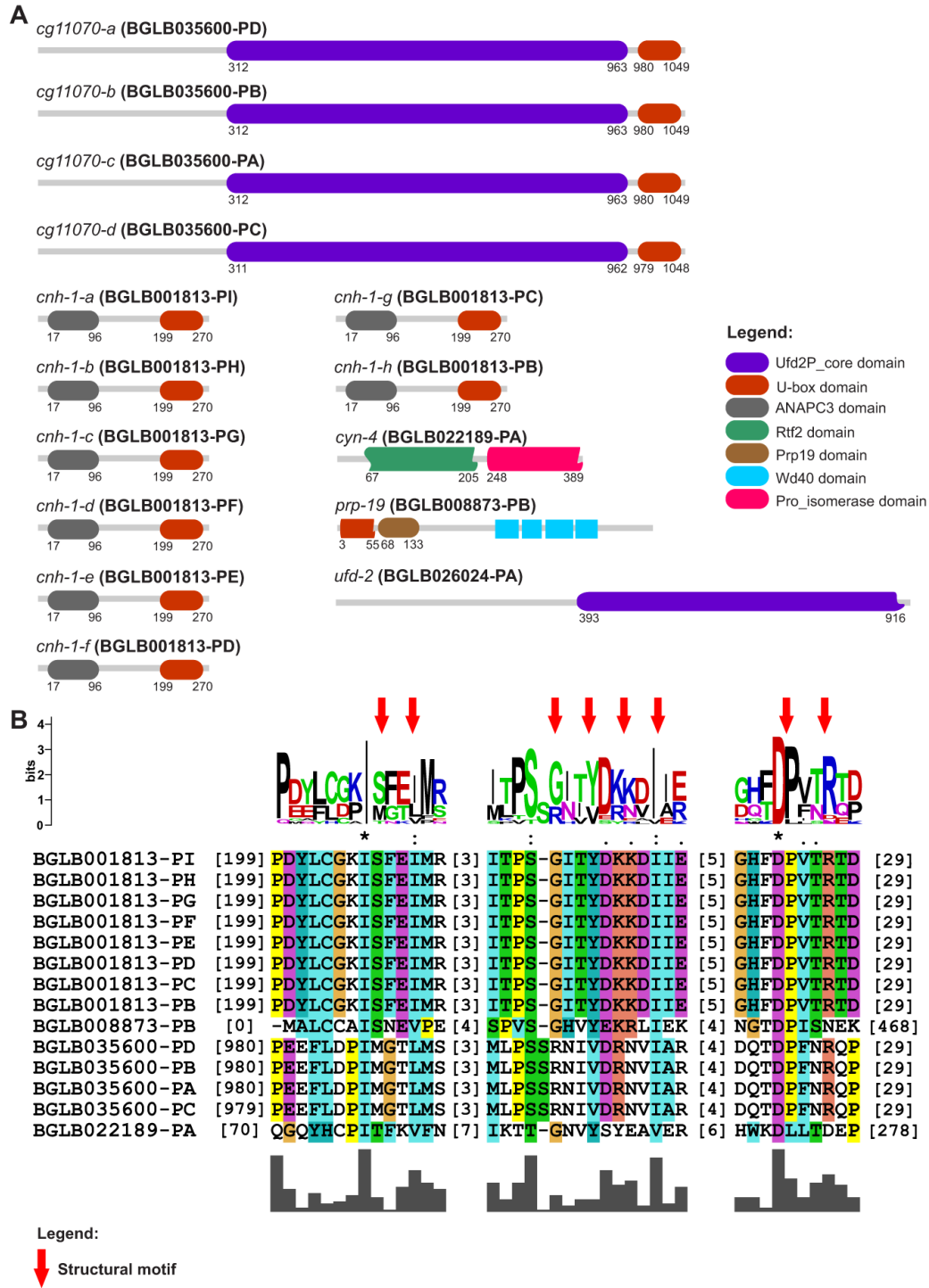


Figure S7. Representation of the evolutionary distribution of E3-HECT sequences for *B. glabrata* against their orthologous organisms.

