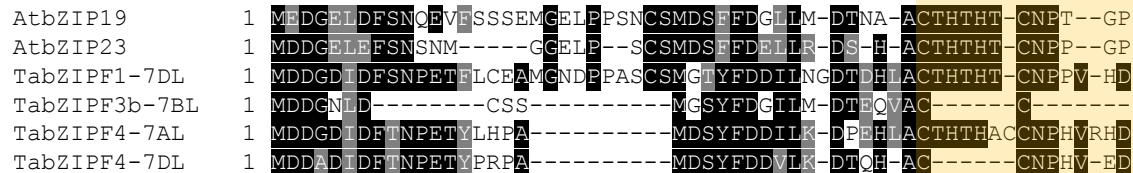


## Group F motif 1



## Group F motif 2



## bZIP domain

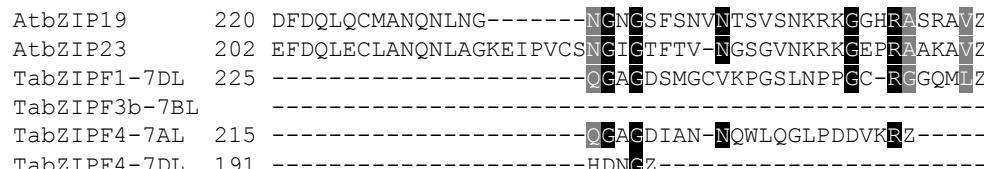
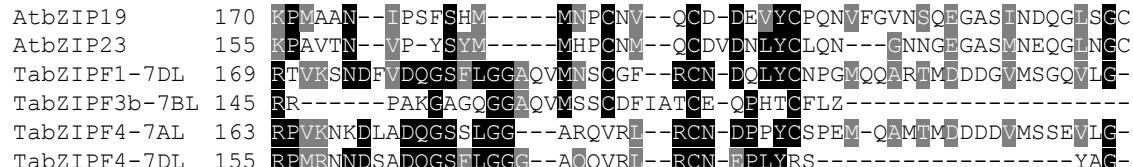


Figure S6. Multiple sequence alignment of cloned group F TabZIPs, AtbZIP19 and AtbZIP23. The Muscle algorithm (Edgar, 2004) was used for the alignment of sequences and the BoxShade software was used to generate this figure. The two group F motifs are labelled with lines above the alignment and shaded 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.