А

В

AtbZIP10 AtbZIP9 AtbZIP25 AtbZIP63 PcCPRF2	1 UNSIFSIDDFS-DPFWETPPIPLNPDSSKPVTADEVSOOOPBWTFEMFLEEISSSAVSSEPLG 1 UDNHTAK-DIG
AtbZIP10 AtbZIP9 AtbZIP25 AtbZIP63 PcCPRF2	63 NNNNAIVGVSSAQSLPSVSGQNDFEDDSRFRDRDSGNLDCAAPMTTKTVIVDSDD RRVIK 32CFDLMNRD TCEUR 70 RSPPPVQSLSRLEETVDETEDVVEIQKPQNHRRLPVDDQGKNRNRAPSSDPVDSSAPVVVDPNQ HAIVK 47VPVDSEE RAFUK 51VPVDSEE RAFUK
AtbZIP10 AtbZIP9 AtbZIP25 AtbZIP63 PcCPRF2	123 NKUETECATVVSLRVGSVKPEDSTSSPETQLQPVQSSPLTQGELGVTSSLP 46 DS LWSEGLFPAGPERDAQSSICENLSADSPVSANKEEVRGGVR
AtbZIP10 AtbZIP9 AtbZIP25 AtbZIP63 PcCPRF2	acidic *
AtbZIP10 AtbZIP9 AtbZIP25 AtbZIP63 PcCPRF2	* * * * 244 ETQUNDEKGEHES LKQUSNMNHKYDE AVGET I KADI EHL AKVEMZETEKEVTGNPMLLGRSSGH 149 ETQUDSUKGDNET YKQUIDATQQFRS GTN EVIKSDVETL VWELADDLAA GSLTSSLNQLLQTHL 257 DTQUGQURAEHET INRUSDMNHKYDA AVDET IRADI ELL TUVMEETEKEVTGNPLHWSRPN 180 ETQUSQURAEHET INRUSDMNHKYDA AVDET VKANI ELL AKVEMZETEKEUTGRNPMFHNMPQIV 227 ETQUSQURAEHES LKRUTDISQRYNDAVDEV KADI ELA KVEMZEETEKEUTGRNPMFHNMPQSNSEI
AtbZIP10 AtbZIP9 AtbZIP25 AtbZIP63 PcCPRF2	314 NNNNRMPITGNNRMDSSSITPAYQPHSNLNHMSNQNIGIPTILPPRLGNNFAAPPSQTSSPLQ 219 SPPSHSISSLHYTGNTSPAITWHSNQNIGIPTILPPRLGNNFAAPPSQTSSPLQ 325 WHSQSLFPGMTLSGQNSSP 325 MGIPFSNTPSASSSIPPNSNHILKP-ANSSTNTSAGLAQNQRVETAN-FLPEQ 250 STVSLPSETSNSPDTSSQVTPEIISSGNKGKALIGCK 297 STIGMQSFSGSPSDTSADTTQDGSKQHFYQPAPTSHMPAQDQKIQNGLLQVPPVDNLQQHSASGPVEGNK
AtbZIP10 AtbZIP9 AtbZIP25 AtbZIP63 PcCPRF2	 377 RIRNGQNHHVTPSANPYGWNTEPQNDSAWPKKCVD 260 GLGNVSSEAVSCVSDIWP 377 VNREGMQNPFAPDSNLYETLPHWNHKH 289 MNRTASMRRVESLEHLQKRIRSVGDQ 367 MERTSSMQRVASLEHLQKRIRGGVSSCEAQVSGKQ

 C
 G-box
 Gm-box
 C-box
 Cm-box
 AtbZIP10/

 AtbZIP10/ DNA
 AtbZIP10/ DNA
 AtbZIP10/ Free probe (G-box)
 AtbZIP10/ Free probe
 Free prob
 Free probe
 F 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 *.