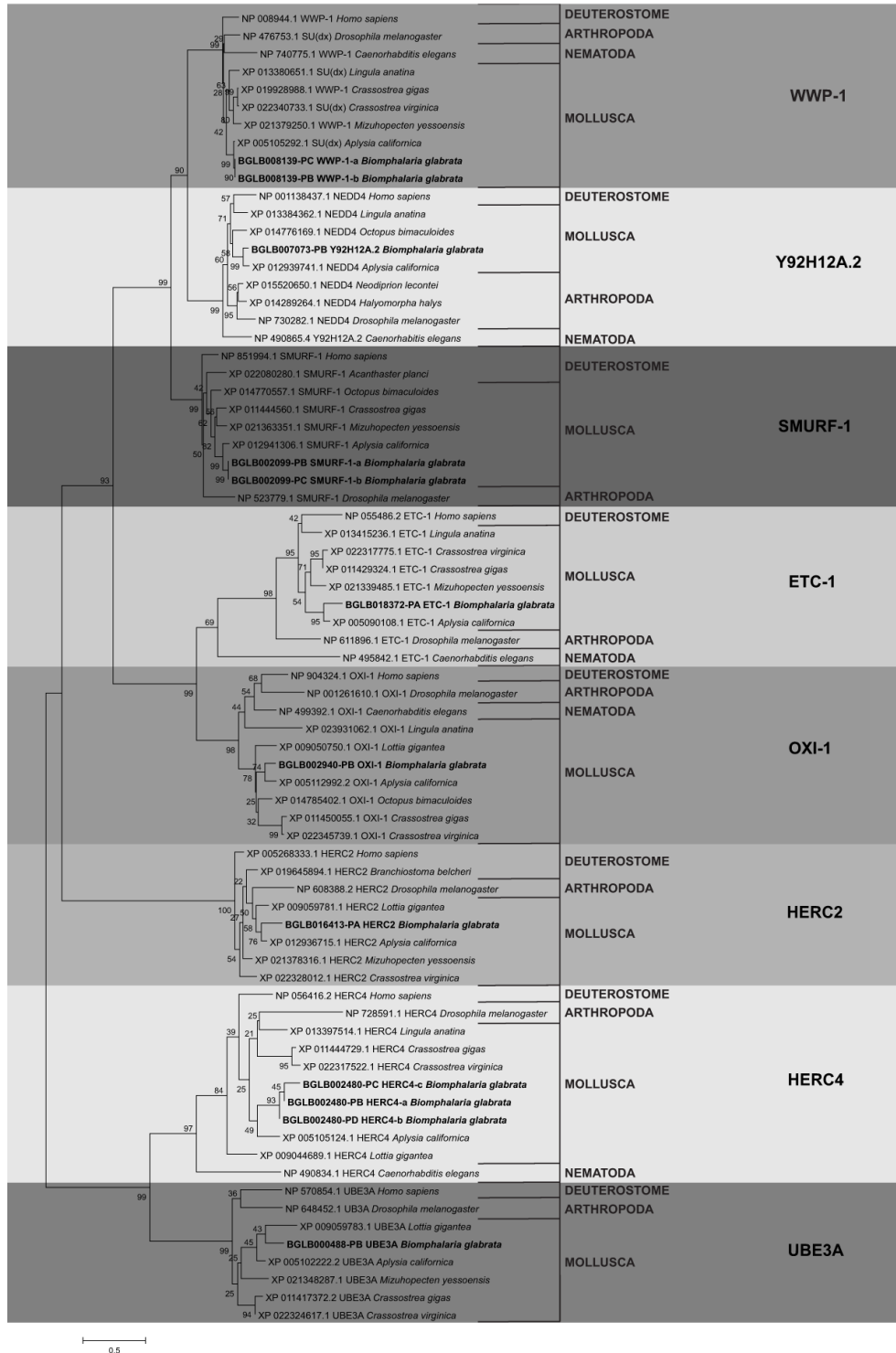


Figure S8. Evolutionary distribution of E3-U-box sequences identified in *B. glabrata* and their orthologous organisms and model organisms.

