

Fig. 1 Suppl. Alignment of amino acid sequences of NHX1 proteins from *Medicago sativa*, *Zygophyllum xanthoxylum*; *Arabidopsis thaliana*, and *Atriplex gmelini*. Amino acids that are identical in all sequences evaluated are indicated by asterisks, highly similar positions in all sequences are indicated by colons, and weakly similar positions in all sequences are indicated by dots. Gray boxes No. 1 and No. 2 indicate the amiloride-binding domain and the C-terminal cytoplasmic regulatory domain, respectively. M1-12 indicates the 12 conserved hydrophobic regions in NHX proteins. degNHX-F and degNHX-R indicate the sites of degenerate primers corresponding to highly conserved amino acid sequences. Gaps were introduced to maximize alignment.

Fig. 2 Suppl. Promoter sequence of *NsNHX1* isolated by TAIL-PCR. *Cis*-elements described as being responsive to biotic and abiotic stresses are marked by *black boxes*.