

1	GACGCACTCCCCTCCTTCAACTAGTGCCTTGCGGCCGGTGGTCCTCCTCTCGATCCAGTT	60
61	CCTCAACCCACCAACACAAATCACCATCCCTCTTCTCTCCCCTCCTCGGCTCCGAACAGC	120
121	AAGGCATGGACAAGCAGCACCTCTTTGGTTGCTCCTACGTGGACGCGCCTTTCTTCGCGG	180
	M D K Q H L F G C S Y V D A P F F A A	
181	CCACTGGCACGTACGATACGACGTGCGGGCGAGCGCGCGCCCGGTGTTTCTTTGCGCATGC	240
	T G	
241	<u>GATGATGCAGCTGCAGGAGTTTCAGTTTCACCGGCCAGGACGCGCATGTGATGCCTTTTT</u>	300
301	<u>TTCTGATTCCGTTTGTGTATGTGCAGGCACGGCGCAGGGGGAGAGCCGGCCTAGAGCGCG</u>	360
	T A Q G E S R P R A R	
361	GCGCAGGCGGCGGAGGGCTGCGAGATGCGGCGGAGGGGACGGTGACGGCGTGGAGATGGA	420
	R R R R R A A R C G G G D G D G V E M D	
421	CGGGGGAGGGGACCCCAAGAAGCGCCGGCTGACCGACGAGCAGGTGGAGGGTCTGGAGCT	480
	G G G D P K K R R L T D E Q V E G L E L	
481	GAGCTTCCGGGAGGAGCGCAAGCTGGAGACCGCCGGAAGGTCCATCTCGCCGCCGAGCT	540
	S F R E E R K L E T G R K V H L A A E L	
541	CGGGCTCGACCCCAAGCAGGTGCGCGTGTGGTTCCAGAACCGGCGGGCGGCCACAAGAG	600
	G L D P K Q V A V W F Q N R R A R H K S	
601	CAAGCTTCTCGAGGAGGAGTTCTCCAAGCTCAAGCACGCCCACGATGCGGCCATCTACA	660
	K L <u>E</u> E E F S K <u>L</u> K H A H D A <u>A</u> I L H	
661	CAAATGCCACCTCGAGAACGAGGTATGCTTGCTCGCACACACTCACACTGCCATACATAT	720
	K C H <u>E</u> N E	
721	<u>GGCGCCGTACATCATCAATTCCCCTCCGTTCTTGACACAAGCTGGCTGACACACACATGAC</u>	780
781	<u>CAGGTGCTGAGGCTGAAGGAGCGGCTGGGAGCGACCGAGGAGGAGGTGCGGCGCCTCAGG</u>	840
	V L R <u>L</u> K E R L G A <u>T</u> E E E V R R <u>L</u> R	
841	TCGGGAGCTGGGAGCCAAGCGGCATCCGGCGACGGCGGAGACGCCGCTGGCGCCGTTGGC	900
	S G A G S Q A A S G D G G D A A G A V G	
901	CTGTGCGGAGGGAGCCCGAGCTCGTCCTTCTCGACGGGAACCTGCCAGCAGCATCTGGT	960
	L C G G S P S S S F S T G T C Q Q H P G	
961	TTCAGCGGCGCAGACGTGCTGGGGCCGGACGATGACCTGATGATGTGCGTCCCCGAGTAT	1020
	F S G A D V L G P D D D L M M C V P E Y	
1021	<u>GGTGGCTACGTGATAGCAGCGTGGTTCGAGTGGTTTAGCCTGTATGGGCTGATTTGAAAT</u>	1080
	G G Y V D S S V V E W F S L Y G L I *	
1081	TGAGACGGGCTGGGCATCAACAGCATGCATAATTTGCATATCGATTACTATTCTAGTTAG	1140
1141	GCATAGTGTTAATTAAGCTGGGATGATCTGTAGGCGTGCCTGTGTTTAATTATGTAGATA	1200
1201	GTGTTGATTAATGGCAAAGCTTGCAAGCTAGCAAGTGTAGTACCGGTAGCTCTCTTGAA	1260
1261	GTTTACAGAGACGATGTGTTGTGTTATCATTGATAGTATATGTTTTACTTCAGC	1313

Supplementary Fig. 1 The structure of *HvHox2*. The translated bases are 126-186, 327-682, and 784-1077bp and the deduced polypeptide consists 236 residues. Intron sequences are *underlined*, and the homeodomain is shown in *bold font*. Leucine zipper motifs are *double underlined*, and *red double lines* indicate the insertion point of the 300bp in *Vrs1*. The stop codon is indicated by an *asterisk*. Genome sequence of *HvHox2* in the two-rowed type (KNG and Haruna Nijo) and six-rowed type (AZ and Morex) were the same as far as determined for the region between nucleotide positions 86 and 1174. Accession AB490233 (cDNA) and AB490234 (genomic DNA).