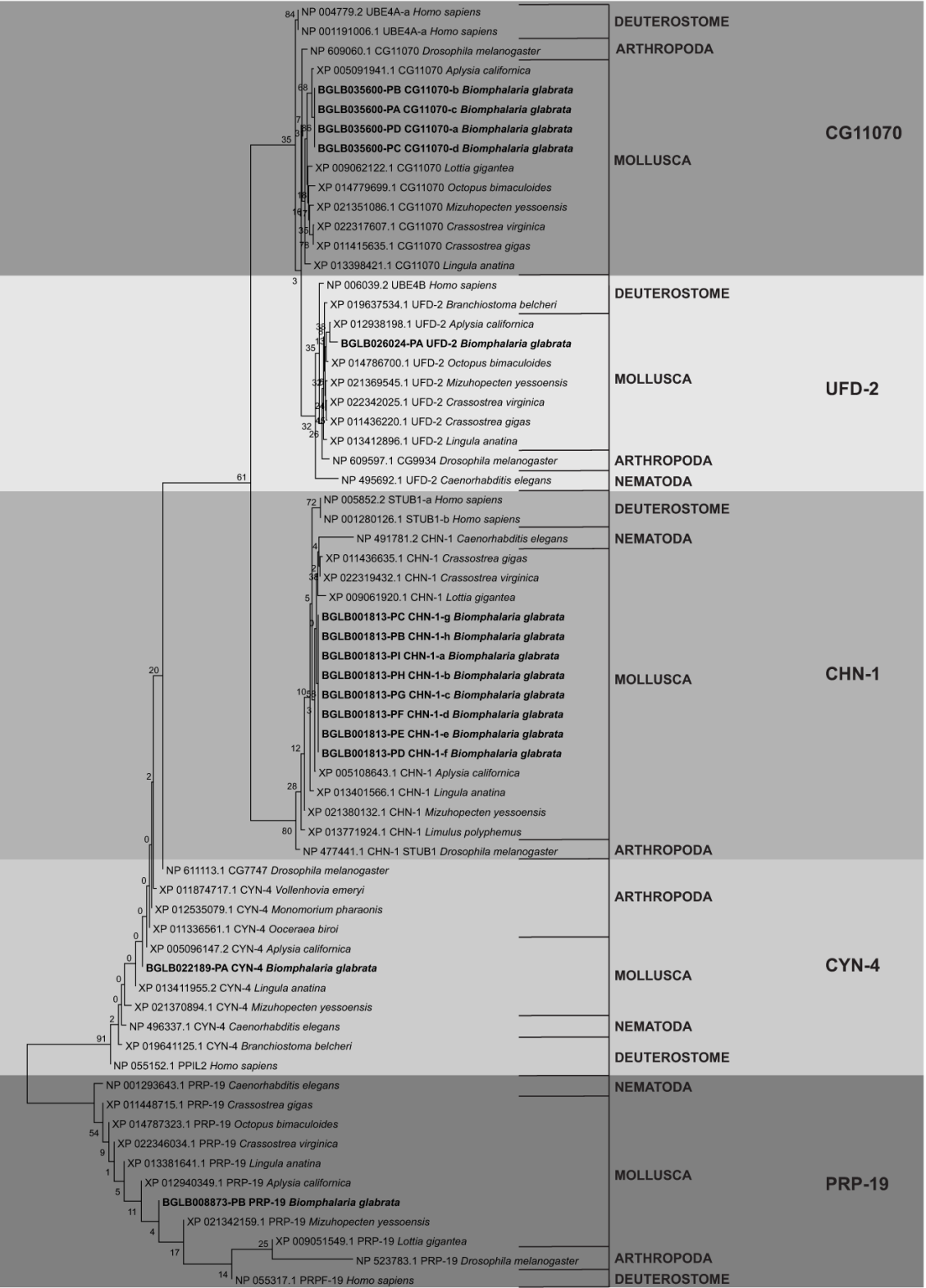


Figure S9. Phylogenetic tree representing a distribution found for the E3-RING finger sequences found in the data of *B. glabrata* against orthologous organisms.

