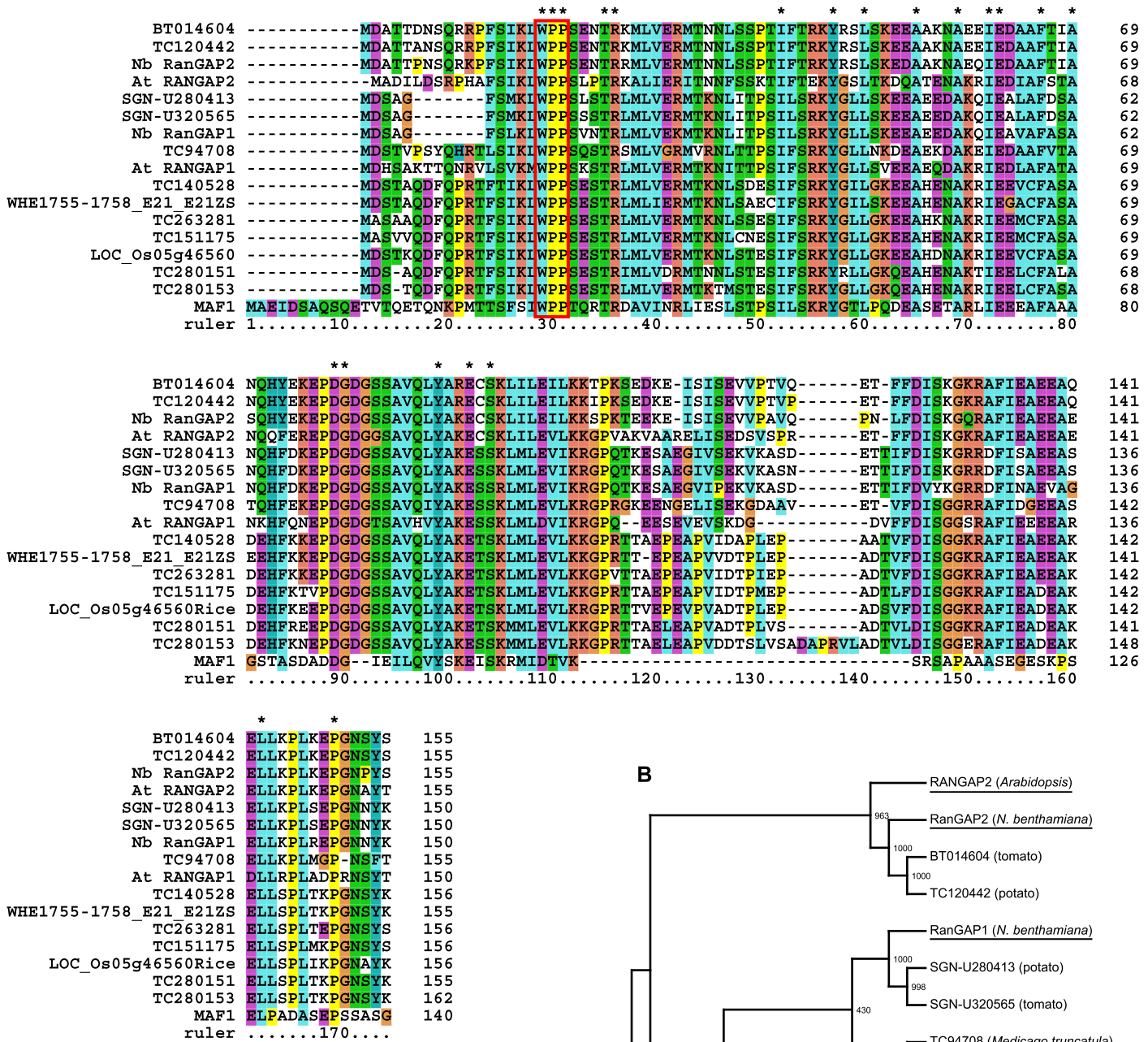


**A**



**Supplemental Figure 3.** Similarity analysis of plant RanGAP Proteins.

N-terminal RanGAP sequences (corresponding to amino acids 1-155 of RanGAP2) were aligned and a neighbour-joining tree was generated using ClustalX (Thompson et al., 1997; Chenna et al., 2003). (A) The WPP motif in the alignment is indicated with a red box. An asterisk above the alignment indicates an absolute conserved residue. (B) Bootstrap values for 1000 replicates are shown. MAF1 (AF118113), a tomato WPP domain protein, was used as an out-group to root the tree. The analysis indicates the presence of the At RANGAP1- and At RANGAP2 homologues in *Nicotiana benthamiana*, tomato and potato as no sequences derived from additional RanGAPs from these species could be found in the public databases. Accession numbers of the sequences were used from NCBI-, SGN- TAIR- and TIGR databases. At RANGAP1 (At3g63130), At RANGAP2 (At5g19320), Nb RanGAP1 (EF396238), Nb RanGAP2 (EF396237).