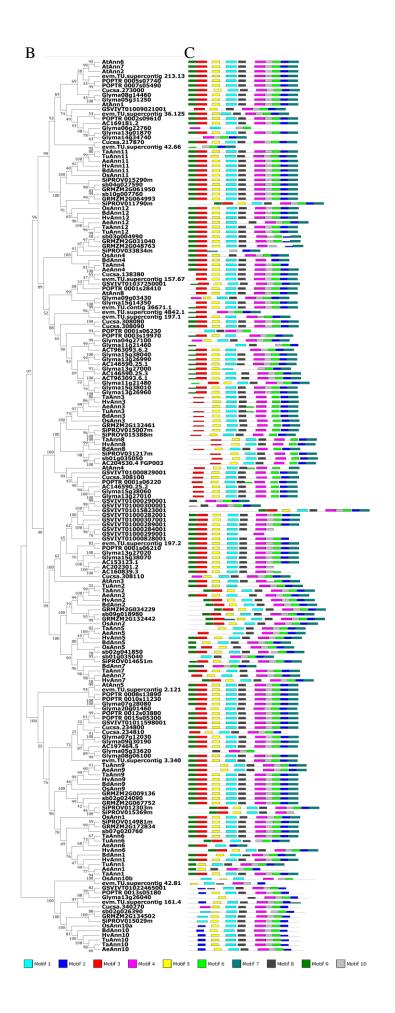
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<u>Motif 1</u>	• 2.1e-1736 • 65 sites	A TRANTREVING KEE CREASE ERAVORING VERALLA VO
<u>Motif 2</u>	• 5.7e-1343 • 50 sites	
<u>Motif 3</u>	• 9.5e-1143 • 45 sites	ASI SV EXY SCR. ALA RKIER AGRE IY IN LA R
<u>Motif 4</u>	• 9.0e-935 • 52 sites	
<u>Motif 5</u>	• 2.4e-833 • 59 sites	
<u>Motif 6</u>	• 3.1e-716 • 52 sites	
<u>Motif 7</u>	• 6.0e-497 • 63 sites	BUEITRSKA
<u>Motif 8</u>	• 1.2e-439 • 50 sites	
<u>Motif 9</u>	• 4.2e-257 • 9 sites	ADEVAL TKA ESOLOGI GYDERTAVAAL AMIRKOPEKRSOFRISE POLIK
<u>Motif 10</u>	• 5.8e-239 • 8 sites	RNOPERSKRIVRI I GODIOLE KLIKSTENNAL ESI M

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Additional file 5: Figure S2. Phylogenetic analysis and predicted structure of annexin proteins of 9 monocots plant and 7 discots plant. A. Ten Conserved sequence motifs identified in the amino acid sequences of 9 monocots plant (wheat, barley, *T.urartu, A.tauschii*, rice, maize, sorghum, *Brachypodium*, and *Setaria*)and 7 discots plant (*Vitis vinifera, Populus trichocarpa, Medicago truncatula, Cucumis Carica, papaya, Arabidopsis, Glycine_max*) as analyzed by MEME tools. The 1, 2, 3 and 4 motifs were found to be functionally associated with calcium-dependent phospho-lipid binding/calcium ion binding. B. Phylogenetic analysis of annexin protein sequences from 9 monocots plant and 7 discots plant. The tree was classified into five groups represented by roman letters (in black boxes) adjacent to the tree branches. C. The distribution of ten conserved motifs represented in the colored boxes was identified in the monocot and discots annexin protein sequences using the MEME 4.6.1 software. The order of the motif corresponds to their position in the individual protein sequences.