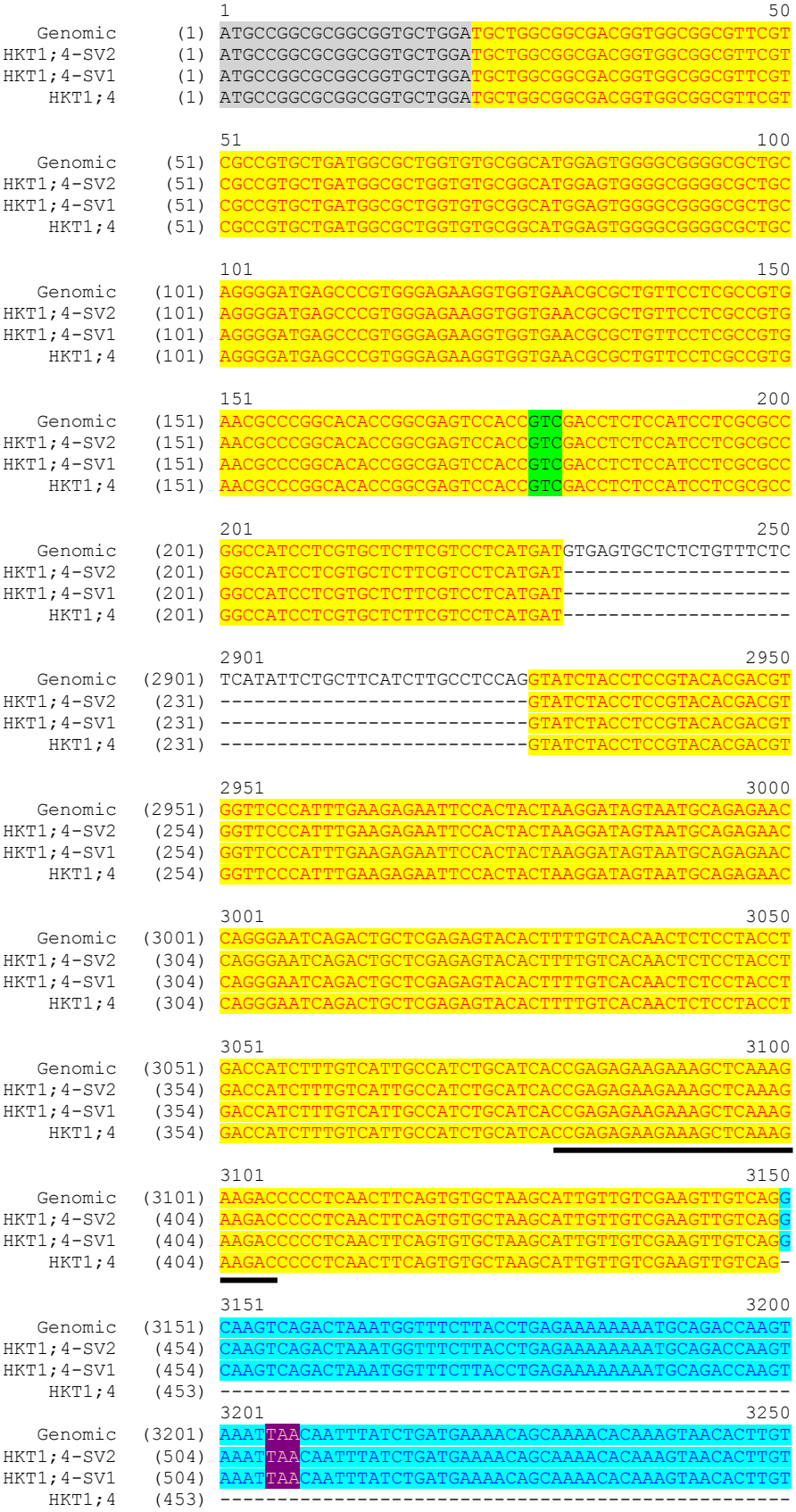
1 50
Genomic (1) ATGCCGGCGCGGCGGTGCTGGATGCTGGCGGCGACGGTGGCGGCGTTCGT
HKT1;4-SV2 (1) ATGCCGGCGCGGCGGTGCTGGATGCTGGCGGCGACGGTGGCGGCGTTCGT
HKT1;4-SV1 (1) ATGCCGGCGCGGCGGTGCTGGATGCTGGCGGCGACGGTGGCGGCGTTCGT
HKT1;4 (1) ATGCCGGCGCGGCGGTGCTGGATGCTGGCGGCGACGGTGGCGGCGTTCGT
51 100
Genomic (51) CGCCGTGCTGATGGCGCTGGTGTGCGGCATGGAGTGGGGCGGGGCGCTGC
HKT1;4-SV2 (51) CGCCGTGCTGATGGCGCTGGTGTGCGGCATGGAGTGGGGCGGGGCGCTGC
HKT1;4-SV1 (51) CGCCGTGCTGATGGCGCTGGTGTGCGGCATGGAGTGGGGCGGGGCGCTGC
HKT1;4 (51) CGCCGTGCTGATGGCGCTGGTGTGCGGCATGGAGTGGGGCGGGGCGCTGC
101 150
Genomic (101) AGGGGATGAGCCCGTGGGAGAAGGTGGTGAACGCGCTGTTCCTCGCCGTG
HKT1;4-SV2 (101) AGGGGATGAGCCCGTGGGAGAAGGTGGTGAACGCGCTGTTCCTCGCCGTG
HKT1;4-SV1 (101) AGGGGATGAGCCCGTGGGAGAAGGTGGTGAACGCGCTGTTCCTCGCCGTG
HKT1;4 (101) AGGGGATGAGCCCGTGGGAGAAGGTGGTGAACGCGCTGTTCCTCGCCGTG
151 200
Genomic (151) AACGCCCGGCACACCGGCGAGTCCACCGTCGACCTCTCCATCCTCGCGCC
HKT1;4-SV2 (151) AACGCCCGGCACACCGGCGAGTCCACCGTCGACCTCTCCATCCTCGCGCC
HKT1;4-SV1 (151) AACGCCCGGCACACCGGCGAGTCCACCGTCGACCTCTCCATCCTCGCGCC
HKT1;4 (151) AACGCCCGGCACACCGGCGAGTCCACCGTCGACCTCTCCATCCTCGCGCC
201 250
Genomic (201) GGCCATCCTCGTGCTCTTCGTCCTCATGATGTGAGTGCTCTCTGTTTCTC
HKT1;4-SV2 (201) GGCCATCCTCGTGCTCTTCGTCCTCATGAT----------
HKT1;4-SV1 (201) GGCCATCCTCGTGCTCTTCGTCCTCATGAT----------
HKT1;4 (201) GGCCATCCTCGTGCTCTTCGTCCTCATGAT----------
2901 2950
Genomic (2901) TCATATTCTGCTTCATCTTGCCTCCAGGTATCTACCTCCGTACACGACGT
HKT1;4-SV2 (231) ----------GTATCTACCTCCGTACACGACGT
HKT1;4-SV1 (231) ----------GTATCTACCTCCGTACACGACGT
HKT1;4 (231) ----------GTATCTACCTCCGTACACGACGT