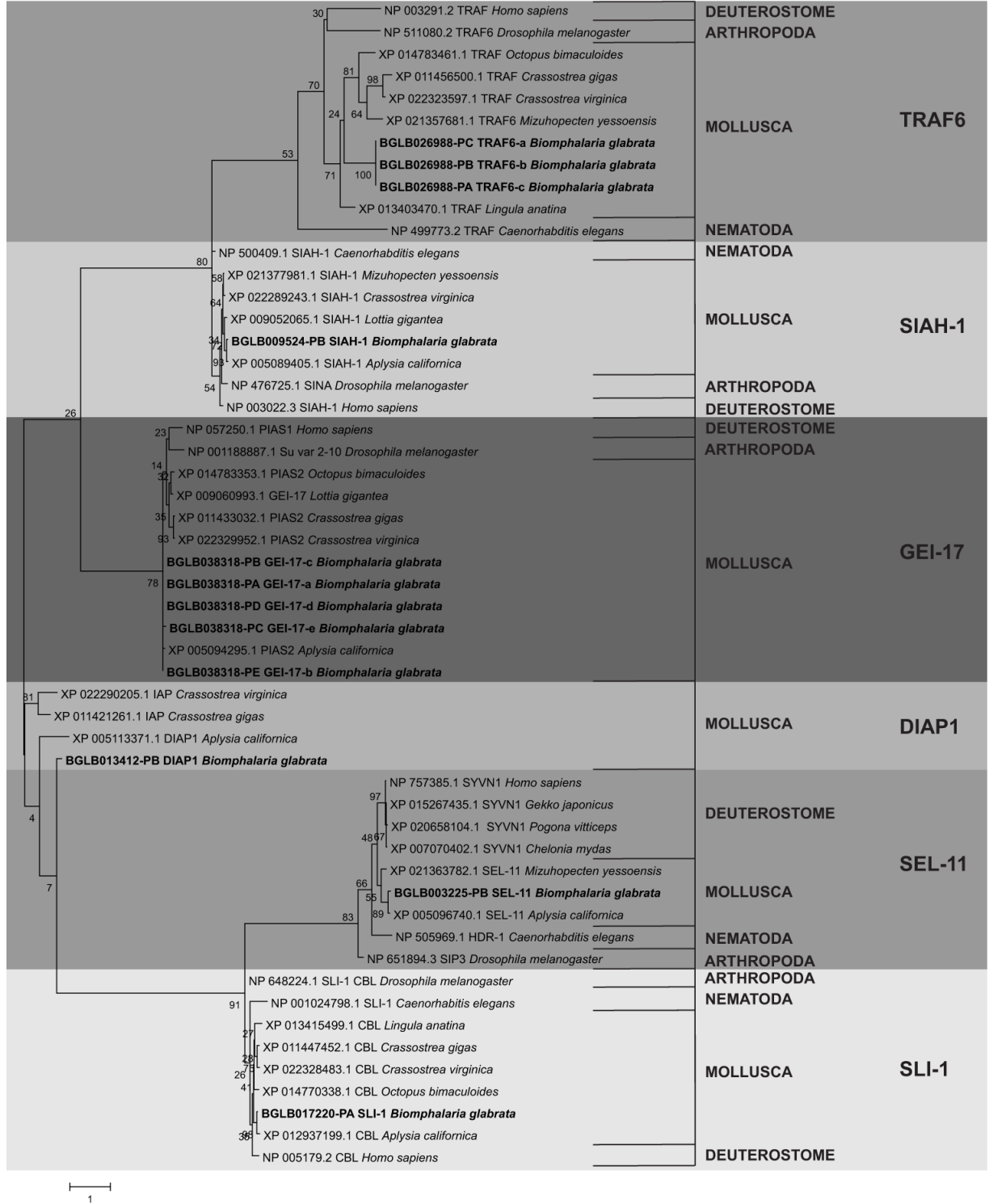


Figure S10. (A) Location and distribution of the Proteasome domain identified in the sequences of the PBS group of *B. glabrata*. **(B)** Active site found in the sequences participating in the PBS group of the *B. glabrata* data.

