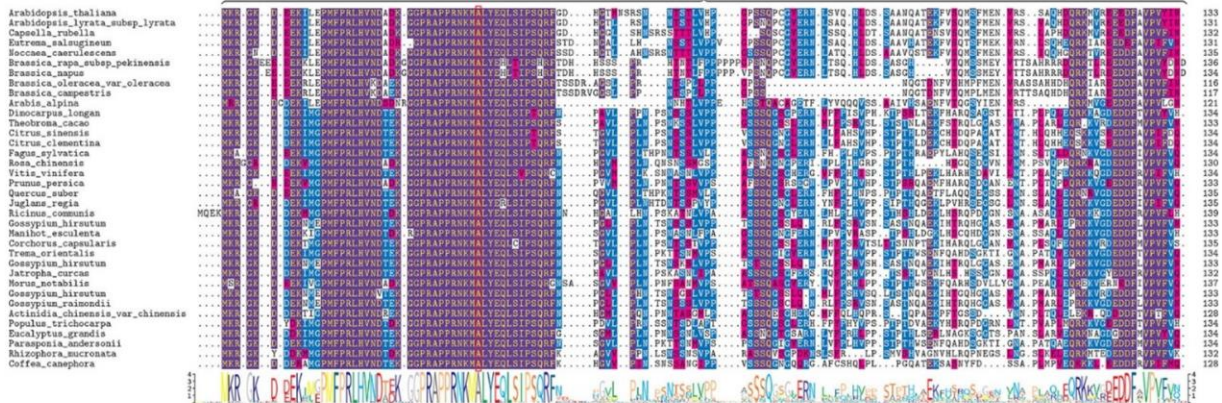


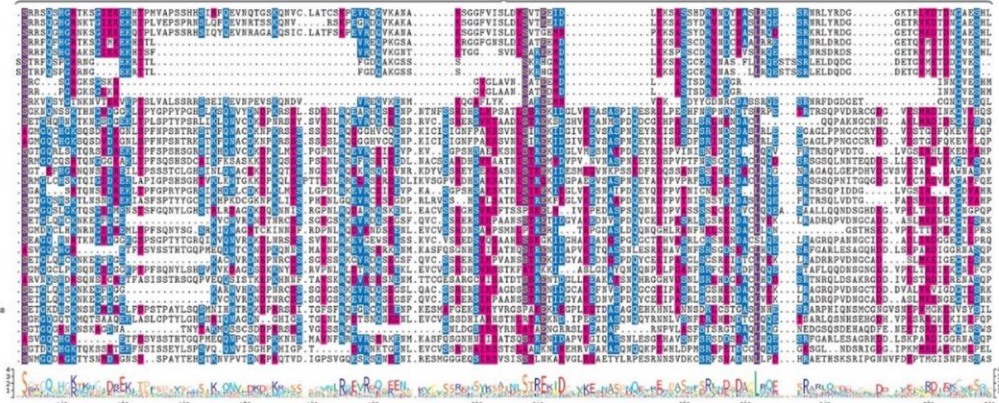
mediates the physical interaction with GI

mediates the physical interaction with PHYB



mediates the physical interaction with GI

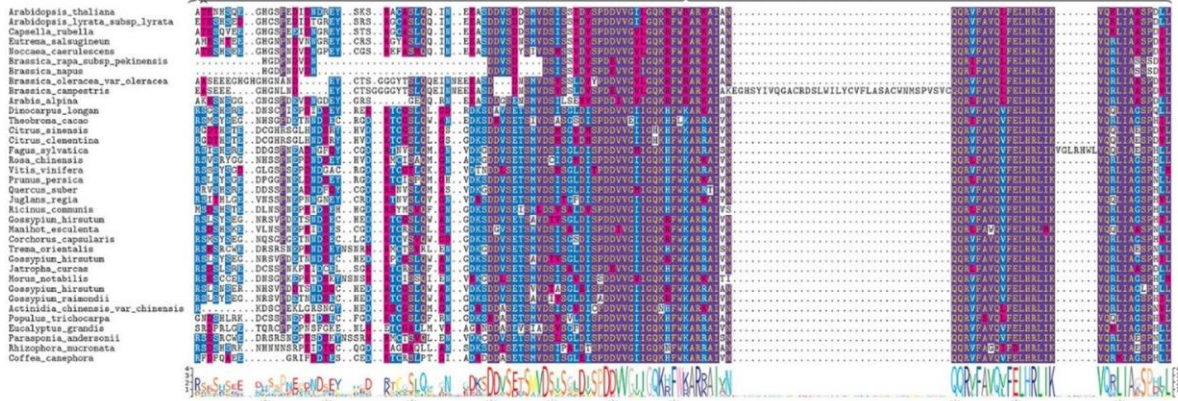
mediates the physical interaction with PHYB



