

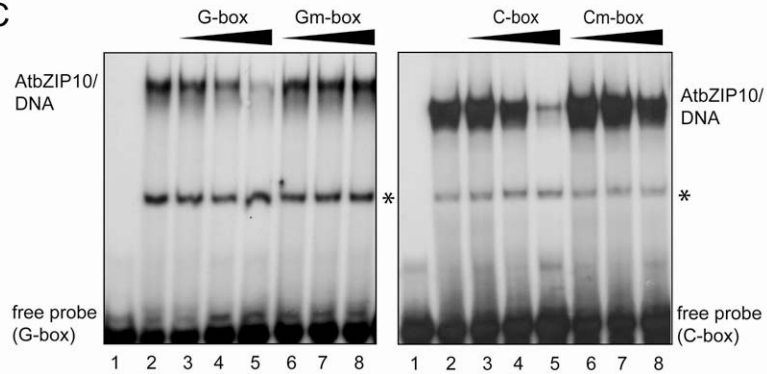
A



B



C



Supplemental Figure 1. *Arabidopsis* group C basic leucine zipper (bZIP) proteins are related to orthologous parsley proteins and bind consensus G- and C-box DNA sequences.

(A) Amino acid alignment of AtbZIP10, 9, 25 and 63 and PcCPRF2. Amino acids identical in all five bZIP factors are red, those common to at least three are yellow. Conservative amino acid exchanges are grey. The overlapping bipartite nuclear localisation sequences (NLS) and the basic DNA-binding domains (basic) are indicated by red and blue bars, respectively. Domains I and II and the acidic domain (acidic) typical of group C bZIP factors are marked by green bars. The amino acids forming the leucine zipper are marked by *.

(B) Coomassie Brilliant blue staining of recombinant AtbZIP10 used in this study. AtbZIP10 was expressed as (His)₆-tagged fusion protein in *E. coli* and purified by Ni-NTA affinity chromatography.

(C) AtbZIP10 specifically binds to G-box and C-box DNA elements in vitro. Electrophoretic mobility shift assay (EMSA) of recombinant AtbZIP10 incubated with either radioactively labelled G-box (left panel, lane 2) or C-box (right panel, lane 2) DNA. AtbZIP10-DNA complexes are indicated. Specificity was determined by competition analyses with increasing amounts (black triangles) of non-labelled wild type G-box (left panel, lanes 3-4) or wild type C-box (right panel, lanes 3-4) DNA, respectively, and mutated G-box (left panel, lanes 6-8) or C-box (right panel, lanes 6-8) DNA. Lanes 1; controls without protein. A non-specific DNA binding activity is marked by *.