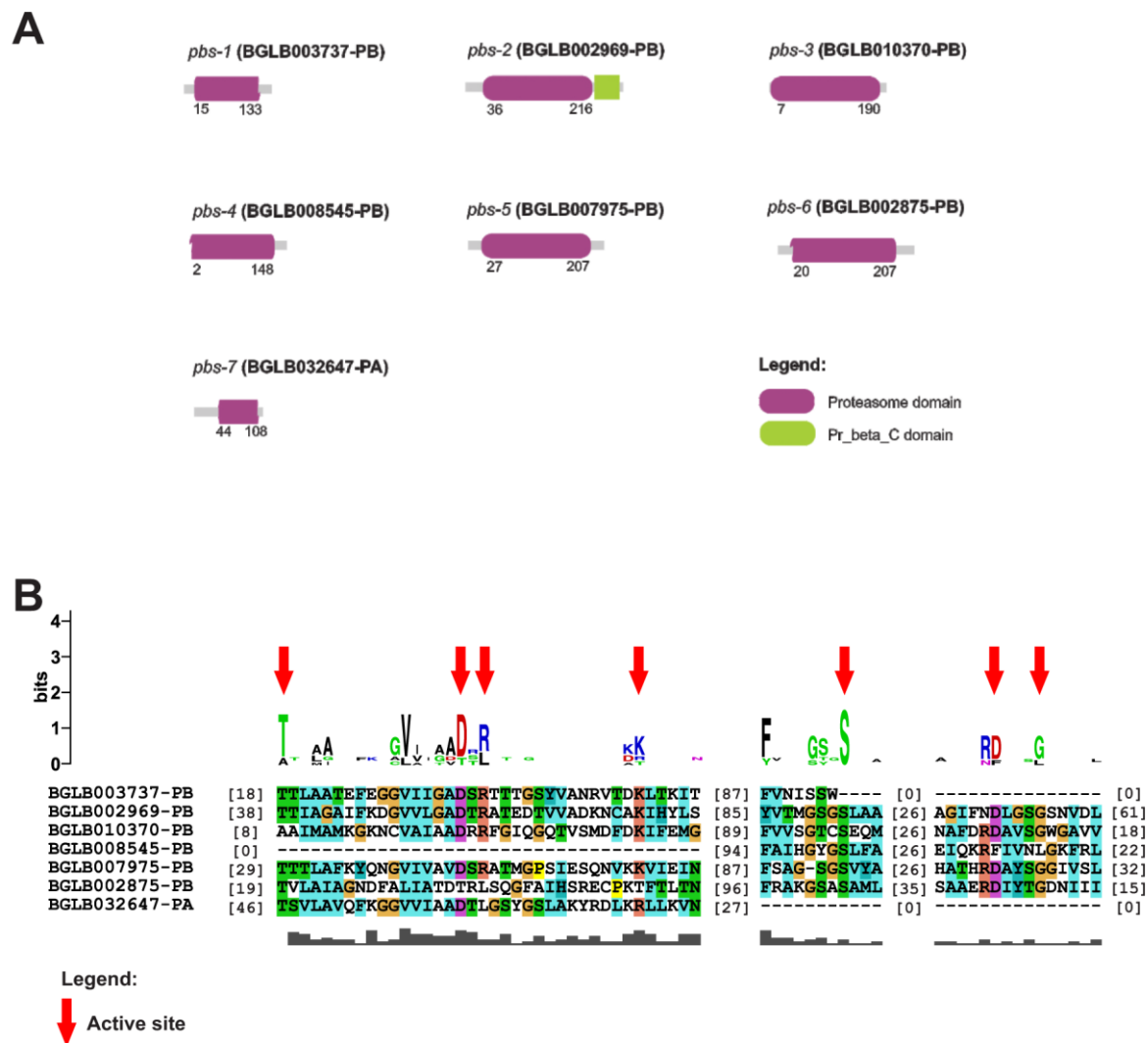


Figure S11. Position and distribution of the AAA domain in the sequences of *B. glabrata* identified as RPT.



