



**Figure S1 Structural model of sequence differences between Arabidopsis A subunit isoforms** (A) A structural model of the RCN1 protein was generated by threading the RCN1 (NP\_173920) amino acid sequence onto the structure of the human A $\alpha$  regulatory subunit protein (Groves et al., 1999; PDB 1B3U). Alpha-helical regions of each HEAT repeat are shown in royal blue, with intra-repeat loops highlighted in yellow-green. Hydrophobic residues contributing to the interaction interface (Ruediger et al., 1994; Groves et al., 1999) are with white space-filling side-chains. Positions at which non-conservative substitutions occur in the PP2AA2 (NP\_189208) and PP2AA3 (NP\_172790) sequences are shown with red space-filling side-chains, and Tyr450 is shown in fuchsia. The amino-terminus is on the left. (B) Protein extracts of yeast cells carrying the constructs indicated were subjected to SDS-PAGE and immunoblotting as described in Figure 1, using anti-RCN1 antibodies to detect the fusion proteins. The positions of the RCN1-YFP (solid arrows) and Tpd3p (hollow arrow) proteins are indicated at right.