

			1	50
Ni-HKT1;4	(1)		MPTSRRALAGGALSMHVAYFLAISCLGYGLLGVLVKVP	EPGAAPRRIDRFF
Po-HKT1;4	(1)		MPTSRRALAGGALSMHVAYFLAISCLGYGLLGVLVKVP	EPGAAPRRIDRFF
Ni-HKT1;4 truncated	(1)		MPTSRRALAGGALSMHVAYFLAISCLGYGLLGVLVKVP	EPGAAPRRIDRFF
			51	100
Ni-HKT1;4	(51)		TAVSAATVSSMSTVEMEVFSNGQLVVLTVLMLLGG	EVFVSLVGLASKWSK
Po-HKT1;4	(51)		TAVSAATVSSMSTVEMEVFSNGQLVVLTVLMLLGG	EVFVSLVGLASKWSK
Ni-HKT1;4 truncated	(51)		TAVSAATVSSMSTVEMEVFSNGQLVVLTVLMLLGG	EVFVSLVGLASKWSK
			101	150
Ni-HKT1;4	(101)		LRSDAMDRSRVESHGDVALADIDGGDVENPTSSGEE	AASRRRPMADATL
Po-HKT1;4	(101)		LRSDAMDRSQRVESHGDVALADIDGGDVENPTSSGEE	AASRRRPMADATL
Ni-HKT1;4 truncated	(101)		LRSDAMDRSRVESHGDVALADIDGGDVENPTSSGEE	AASRRRPMADATL
			151	200
Ni-HKT1;4	(151)		RHNAVRALFYIVLAIFAVVHVVGAVAVAAAYVLAS	PGARRTLGDKSLNTWT
Po-HKT1;4	(151)		RHNAVRALFYIVLAIFAVVHVVGAVAVAAAYVLAS	PGARRTLGDKSLNTWT
Ni-HKT1;4 truncated	(151)		RHNAVRALFYIVLAIFAVVHVVGAVAVAAAYVLAS	PGARRTLGDKSLNTWT
			201	250
Ni-HKT1;4	(201)		FAVFTTVSTFVSNCGFMPTNENMVVFKRDAPLQ	LLLVPQVLAGNTLFAPLL
Po-HKT1;4	(201)		FAVFTTVSTFVSNCGFMPTNENMVVFKRDAPLQ	LLLVPQVLAGNTLFAPLL
Ni-HKT1;4 truncated	(201)		FAVFTTVSTFVSNCGFMPTNENMVVFKRDAPLQ	LLLVPQVLAGNTLFAPLL
			251	300
Ni-HKT1;4	(251)		AACVWAAAAATRREELVEMAREGGRAAAAGYAH	LMPARRCWMLAATVAAF
Po-HKT1;4	(251)		AACVWAAAAATRREELVEMAREGGRAAAAGYAH	LMPARRCWMLAATVAAF
Ni-HKT1;4 truncated	(251)		AACVWAAAAATRREELVEMAREGGRAAAAGYAH	LMPARRCWMLAATVAAF
			301	350
Ni-HKT1;4	(301)		VAVLMALVCGMEWGGALQGMSPWEKVVNALFLAV	NARHTGESTV DLSILA
Po-HKT1;4	(301)		VAVLMALVCGMEWGGALQGMSPWEKVVNALFLAV	NARHTGESTV DLSILA
Ni-HKT1;4 truncated	(301)		VAVLMALVCGMEWGGALQGMSPWEKVVNALFLAV	NARHTGESTV DLSILA
			351	400
Ni-HKT1;4	(351)		PAILVLFVLMYLPPTYTWFPEENSTTKDSNAEN	QIRLLESTLTSQLS
Po-HKT1;4	(351)		PAILVLFVLMYLPPTYTWFPEENSTTKDSNAEN	QIRLLESTLTSQLS
Ni-HKT1;4 truncated	(351)		PAILVLFVLMYLPPTYTWFPEENSTTKDSNAEN	QIRLLESTLTSQLS
			401	450
Ni-HKT1;4	(401)		YLTIFVIAICITERRRLKEDPLNFSVLSIVVEV	VSAYGNVGFSGYSCSR
Po-HKT1;4	(401)		YLTIFVIAICITERRRLKEDPLNFSVLSIVVEV	VSAYGNVGFSGYSCSR
Ni-HKT1;4 truncated	(401)		YLTIFVIAICITERRRLKEDPLNFSVLSIVVEV	VSAYGNVGFSGYSCSR
			451	500
Ni-HKT1;4	(451)		QINPDHLCTDKWTGFVGRWSDSGKLILIFVMFF	GRLKKFSMKGGKAWKLS
Po-HKT1;4	(451)		QINPDHLCTDKWTGFVGRWSDSGKLILIFVMFF	GRLKKFSMKGGKAWKLS
Ni-HKT1;4 truncated	(451)		QVN-----	

Figure S6. OsHKT1;4 protein sequence comparison. The Pokkali (Po) *OsHKT1;4* transcript encoding a functional protein was fully sequenced and its nucleotide sequence translated into an amino acid sequence. Po-*OsHKT1;4* encodes for a 500 amino acid protein which share 99.8% homology with the *OsHKT1;4* protein from Nipponbare (Ni). The sole difference between the two functional *OsHKT1;4* proteins is a R to Q substitution in position 110 in Pokkali. The structural modeling of the *OsHKT1;4* protein predicts that this substitution is localized in the cytoplasm-exposed loop inter-connecting membrane α -helices between the first two domains of the protein and thus does not affect Na^+ transport rate. Ni-*OsHKT1;4* and Po-*OsHKT1;4* were aligned against a predicted truncated protein generated by the splice variants. This predicted splice variant protein is 47 amino acid residues shorter and differs from the full-length *OsHKT1;4* protein in its 19 C-terminal residues. The protein sequences were aligned using Align X (Invitrogen). Homologous regions are highlighted in yellow or blue. The conserved Val residue in position 344 is highlighted in green.