mediates the physical interaction with GI

mediates the physical interaction with PHYB

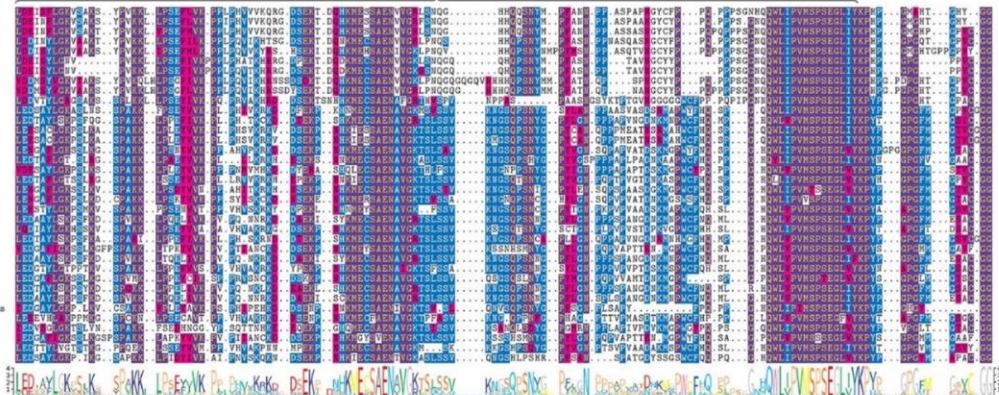
mediates the physical interaction with ELF4 and is crucial for ELF3 nuclear localization

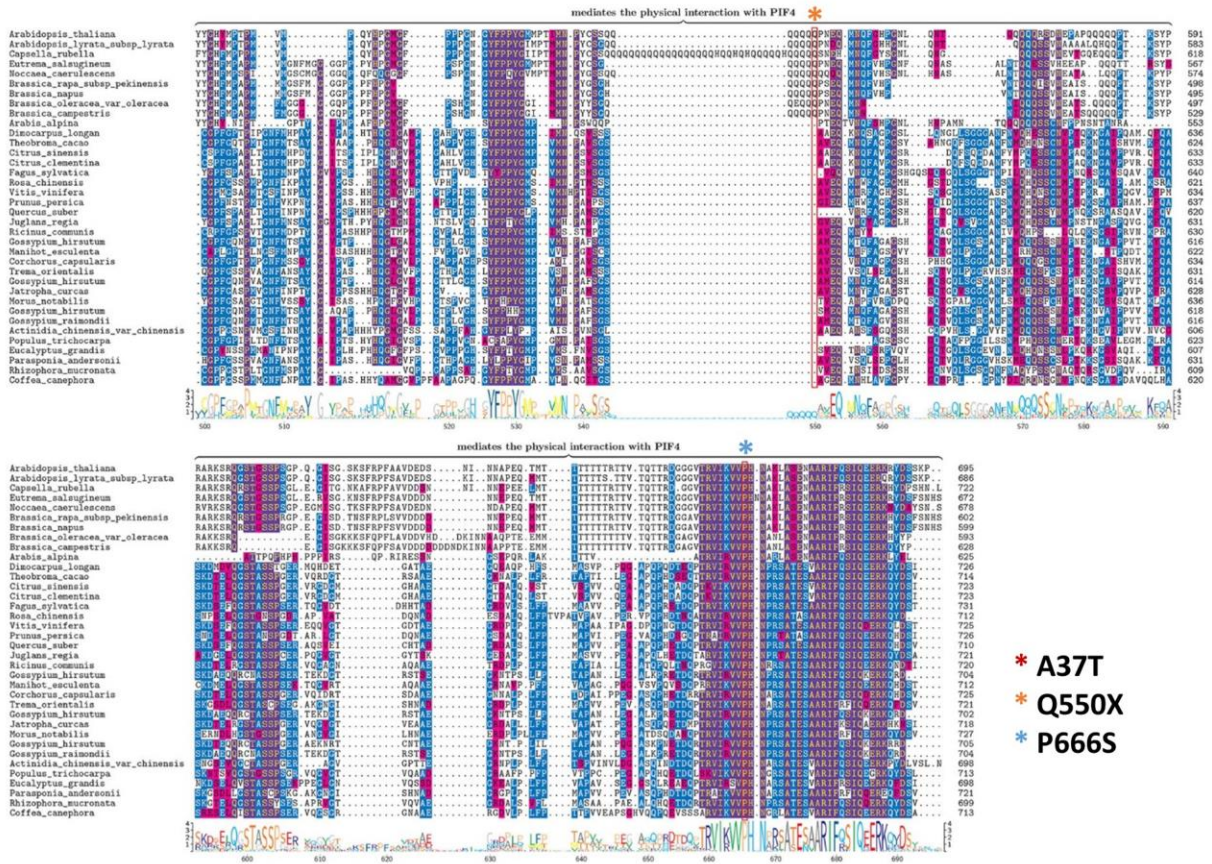


mediates the physical interaction with GI

mediates the physical interaction with PIF4

mediates the physical interaction with ELF4 and is crucial for ELF3 nuclear localization





Supplementary Figure S1. Alignment of plant ELF3 homologs. Amino acid sequence of Arabidopsis ELF3 (AT2G25930.1) was used as query sequence in BLAST against the UniProtKB database (<https://www.uniprot.org/>). Among top 50 sequences (E-value cutoff 10^{-124}), one gene for each species, which were best matched with AtELF3, was selected and total 36 ELF3 orthologs were represented. The alignment image was rendered using TeXshade (Beitz, 2000). Note that the amino acid residues corresponding to the substitution mutations identified in this study (asterisks and red box) are highly conserved across the homologs. The known interaction regions of ELF3 are shown above the aligned sequences, if identified. Sources for delimiting the regions of interaction with known ELF3 partners are as follows: ELF3 homodimerization, PHYB (Liu et al., 2001); ELF4, LUX (Nusinow et al., 2011); PIF4 (Nieto et al., 2015); GI, COP1 (Yu et al., 2008).