



File S2. Phylogenetic tree drawn by the Neighbor-Joining method. Amino acid sequences listed in File S1 were aligned using ClustalW (<http://clustalw.ddbj.nig.ac.jp/index.php?lang=ja>) and tree data were obtained. The tree was drawn using FigTree software (<http://tree.bio.ed.ac.uk/software/figtree/>). The tree includes: P-type PPR proteins from *Arabidopsis thaliana* (O'Toole et al., Mol. Biol. Evol., 2008, 25: 1120-1128); soybean PPR-type Rf-like (RFL) proteins (Fujii et al., PNAS, 2011, 108: 1723-1728); poplar RFL proteins (Fujii et al., PNAS, 2011, 108: 1723-1728); petunia RF protein (Bentolila et al., PNAS, 2002, 99: 10887-10892); radish RF protein (Brown et al. Plant J., 2003, 35: 262-272; Desloire et al., EMBO Rep., 2003, 4: 588-594; Koizuka et al., Plant J., 2003, 34: 407-415); and bvORF16. Clades including bvORF16 and AT5g42310 (At_CRP1), and RF and RFL are colored by green and red, respectively.