

```

AtbZIP19      1  MEDGELIDFSNQEVVTSSEMGELEPPSNCSMDSFDFGILM-DTNA-ACHTHHT-CNPT--GP
AtbZIP23     1  MDDGLELDFNSNM-----GGELP--SCSMDSFDFEILR-DS-H-ACHTHHT-CNPP--GP
TabZIPF1-7DL 1  MDDGDIDFSNPETFLCEAMGNPDPASCMSGTYFDLILNGDTHLACTHHT-CNPFV-HD
TabZIPF3b-7BL 1  MDDGNLD-----CSS-----MGSYFDGILM-DTEQVAC-----C-----
TabZIPF4-7AL 1  MDDGDIDFTNPETYLHPA-----MDSYFDDILK-DPEHLACTHTHACCNPHVVRHD
TabZIPF4-7DL 1  MDDADIDFTNPETYPRFA-----MDSYFDDVLR-DTQH-AC-----CNPHV-ED

```

## Group F motif 2

```

AtbZIP19     56  ENTHTHTCFHVHTKILPDESDE-----KVSTDDTAESC GKKG EKRELG NREAVRKYREK
AtbZIP23     48  ENTHTHTCIHVHTKILPD-----KVSTDDTSESSGKK---RELG NREAVRKYREK
TabZIPF1-7DL 59  LAHHTHTCVHVHTKIISA-SDDA-----AETSESLPESK--K--QRPSGNRAAVRKYREK
TabZIPF3b-7BL 29  --THHTHTCIHVHVKIAASASSDAGAETPAEFEDAHVTSRSKR--RPSGNQA AAVRKYREK
TabZIPF4-7AL 50  LAHHTHTCVHVHTKIIRESSDDV-----PETSESPQENNGPK--KREPGNRAAVRKYREK
TabZIPF4-7DL 42  LAHHAHTCVHVHTKIIFAESDDV-----AETSESPQQNSGAK--KRPSGNRAAVRKYRDK

```

## bZIP domain

```

AtbZIP19     110  KKAKAASLEDEVARLRVAVNQQLVKKRLQNQATLEAEVSRCLKCLLVDIRGRIDGEIGSFYQ
AtbZIP23     95  KKAKAASLEDEVMLRKA VNNQLLKR LQGQAALAEVTRLKCLLVDIRGRIDGEIGAFYQ
TabZIPF1-7DL 109  KKAHTALLEEEVAHLKAVNQQLVKKLQSHSALAELVARLRCLLVDIRGRIDGEIGTFYQ
TabZIPF3b-7BL 85  KKAHTALLEEEAARLRAMNKLAKKVDHAALEAEARLRCLLVDIRGRIDGEIGAFYQ
TabZIPF4-7AL 103  KKAHTALLEEEVARLKALNKQLVRR LQSHSALAEAEARLRCLLVDIRGRIDGEIGAFYK
TabZIPF4-7DL 95  RKARTALLEEEVARL KALNRQLV RKLQSHSALQAELASRLRYLLVDIRGRIDGEIGVFYQ

```

```

AtbZIP19     170  KPMAAN--TPSFSHM-----MNPCNV--QCD-DEVYCPQNVFGVNSQHGASINDQGLSGC
AtbZIP23     155  KPAVTN--VP-YSYM-----MHPCNV--QCVDNLYCLQN---GNNGEGASMNEQGLNGC
TabZIPF1-7DL 169  RTVKSND EVDQGSFLGGAQVMNSCGF--RCN-DQLYCNPGMQQARMLDDGVMSGQWLG
TabZIPF3b-7BL 145  RR-----PAKAGQGGAQVMSSCDFIATCE-QPHTCFLZ-----
TabZIPF4-7AL 163  RPVKNKDLADQGSFLGG--ARQVRV--RCN-DPPYCSPEM-QAMIMDDDVMSSFVWG
TabZIPF4-7DL 155  RPMRNDSDADQGSFLGG--AQVRV--RCN-EPLYRS-----YAG

```

```

AtbZIP19     220  DFDQLQCMANQN L NGNGSFSNVNTSVSNKRKGGHRASRAVZ
AtbZIP23     202  EFDQLECLANQN LAGKEIPVCSNGICTFTV-NGSGVNRKKGEPRAAKAVZ
TabZIPF1-7DL 225  -----QGACDSMGCVKPGSLNPPGC-RCGQMLZ
TabZIPF3b-7BL -----
TabZIPF4-7AL 215  -----QGACDIAN-NQWLQGLPDDVKRZ-----
TabZIPF4-7DL 191  -----HDNGZ-----

```

Figure S6. Multiple sequence alignment of cloned group F TabZIPs, AtbZIP19 and AtbZIP23. The Muscle algorithm (Edgar, 2004) was used for the alignment of sequences and the BoxShade software was used to generate this figure. The two group F motifs are labelled with lines above the alignment and shaded in yellow and green in consensus with the sequence prediction by Jakoby et al., (2002); motif 1 C[ST]HTH[ST]CNP[PT]GPE, motif 2 H[ST]HTC[FL]H[AV]HT. The bZIP domain common to all bZIP groups is also labelled and shaded in blue, the consensus of which is N-x<sub>7</sub>-R/K-x<sub>9</sub>-L-x<sub>6</sub>-L-x<sub>6</sub>-L, shown in red.