Figure S12. (A) Presence and distribution of the domains conserved found in the sequences of *B. glabrata* identified as RPN. **(B)** Active site indicated by arrows on the amino acid residues involved in its formation.

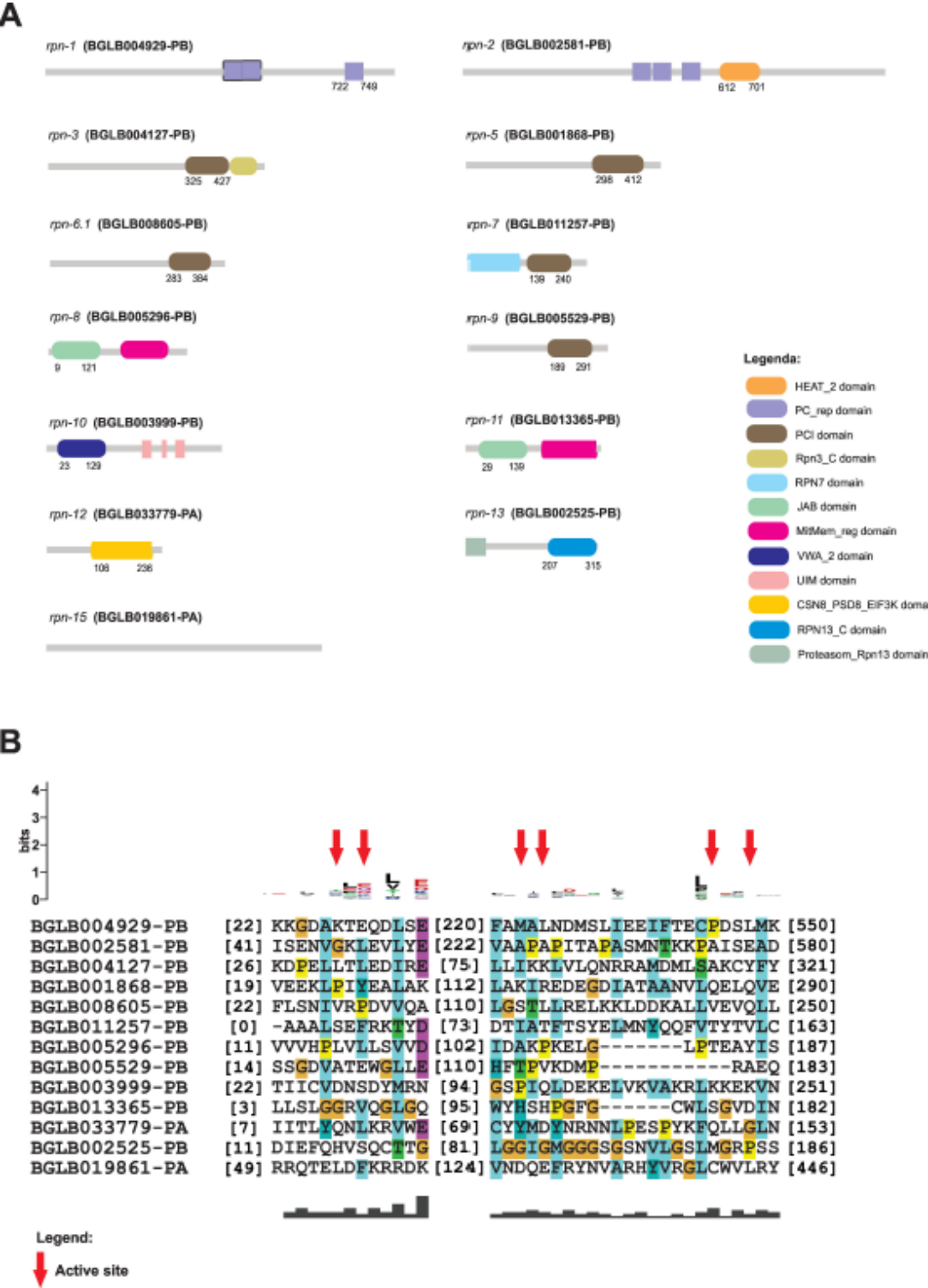


Figure S13. Phylogenetic tree generated from the PBS sequences identified in *B. glabrata* and its orthologs.

