

Fig. S4

WT	TCGTTACAGTGTTACTGGTCGCTCTGATCACC	GATCACC	CGCGCTCTCCTA	CGG	CGCACGGCCAGACGTGGCACGGCGACCTCGCG	280
22-1	TCGTTACAGTGTTACTGGTCGCTCTGATCACC-----				AGACGTGGCACGGCGACCTCGCG	229
22-3	TCGTTACAGTGTTACTGGTCGCTCTGATCACC-----				AGACGTGGCACGGCGACCTCGCG	227
22-5	TCGTTACAGTGTTACTGGTCGCTCTGATCACC-----				AGACGTGGCACGGCGACCTCGCG	228
22-6	TCGTTACAGTGTTACTGGTCGCTCTGATCACC-----				AGACGTGGCACGGCGACCTCGCG	227
22-7	TCGTTACAGTGTTACTGGTCGCTCTGATCACC-----				AGACGTGGCACGGCGACCTCGCG	230
WT	TCGTTACAGTGTTACTGGTCGCTCTGATCACC	GATCACC	CGCGCTCTCCTA	CGG	CGCACGGCCAGACGTGGCACGGCGACCTCG	278
27-1	TCGTTACAGTGTTACTGGTCGCTCTGATCACC	CGCGCTCTGATCACC	CGCGCTCTGATCACC	CGCGCTCTGATCACC	CGCACGGCGACCTCG	253
27-5	TCGTTACAGTGTTACTGGTCGCTCTGATCACC-----				AGACGTGGCACGGCGACCTCG	225
WT	TCGTTACAGTGTTACTGGTCGCTCTGATCACC	GATCACC	CGCGCTCTCCTA	CGG	CGCACGGCCAGACGTGGCACGGCGACCTCGCG	280
29-8	TCGTTACAGTGTTACTGGTCGCTCTGATCACC-----				TACGGCGCACGGCCAGACGTGGCACGGCGACCTCGCG	242
29-3	TCGTTACAGTGTTACTGGTCGCTCTGATCACC-----				TACGGCGCACGGCCAGACGTGGCACGGCGACCTCGCG	243
WT	TCGTTACAGTGTTACTGGTCGCTCTGATCACC	GATCACC	CGCGCTCTCCTA	CGG	CGCACGGCCAGACGTGGCACGGCGACCTCGCG	280
34-1	TCGTTAC-----				CTACGGCGCACGGCCAGACGTGGCACGGCGACCTCGCG	220
34-2	TCGTTAC-----				CTACGGCGCACGGCCAGACGTGGCACGGCGACCTCGCG	219
34-3	TCGTTAC-----				CTACGGCGCACGGCCAGACGTGGCACGGCGACCTCGCG	219
34-5	TCGTTAC-----				CTACGGCGCACGGCCAGACGTGGCACGGCGACCTCGCG	218
34-6	TCGTTAC-----				CTACGGCGCACGGCCAGACGTGGCACGGCGACCTCGCG	220
34-7	TCGTTAC-----				CTACGGCGCACGGCCAGACGTGGCACGGCGACCTCGCG	219
34-8	TCGTTAC-----				CTACGGCGCACGGCCAGACGTGGCACGGCGACCTCGCG	220
34-9	TCGTTAC-----				CTACGGCGCACGGCCAGACGTGGCACGGCGACCTCGCG	219
34-10	TCGTTAC-----				CTACGGCGCACGGCCAGACGTGGCACGGCGACCTCGCG	219
WT	TCGTTACAGTGTTACTGGTCGCTCTGATCACC	GATCACC	CGCGCTCTCCTA	CGG	CGCACGGCCAGACGTGGCACGGCGACCTCGCG	280
54-4	TCGTTACAGTGTTACTGGTCGCTCTGATCACC	CGCGCTCTGATCACC	CGCGCTCTGATCACC	CGCGCTCTGATCACC	GGCGCACGGCCAGACGTGGCACGGCGACCTCGCG	248
WT	TCGTTACAGTGTTACTGGTCGCTCTGATCACC	GATCACC	CGCGCTCTCCTA	CGG	CGCACGGCCAGACGTGGCACGGCGACCTCGCG	280
57-6	TCGTTACAGTGTTACTGGTCGCTCTGATCACC	CGCGCTCTGATCACC	CGCGCTCTGATCACC	CGCGCTCTGATCACC	ACGGCGCACGGCCAGACGTGGCACGGCGACCTCGCG	251
57-7	TCGTTACAGTGTTACTGGTCGCTCTGATCACC	CGCGCTCTGATCACC	CGCGCTCTGATCACC	CGCGCTCTGATCACC	ACGGCGCACGGCCAGACGTGGCACGGCGACCTCGCG	250
57-9	TCGTTACAGTGTTACTGGTCGCTCTGATCACC	CGCGCTCTGATCACC	CGCGCTCTGATCACC	CGCGCTCTGATCACC	ACGGCGCACGGCCAGACGTGGCACGGCGACCTCGCG	251
WT	TCGTTACAGTGTTACTGGTCGCTCTGATCACC	GATCACC	CGCGCTCTCCTA	CGG	CGCACGGCCAGACGTGGCACGGCGACCTCGCG	280
63-1	TCGTTACAGTGTTACTGGTCGCTCTGATCACC	CGCGCTCTGATCACC	CGCGCTCTGATCACC	CGCGCTCTGATCACC	ACGGCGCACGGCCAGACGTGGCACGGCGACCTCGCG	250
63-6	TCGTTACAGTGTTACTGGTCGCTCTGATCACC	CGCGCTCTGATCACC	CGCGCTCTGATCACC	CGCGCTCTGATCACC	ACGGCGCACGGCCAGACGTGGCACGGCGACCTCGCG	251

WT	TCGTTACGTGTTACTGGTCGCTCTGATCACC	CGCGGCGTCTCCTACCG	CGCACGGCCAGACGTGGCACGGCGACCTCGCG	280
78-1	TCGTTACGTGTTACTGGTCGCTCTGATCACC	CGCGGCGTCT-----GGCGACCTCGCG		228
78-5	TCGTTACGTGTTACTGGTCGCTCTGATCACC	CGCGGCGTCT-----GGCGACCTCGCG		228

Fig. S4 Sequence alignment of the *HvCKX1* gene fragments cloned from selected T₁ plants. Target sequence is marked in yellow and PAM motif in light blue; deletions are indicated by dashes.