Suppl. Fig. 2. An initial alignment of calmodulin sequences was made using MAFFT v7.149b with the L-INS-i option (Katoh & Standley 2013). Using this aligned sequences, a Neighbor-Joining (Saitou & Nei 1987) tree was generated in MEGA-6 (Tamura et al. 2013) with the Kimura 2-parameter method (Kimura 1980). The rate of variation among sites was modelled with a gamma distribution (shape parameter = 0.34). The tree then served as a guide-tree in the second alignment using PRANK v.140710 (Löytynoja & Goldman 2005) using the +F option. A phylogenetic reconstruction was conducted using Maximum Likelihood analysis in raxmlGUI v1.5 using the GTR+Γ model (Silvestro & Michalak 2011). The partial calmodulin dataset was partitioned to exons and introns. The analysis was run with 500 bootstrap replicates.

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