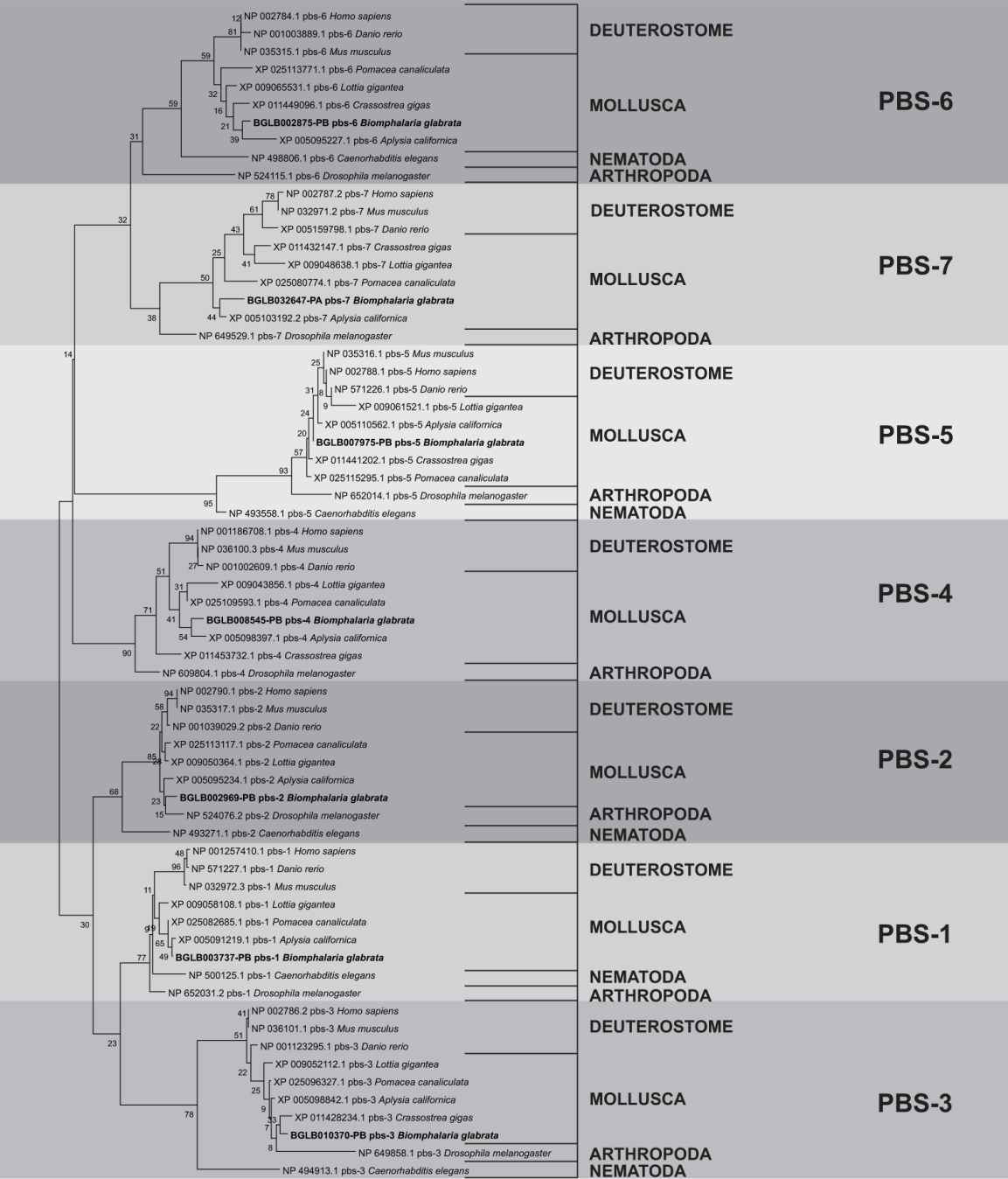


Figure S14. Representation of the evolutionary distribution of RPN sequences for *B. glabrata* against their orthologous organisms.

