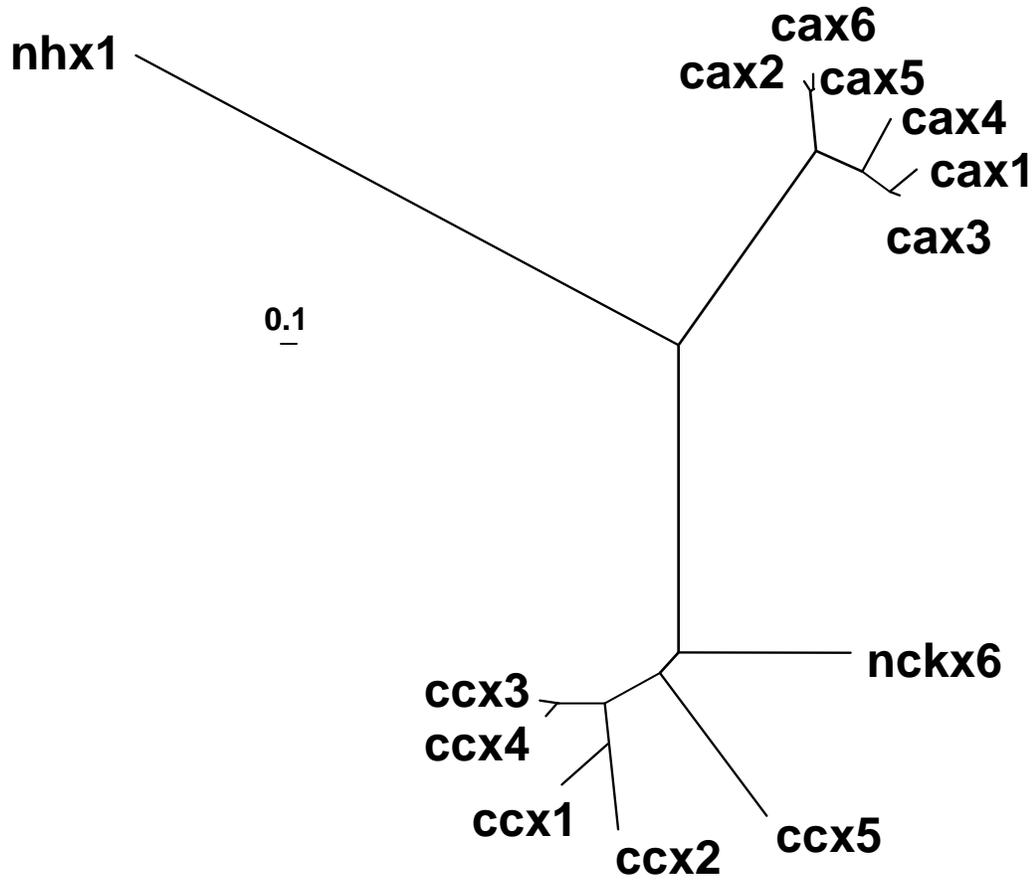


Supplemental Figure 1

A



Supplemental Figure 1

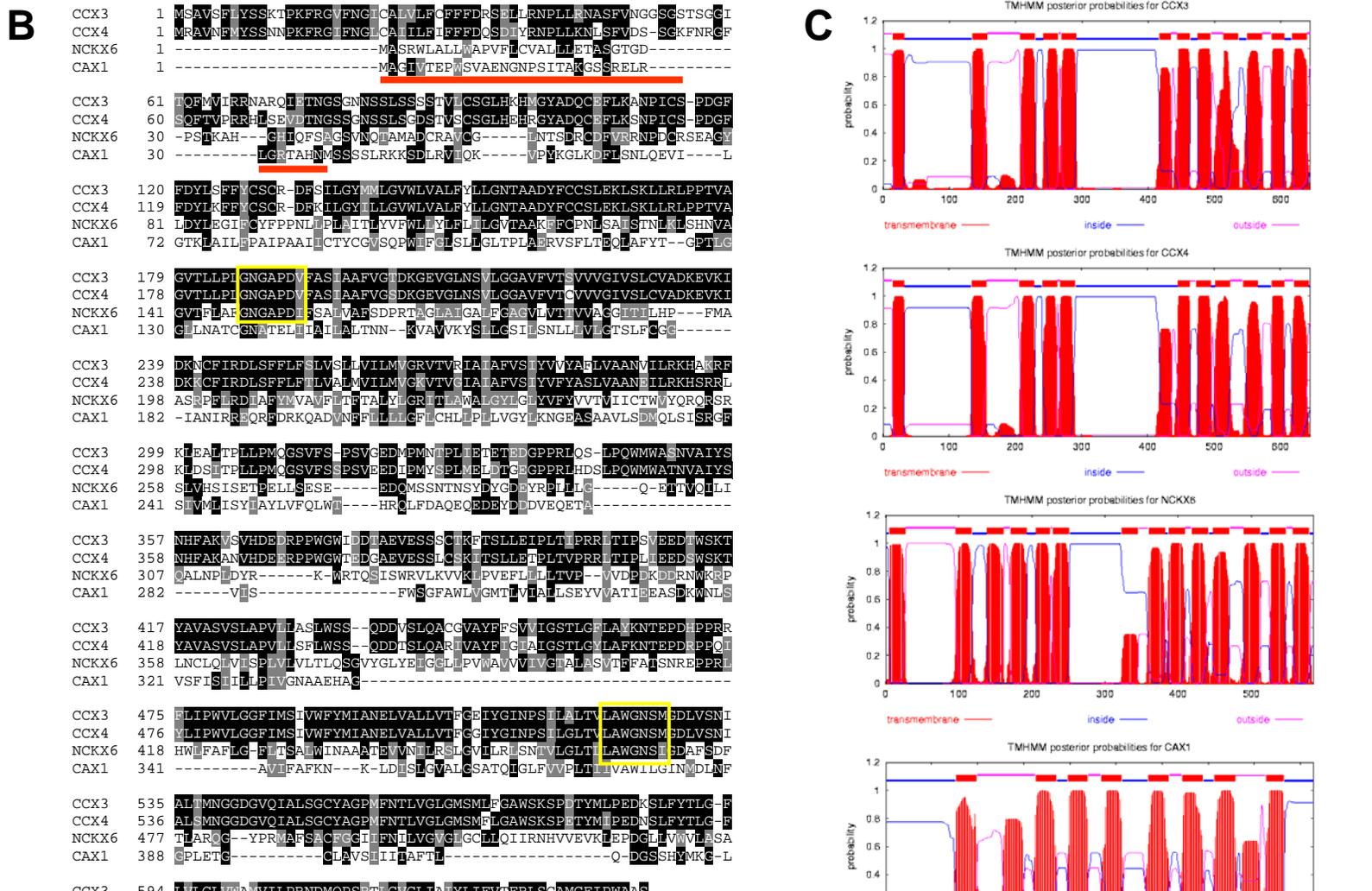


Figure S1. A, Phylogenetic tree showing the relative distance of predicted CAX to CCX proteins, including *HsNCKX6* (Phylip package from the protest software program ; Felsenstein, 1989) Bar represents percent change in amino acids. B, Protein sequence comparison of *AtCCX3* and *AtCCX4* to *AtCAX1* and *HsNCKX6*. Alignment of deduced amino acid sequences were performed using ClustalW 1.8 program (Thompson *et al.*, 1994). The autoregulatory domain of CAX1 is underlined in red. The yellow boxes mark the highly conserved $\alpha 1$ and $\alpha 2$ domains that are absent from *AtCAX1*. C, Predicted topology of *HsNCKX6*, *AtCAX1*, *AtCCX4* (*At1g54115*) and *AtCCX3* (*At3g14070*) analysis done using TMHMM algorithm (Sonnhammer *et al.*, 1998; Krogh *et al.*, 2001); <http://www.cbs.dtu.dk/services/TMHMM/>)

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