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AtHKT1;1  30:LFFSFLGFLALKITKPRTTSRPHDFDLFFTSVSAITVSSMSTVDMEVFSN:79
HvHKT1;1  91:LSISFAGFLALKNLRPLNKPSPRNLDLMFTSVSTVTVSSMATVEMEEFSG:140
OsHKT1;1  81:VIISFAGFLALKNLKPQKPGPKDLDLLFTSVSTLTVSSMATVEMEDLSD:130
SitHKT1;1 81:MAISFAGFVALKNLNPHGKPVPSDFDLMFTSVSTATVSSMSTIQMEDLSD:130
SvHKT1;1  81:MVTSEFVGFLALKNLQSLGKPVLRDLDLMFTSVSTVTVSSMSTVQMEDLSE:130

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$P_A$

Fig. S1. Alignment of partial amino acid sequences of selected class I HKTs. Amino acid sequences of AtHKT1;1 (AK228564.1), HvHKT1;1 (JF496205.1), OsHKT1;1 (XP\_015641242.1), SitHKT1;1 (XM\_014805535.2), and SvHKT1;1 (LC545616) were aligned. Conserved serine residues among class I HKT sequences are surrounded by a square. The pore A loop region ( $P_A$ ) is colored pink.

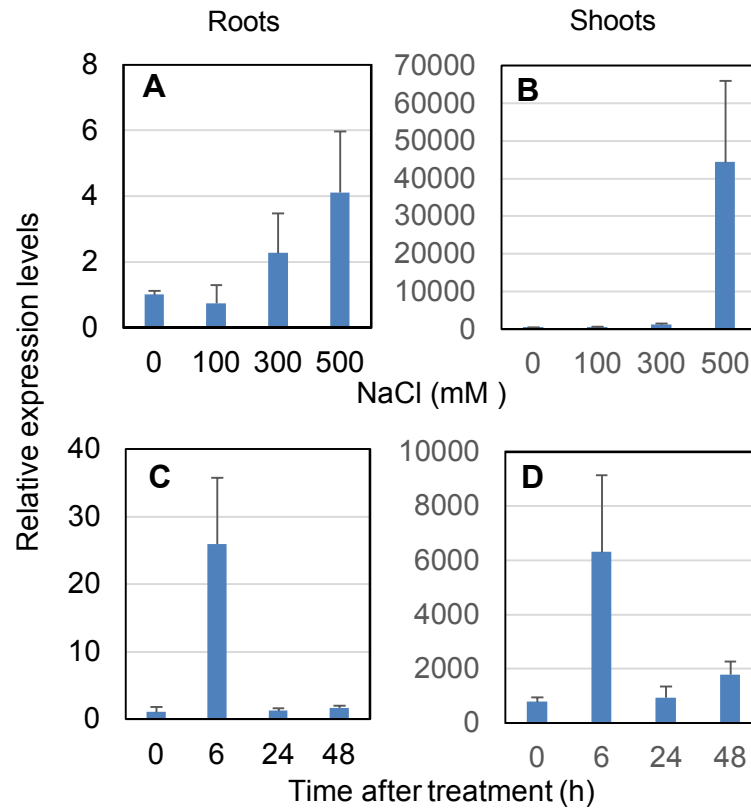


Fig. S2. Expression profiles of *SvHKT1;1* gene in *Sporobolus virginicus*.

The expression profiles of *SvHKT1;1* gene in roots and shoots of hydroponically grown *S. virginicus* were determined using qRT-PCR under different salt stress conditions (A, B) or at different time points after salt treatment (C, D). Plants grown in 1/2 MS medium were transferred to 1/2 MS medium supplemented with 0, 100, 300, or 500 mM NaCl and the roots (A) and shoots (B) were harvested at 48 h after the treatment. Plants grown in 1/2 MS medium were transferred to 1/2 MS medium supplemented with 500 mM NaCl and the roots (C) and shoots (D) were harvested at indicated time points. Expression levels relative to that in roots at 0 h after treatment (1.0) are shown. The *Actin* was used as a reference gene. Data are presented as mean  $\pm$  SE (n = 3, biological replicates).

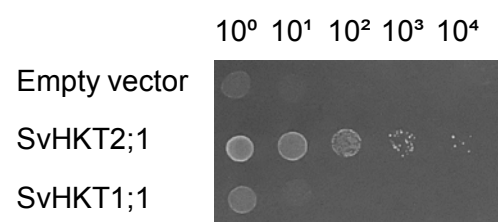


Fig. S3. Growth of yeast strain 9.3 transformed with the empty vector or the plasmid containing *SvHKT2;1* or *SvHKT1;1* gene.

SC/-His medium supplemented with 0.2 mM K<sup>+</sup> (0.7 mM Na<sup>+</sup>) were inoculated with serially diluted yeast cell suspensions and incubated for 3 d.