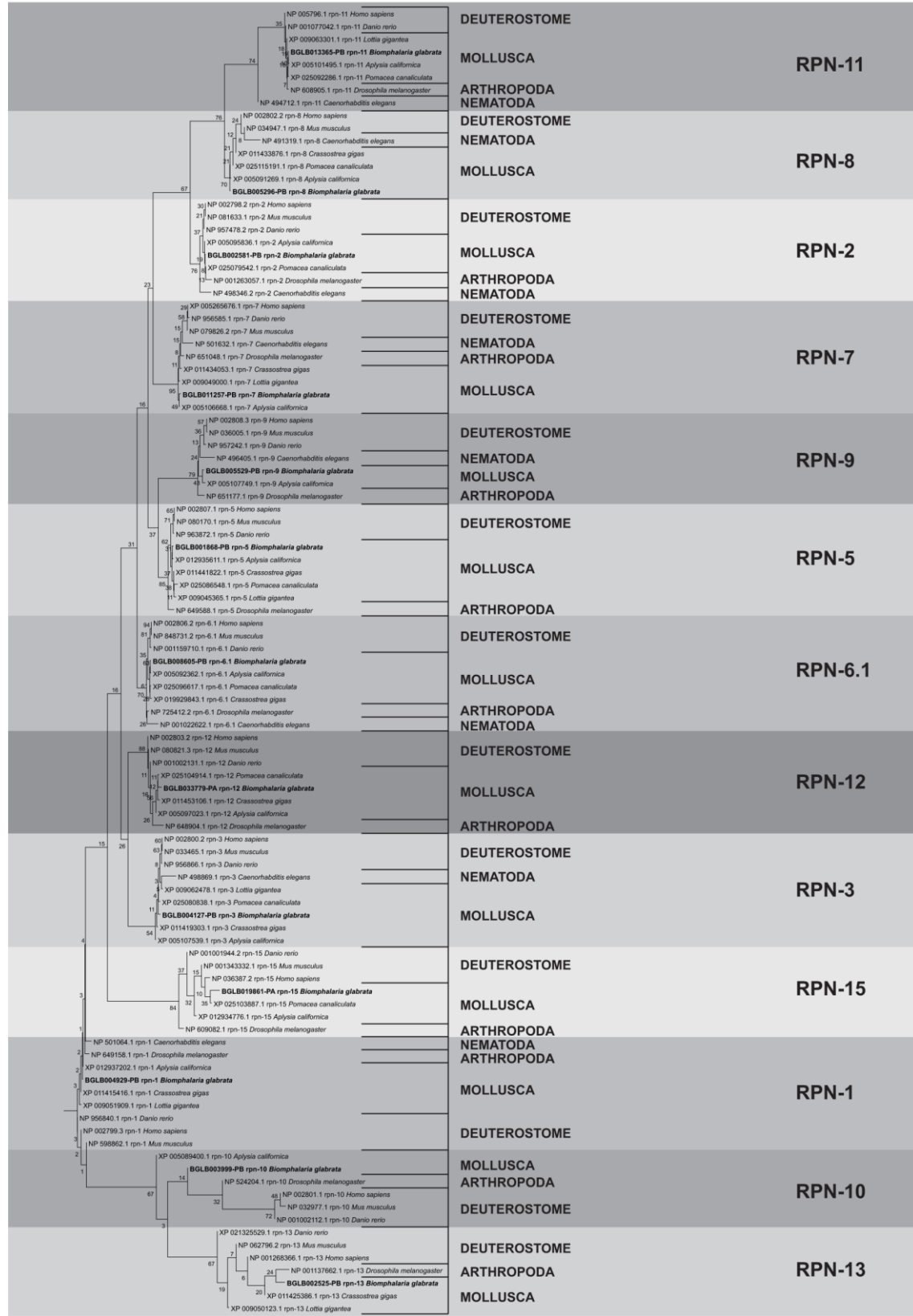


Figure S15. Evolutionary distribution of RPT sequences identified in *B. glabrata* and their orthologous organisms and model organisms.

