Table 1 Suppl. Different transporter gene promoters and their activity and localization.

Gene family	Gene source	Gene and size	Motif/elements	Localization	Activity	Reference
NHX	*Arabidopsis thaliana*	*AtNHX1* 1900 bp	ABRE(putative)	all tissues except root tips, strong activity in root hairs and leaves	NaCl, KCl, ABA	Shi and Zhu (2002)
		AtNHX1 *AtNHX2*	MYC/MYB MYC/MYB	- -	- -	Yokoi *et al.* (2002)
	Beta vulgaris	*BvNHX1* 2464 bp	MYB 1AT, MYC, MYB ST1, and napA	hydathodes, trichomes, root tips and elongation regions, sepals, anthers, fruit pedicels,	Na_2SO_4, NaCl, KCl, mannitol	Adler *et al.* (2010)
	Oryza sativa	*OsNHX1* 2100 bp	ABRE (CACGTGGC), as1 MYCRS, MYBRS	stele, lateral roots, vascular bundles, water pores, basal part of seedling shoots, guard cells and trichomes	NaCl, mannitol, ABA	Fukuda *et al.* (2011)
	Oryza sativa	*OsNHX2* -	ABRE (CACGTGGC), ABRE (CCACGTGG), as1, MYCRS, MYBRS	-	-	
	Oryza sativa	*OsNHX3* -	ABRE (ACGTCGGC), as1, MYCRS	-	-	
	Oryza sativa	*OsNHX5* 1500 bp	MYCRS, MYBRS	stele, lateral roots, vascular bundles, water pores, basal part of seedling shoots, root tips and pollen grains	NaCl, ABA	
SOS1	*Arabidopsis thaliana*	*AtSOS1* 981 bp	ABRE RATCAL, TBOXATGAPB DPBFCOREDCDC3 ABRE, ARE, AG, AP1, ARR1AT, PIF3, CDC5, Athb-1, Athb-5, AtMYB77, box b, MYB4, Myba, PtMYB4, LTR, LTRECOREATCOR15, MYB1AT, MYCCONSENSUSAT, WA, ACGTAT ERD1, box 4, GT1CONSENSUS, MYBCORE, WBOXATNPR1 and certain light responsive elements	-	-	Oh *et al.* (2010)
	Brassica juncea	*BjSOS2* 713 bp	ABRE, GARE, TCA, MYCCONSENSUSAT, MYBCORE, Aux RR-core and TGA	shoots and roots	NaCl, desiccation, heat, cold, ABA	Kaur *et al.* (2015)
	Salichornia brachiata	*SbUSOS1* 734 bp	DOF, GT elements, ABRE, root specific, (RHE transcription factors) and RAV1-A/RAV1-B	leaf bases and stems	NaCl	Goyal *et al.* (2013)*
	Thellungiella parvula	-	ASF1, TGA box, ARF, AGL3, AG, PY-Box, ARR1AT, PIF3, Rav1, Athb-1,5&9, MYB4, CCA1, LTRECOREATCOR15, GA-3, ARR10, TC-	-	-	Oh *et al.* (2010)