2951 3000
Genomic (2951) GGTTCCCATTTGAAGAGAATTCCACTACTAAGGATAGTAATGCAGAGAAC
HKT1;4-SV2 (254) GGTTCCCATTTGAAGAGAATTCCACTACTAAGGATAGTAATGCAGAGAAC
HKT1;4-SV1 (254) GGTTCCCATTTGAAGAGAATTCCACTACTAAGGATAGTAATGCAGAGAAC
HKT1;4 (254) GGTTCCCATTTGAAGAGAATTCCACTACTAAGGATAGTAATGCAGAGAAC
3001 3050
Genomic (3001) CAGGGAATCAGACTGCTCGAGAGTACACTTTTGTCACAACTCTCCTACCT
HKT1;4-SV2 (304) CAGGGAATCAGACTGCTCGAGAGTACACTTTTGTCACAACTCTCCTACCT
HKT1;4-SV1 (304) CAGGGAATCAGACTGCTCGAGAGTACACTTTTGTCACAACTCTCCTACCT
HKT1;4 (304) CAGGGAATCAGACTGCTCGAGAGTACACTTTTGTCACAACTCTCCTACCT
3051 3100
Genomic (3051) GACCATCTTTGTCATTGCCATCTGCATCACCGAGAGAAGAAAGCTCAAAG
HKT1;4-SV2 (354) GACCATCTTTGTCATTGCCATCTGCATCACCGAGAGAAGAAAGCTCAAAG
HKT1;4-SV1 (354) GACCATCTTTGTCATTGCCATCTGCATCACCGAGAGAAGAAAGCTCAAAG
HKT1;4 (354) GACCATCTTTGTCATTGCCATCTGCATCACCGAGAGAAGAAAGCTCAAAG
3101 3150
Genomic (3101) AAGACCCCCTCAACTTCAGTGTGCTAAGCATTGTTGTCGAAGTTGTCAGG
HKT1;4-SV2 (404) AAGACCCCCTCAACTTCAGTGTGCTAAGCATTGTTGTCGAAGTTGTCAGG
HKT1;4-SV1 (404) AAGACCCCCTCAACTTCAGTGTGCTAAGCATTGTTGTCGAAGTTGTCAGG
HKT1;4 (404) AAGACCCCCTCAACTTCAGTGTGCTAAGCATTGTTGTCGAAGTTGTCAG-
3151 3200
Genomic (3151) CAAGTCAGACTAAATGGTTTCTTACCTGAGAAAAAAAATGCAGACCAAGT
HKT1;4-SV2 (454) CAAGTCAGACTAAATGGTTTCTTACCTGAGAAAAAAAATGCAGACCAAGT
HKT1;4-SV1 (454) CAAGTCAGACTAAATGGTTTCTTACCTGAGAAAAAAAATGCAGACCAAGT
HKT1;4 (453) ----------
3201 3250
Genomic (3201) AAATTAACAATTTATCTGATGAAAACAGCAAAACACAAAGTAACACTTGT
HKT1;4-SV2 (504) AAATTAACAATTTATCTGATGAAAACAGCAAAACACAAAGTAACACTTGT
HKT1;4-SV1 (504) AAATTAACAATTTATCTGATGAAAACAGCAAAACACAAAGTAACACTTGT
