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MEICEAGSESPDDAVIEFGVALVIGIASRHLIRGTRV<mark>P</mark>YIVALIVIGVALCCIEYGTKHGIGKLGAGIRIWSAINPDLLLAVFLEALLFE ..MEEAGS.SPDDAVI<mark>I</mark>FGV<mark>S</mark>IVIGI<mark>G</mark>SRHLIRGTRV<mark>I</mark>YIVALIVIGVALCSIEYGTKHGIGKLGAGIRIWAAVNPDLLLAVFLEALLFE 90 TaSOS1 PtSOS1 87 TM 3 TM 1 TM 2 SSFSMEVHQIKKQNACKVLLA<mark>V</mark>FCVV<mark>I</mark>STVLIG<mark>AVKLTFFYLWA</mark>NKTSFLE<mark>S</mark>GLLSATDFVAVVALLK<mark>D</mark>LGASKKLSTI<mark>I</mark>EGESIMND SSFSMEVHQIKKC<mark>T</mark>AQMVLLA<mark>D</mark>FCVV<mark>I</mark>STVLIG<mark>S</mark>AVKLTFPY<mark>N</mark>NE</mark>KKTSFLE<mark>G</mark>GLLSATDFVAVVALLK<mark>V</mark>LGASKKLSTI<mark>V</mark>EGESIMND TaSOS1 180 PtSOS1 177 TM 3 TM 4 TM 5 TAIVVYQLFYRMV<mark>IC</mark>KTFDAGSIIKFISQVSLGAVALGIAFGIASVLWLGFIFNDTIIEISLTLAVSYIAFFTAQDA<mark>T</mark>EVSGVLAVMTLG TAIVV<mark>C</mark>QLFYRMV<mark>EC</mark>TTFDAGSIIKFL<mark>I</mark>QVSLGAVALGIAFGIASVLWLGFIFNDTIIEISLTLAVSYIAFFTAQDA<mark>F</mark>EVSGVLAVMTLG TaSOS1 270 PtSOS1 267 TM 7 TM MFYAAFAKTAFKGDSQ<mark>Q</mark>SLHHEWEN<mark>V</mark>AYIANTLIFILSCVVIADGVLQDNIHFERHG<mark>I</mark>SWGFI<mark>VI</mark>LY<mark>VFVQIS</mark>RAVVVQVI<mark>Y</mark>PLLRHFGY MFYAAFAKTAFKGDSQ<mark>D</mark>SLHHFWEM<mark>I</mark>AYIANTLIFILSCVVIADGVLQDNIHFERHG<mark>A</mark>SWGFI<mark>IVLYA</mark>FVLTARAVVVTVI<mark>E</mark>PLLRHFGY TaSOS1 360 PtSOS1 357 TM 7 TMS TM TKEATVI VÜSGLRGAVALSLSLSVKRASD<mark>SVC</mark>TYI<mark>KP</mark>EVGTMEVFFTGGIVFLTLT<mark>I</mark>NGSTTQFILHLLGLGKLSATKIRVLKYT VKEATVI VÜSGLRGAVALSLSLSVKRASD<mark>AD</mark>CPYI<mark>RS</mark>EVG<mark>V</mark>MEVFFTGGIVFLTLT<mark>V</mark>NGSTTQFILHLLGLGKLSATKIRVLKYT TaSOS1 450 447 PtSOS1 RΥ TM 10 TM 11 EM<mark>unkat</mark>eafgdlrddeelg<mark>ev</mark>dev<mark>nvkkyitcinnledeçahphiv</mark>pdkd<mark>dhi</mark>htmni<mark>k</mark>dtrvrlingvçaayw<mark>g</mark>mleegritqstani Em<mark>onkar</mark>eafgdlrddeelgr<mark>d</mark>evv<mark>uvkkyitcinnledeçahphda</mark>pdkd<mark>env</mark>htmni<mark>r</mark>dtrvrlingvçaaywemleegritqstani TaSOS1 540 537 PtSOS1 IMRSVDEAMDIVS<mark>S</mark>QSICDWKGLRSNVHFF<mark>N</mark>YYRFLQMSRLPRR<mark>I</mark>VTYFTVERLELGCYICAAFLRAHRIARRQIHDFLGDSEIARIVID IMRSVDEAMDIVS<mark>I</mark>QSICDWKGLRSNVHFF<mark>R</mark>YYRFLQMSRLPRF<mark>V</mark>VTYFTVERLELGCYICAAFLRAHRIARRQIHDFLGDSEIARIVID TaSOS1 630 PtSOS1 627 ESTA<mark>VGE</mark>GAKKFLEDVF<mark>V</mark>TFPQVI<mark>E</mark>ALKTRQVTYAVLTHLSEYIQDLGKTGLLEEKE<mark>I</mark>VHIDDALQTDLKKLKENPPI<mark>VKMERVE</mark>ELINT ESTA<mark>A</mark>GB<mark>E</mark>AKKFLEDVR<mark>I</mark>TFPQVI<mark>E</mark>ALKTRQVTYAVLTHLSEYIQDLGKTGLLEEKE<mark>N</mark>VHIDDALQTDLKKLKENPPI<mark>A</mark>KMFRV<mark>S</mark>ELINT TaSOS1 720 PtSOS1 717 HPIVGA<mark>LSAL</mark>VRDPLLS<mark>NTKETIKVHGTILYE</mark>EGSK<mark>R</mark>TGIWLVSTGIVKWTS<mark>RNC</mark>TRHSLDPILSHGSTLGLYEAL<mark>T</mark>GKPYICDIITES HPIVGAL<mark>HA</mark>VRDPLLS<mark>CTKETIKVHGTILYE</mark>EGSK<mark>E</mark>TGIWLVSTGIVKWTS<mark>CRLSTRHSLDPILSHGSTLGLYEALV</mark>GRPYICDIITES TaSOS1 810 PtSOS1 807 Cyclin Nucleotide Binding Domain VVHCFFIEAEKIEQIRQSDPSIEDE<mark>N</mark>WQESAIVIARI<mark>I</mark>IPQIFEKNAMREMRVLISERS<mark>SMN</mark>YYIKGEAIEIGHNNYC</mark>ILLEGFIKT<mark>ENR</mark> VVHCFFIEAEKIEQIRQSDPSIEDE<mark>I</mark>WQESAIVIARI<mark>E</mark>IPQIFEKNAMREMRVLISERS<mark>INNI</mark>YIKGE<mark>D</mark>IEIGHNYVCILLEGFIKI<mark>N.Q</mark> TaSOS1 900 PtSOS1 896 Cyclin Nucleotide Binding Domain TLITAFAVLIPSNTDINIFGLQSS<mark>ANNQ</mark>IDYCYTAPSYCVEARARAI<mark>IFEIGRLDIPAD</mark>IQRSASLLS<mark>ST</mark>LG<mark>E</mark>SRTQSKE<mark>E</mark>VGLLRWEBS TLIT<mark>P</mark>FAVLIPSNTDIN<mark>V</mark>FGLQSS<mark>VMNH</mark>IDYCYTAPSYCVEARARAI<mark>I</mark>FDI<mark>RSPEA</mark>ES<mark>DM</mark>QRSASLLS<mark>PR</mark>LGF<mark>B</mark>RTQSKEEIGLLRWE<mark>C</mark>S TaSOS1 990 PtSOS1 986 er.rssgegnaslaetroopgsfsaralovsmyg<mark>.smtigher</mark>roprlahvdgnokhsvsvervpsr<mark>.aad</mark>TRPLLSvrsegsnamkr Phersropgneslaetgropgsfsaralovsmyg<mark>smadd</mark>dmhtr<mark>oprpprvda</mark>nokhsssypkvpsr<mark>plsn</mark>TRPLLSvcsegsnamkr TaSOS1 1077 PtSOS1 1076 R......SAFAFATAFALAPFFPFLA<mark>EGOORFA</mark>VGEDDDSSDESVGEEVIVRVDSPSMIS<mark>ENPPSGPF</mark>RG R<mark>SAFAFAF</mark>AFAFAFAFAFAFAFAFF.ALAAGRHHFATTEDGNSSDES<mark>AGEEVIVRVDSPSMIA</mark>FQF...PF<mark>Q</mark>G 1141 1142 TaSOS1 PtSOS1