			rich repeats, AtMYC2, MYCATERD1, MYCCONSENSUSAT, WA, GT2, ACE, GA, ATCT, motif VI, ERE, ACGTAT ERD1, GAREAT, HSE, ATCT motif, box 4, G-box, box 1, GATABOX, CGTCA-motif, CCA1,			
	Thellungiella salsuginea	-	ABRE RATCAL, DPBFCOREDCDC3, ABRE, I-box, E5-core, ASF1 motif , CAMV,ARE, box 1, AP1, ARR1AT, PIF3, ANT,LTR, Athb-9, ARR10, TC-rich repeats, AtMYC2 , G-box, MYCATERD1, MYB1AT, box 4, MYCCONSENSUSAT,WA,PB1,TA rich region, ERE, ACGTAT ERD1, GAREAT,GA-motif, GATA-motif, TCT-motif, GATABOX, CGTCA-motif, MBS, MYBCORE, S1, TCA-element, SURECOREATSULTR11, SV40COREENHAN	-	-	
	Triticum aestivum	*prSOS1-D* 2661 bp *PrSOS1-AB* 2745 bp	ABRELATERD, ACGTATERD1, ABRERATCAL, MYBCORE, MYBCOREATCYCB1, DOFCOREZM, WRKY7lOS GT1GMSCAM4, TATABOX, BS1EGCCR	seedling stage: roots, root tips, stems, leaves mature stage: shoots, roots	NaCl, mannitol, ABA	Feki *et al.* (2014)
HPPase	*Zea mays*	*ZmGAPP* 1468 bp	Box E, CuRE, LTRE , GTGA, GAGAC, G-Box , MBS/ MYB, Sp1,GCC-box, GC, GARE, Pollen1lelat52, O2-site, TGTCACA, CAAT-box, GCN4, Gap-box, Skn-1, TGACG, GT-1 and ACE	all tissues	NaCl, PEG	Hou *et al.* (2016)
	Arabidopsis thaliana	*AVP2/AVPL1* 1400 bp	-	mainly trichomes and stamen filaments	-	Mitsuda *et al.* (2001)
		AVP1 1700 bp	DOF2	in young seedlings: root apical meristem, leaf primordia, cotyledons and leaves in adult plants: source leaves, leaf and flower primordia, roots, reproductive tissues; conspicuously in phloem tissue of leaf vascular	-	Pizzio *et al.* (2015)

				bundles		
	Thellungiella halophila	*TsVP1* 2200 bp	SP1, ACE, AE Box, AAAC, HD-Zip1, ARE, MBS, ABRE, G-box, AT-rich sequence, Box-4, Box-1, HSE, GT1, TCA, CGCTA, Box III, TC	almost all tissues except seeds	NaCl	Sun *et al*. (2010)
	Oryza sativa	*OVP3* 2100 bp	AAACAAA, AGCAGC, TCATCAC and GTTHGCAA, GTGGGCCCG, GCBP-2, TATA-like	higher in roots (stelar region) than leaves	anoxia	Liu *et al*. (2010)
VATPase c	*Pennisetum glaucum*	*PgVHA-c1* 1037 bp	TATA-box, CAAT, GC- motif binding region, GC repeats, putative TCA-Box, LTRE like,DRE like, ABRE like sequences	shoot hairs, panicles, young anthers, basal part of stamens and gynoecium, stamen and petal hairs	-	Tyagi *et al.* (2005)
HKT	*Triticum monococcum*	*TmHKT1;5*	CAAT, CATT, circadian, G-box, LTR,TC-rich repeats, ERE, ARE, skn-1, ACE, I-box, MNF-1, O2- site, ATCT, CCAAT- box, CGTCA- box, Sp1, TGACG, GARE	roots	NaCl	Babgohari *et al*. (2014)*
	Triticum aestivum	*TaHKT1;5*	CAAT box, CATT motif, circadian, G-box, LTR,AE-box, AE-box, MRE, , LTR,TC-rich repeats, ERE, Box-1, Box-4, HSE,ERE,TATA-box, skn-1motif, ACE, MNF-1, , ATCT-motif, CCAAT- box, CGTCA- box, Sp1, TGA- element, TGACG motif, GARE- motif, CCGTCC- box, A-box	more in leaves	NaCl, heat	Babgohari *et al*. (2014)*
	Solanum lycopersicum	*SlHKT1;1* 1319 bp	ARE, CAAT, CACTFT*PPCA1*, MYB1AT, MYB2AT, MYBCONSENSUSAT,MYBCORE, PREATPRODH, PRECONSCRHSP70A, SEF4MOTIFGM7S, POLASIG, SORLREP3AT, TATA- box, TCA-element.	salinity treatment reduces expression in leaves and stems but increases in roots	NaCl	Asins *et al*. (2013)*
	Solanum lycopersicum	*SlHKT1;2* 814 bp	ARR1AT, CAAT, HSE, CACTFTPPCA1, PRECONSCRHSP70A			Asins *et al*. (2013)*

*The promoter was not overexpressed in plants.