HKT1;4 (453) ----------

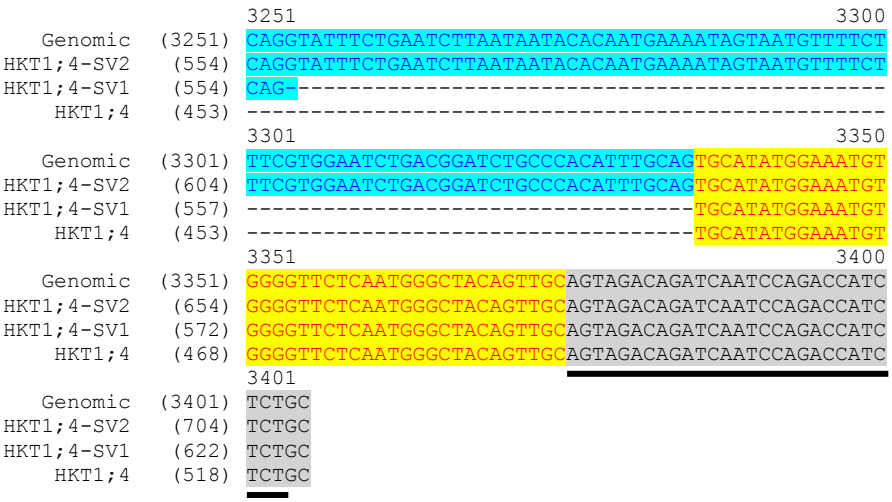

Figure S5. Sequences of *OsHKT1;4* splice variants. A predicted 522 bp fragment spanning over the *OsHKT1;4* transcript three exons was amplified by RT-PCR from RNA purified from salt treated Nipponbare and Pokkali sheath tissue. Three amplification products were recovered from each line: the predicted 522 bp fragment (HKT1;4) and two other fragments of superior sizes (HKT1;4-SV1 and HKT1;4-SV2). No sequence variation was observed between the fragments of similar size across the two lines (data not shown). Here, an alignment of the three splice forms is presented against the genomic sequence of the *OsHKT1;4* gene (Genomic). The increased length of both splice variants is due to alternative splicing of the second intron. Whereas *SV1* is splicing a second shorter intron, only one intron, the first, is spliced in *SV2*. Both variants are translated into an identical truncated protein due to the presence of an in frame STOP codon in the 5'-end of *OsHKT1;4* second intron. Sequence alignment was performed using Align X (Invitrogen). Homologous sequences are highlighted in yellow or blue. The full length second intron is highlighted in blue. The conserved codon encoding a Val residue in position 344 of the OsHKT1;4 protein is highlighted in green. The in frame STOP codon in the second intron is highlighted in purple. The RT-PCR primers are highlighted in grey. The sequences of the primers used to perform the HPLC molecular count ratio between the three splice forms are underlined in black.