Supplementary material

Fig. S1. Sequence alignment of PtSOS1 with other SOS1 from higher plants. Sources of plasma membrane Na^+/H^+ antiporters and their GenBank accession numbers are as follows: PtSOS1 (*Puccinellia tenuiflora*, GQ452778) and TaSOS1 (*Triticum aestivum*, AY326952). The sequences were aligned with DNAMAN 6.0 software. Amino acid residues highlighted in black are conserved in the two

transporters. The identical and different amino acid residues were indicated with white and green, respectively. The eleven putative trans-membrane domains (TM 1-TM 11) and cyclic nucleotide binding domain are underlined, respectively.

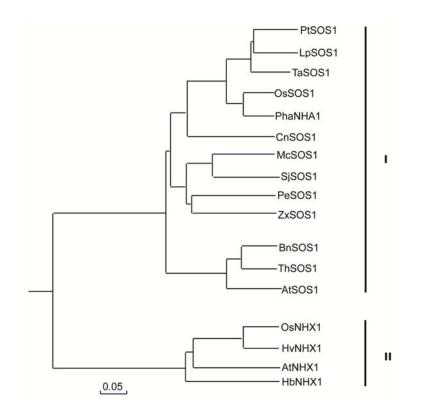


Fig. S2. Phylogenetic tree of the SOS1. The tree was constructed by the Neighborjoining method. The proteins are as follows: PtSOS1 (*Puccinellia tenuiflora*, GQ452778), TaSOS1(*Triticum aestivum*, AY326952), OsSOS1 (*Oryza sativa*, AY785147), PhaNHA1 (*Phragmites australis*, AB244217), LpSOS1 (*Lolium perenne*, AY987046), CnSOS1(*Cymodocea nodosa*, AJ427294), PeSOS1 (*Populus euphratica*, DQ517530), SjSOS1 (*Suaeda japonica*, AB198179), ZxSOS1 (*Zygophyllum xanthoxylum*, GU177864), BnSOS1 (*Brassica napus*, EU487184), McSOS1 (*Mesembryanthemum crystallinum*, EF207776), ThSOS1 (*Thellungiella halophila*, EF207775), AtSOS1 (*Arabidopsis thaliana*, AF256224), HvNHX1 (*Hordeum vulgare*, AB089197), OsNHX1 (*Oryza sativa*, AB021878), HbNHX1 (*Hordeum brevisubulatum*, DQ285410) and AtNHX1 (*Arabidopsis thaliana*, AF510074).