Figure S1. Distribution of *HvWRKY* genes on barley chromosomes. Different color fonts represent different groups (group I is green, group II is red, group III is blue), and the unit of scale on the left is megabases (Mb). Four *HvWRKY* genes (*HvWRKY83*, *HvWRKY84*, *HvWRKY85* and *HvWRKY86*) had no chromosome location information. Tandem duplication gene pairs are linked with a pink background.

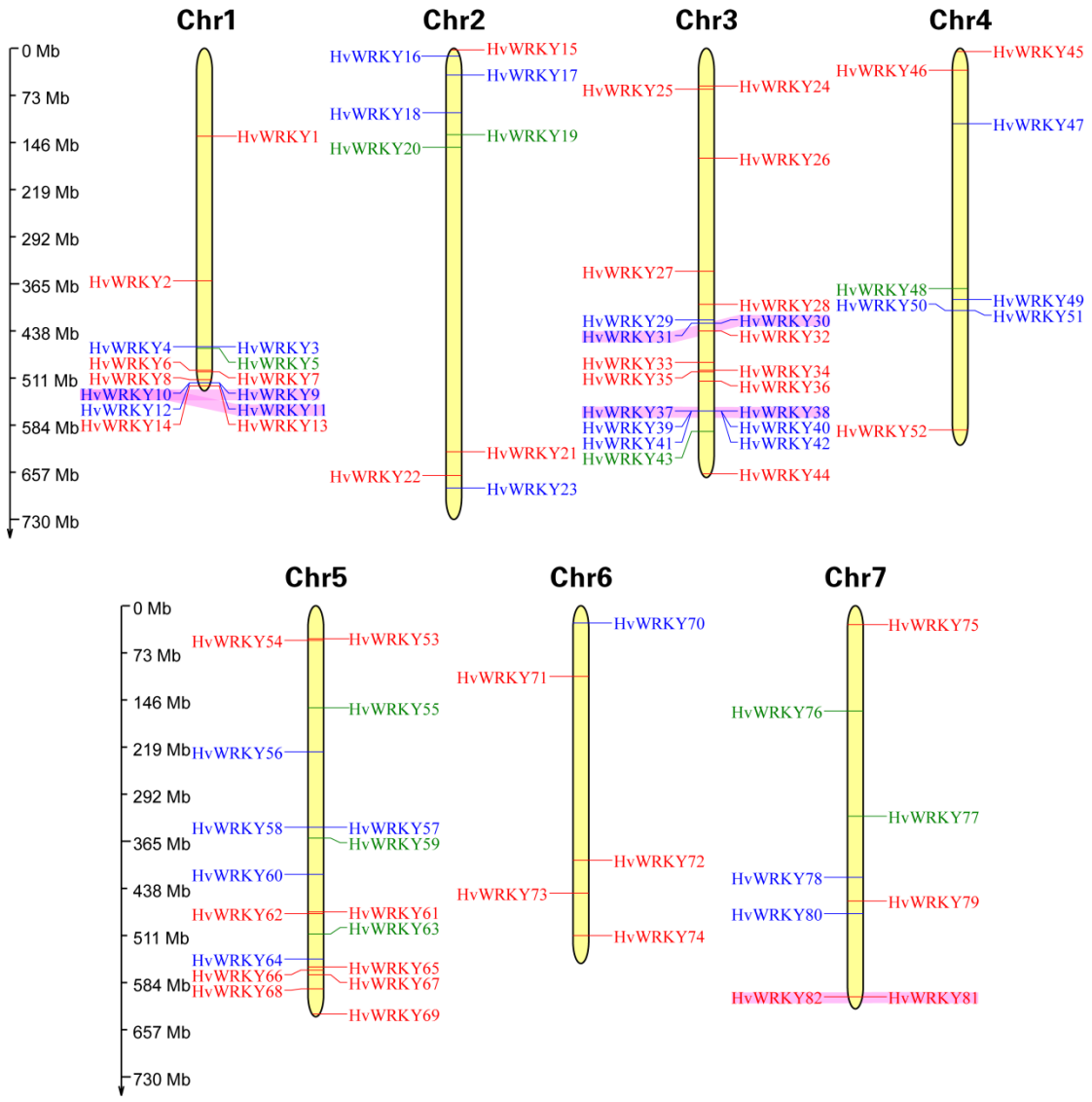
Figure S2. Comparison of the average number of introns in WRKY gene family members of each group or subgroup. The significance level was calculated by one-way ANOVA and compared by student Newman Keuls (S-N-K) test method.

Figure S3. *cis*-Elements distribution of HvWRKYs promoters. Promoter sequences (-2000bp) of 86 *HvWRKY* genes were analyzed by PlantCARE.

Table S1. The primer sequence used in qRT-PCR.

Table S2. Basic information of protein and nucleic acid of WRKY gene family members in barley. Sheet 1 includes gene ID, group information, protein properties, predicted subcellular localization, heptapeptide core motif and zinc finger motif type of *HvWRKY1-HvWRKY86*. Sheet 2 includes protein sequences and coding sequences (CDS) of 86 HvWRKYs . Sheet3 is the position distribution of HvWRKYs on barley chromosomes.

Figure S1


Chr1
Chr2
Chr3
Chr4
0 Mb
73 Mb
146 Mb
219 Mb
292 Mb
365 Mb
438 Mb
511 Mb
584 Mb
657 Mb
730 Mb
HvWRKY1
HvWRKY2
HvWRKY3
HvWRKY4
HvWRKY5
HvWRKY6
HvWRKY7
HvWRKY8
HvWRKY9
HvWRKY10
HvWRKY11
HvWRKY12
HvWRKY13
HvWRKY14
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HvWRKY52
Chr5
Chr6
Chr7
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HvWRKY81
HvWRKY82

Figure S2

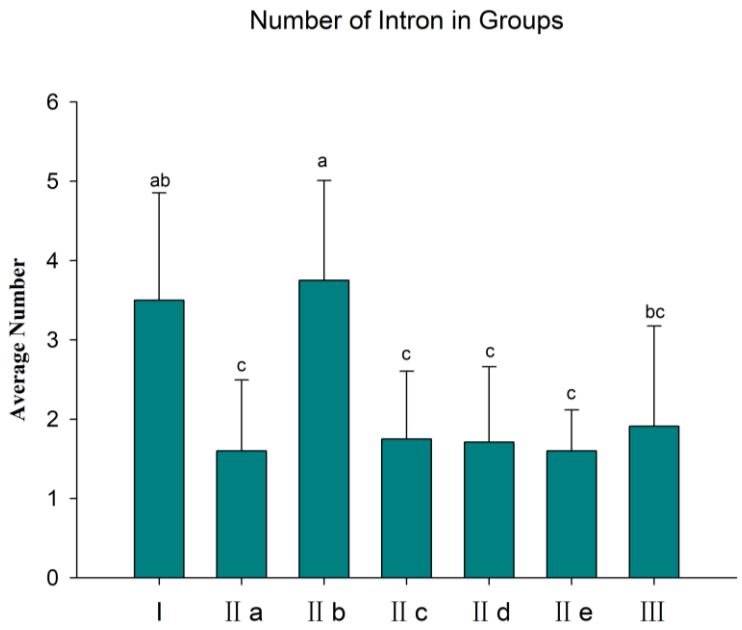
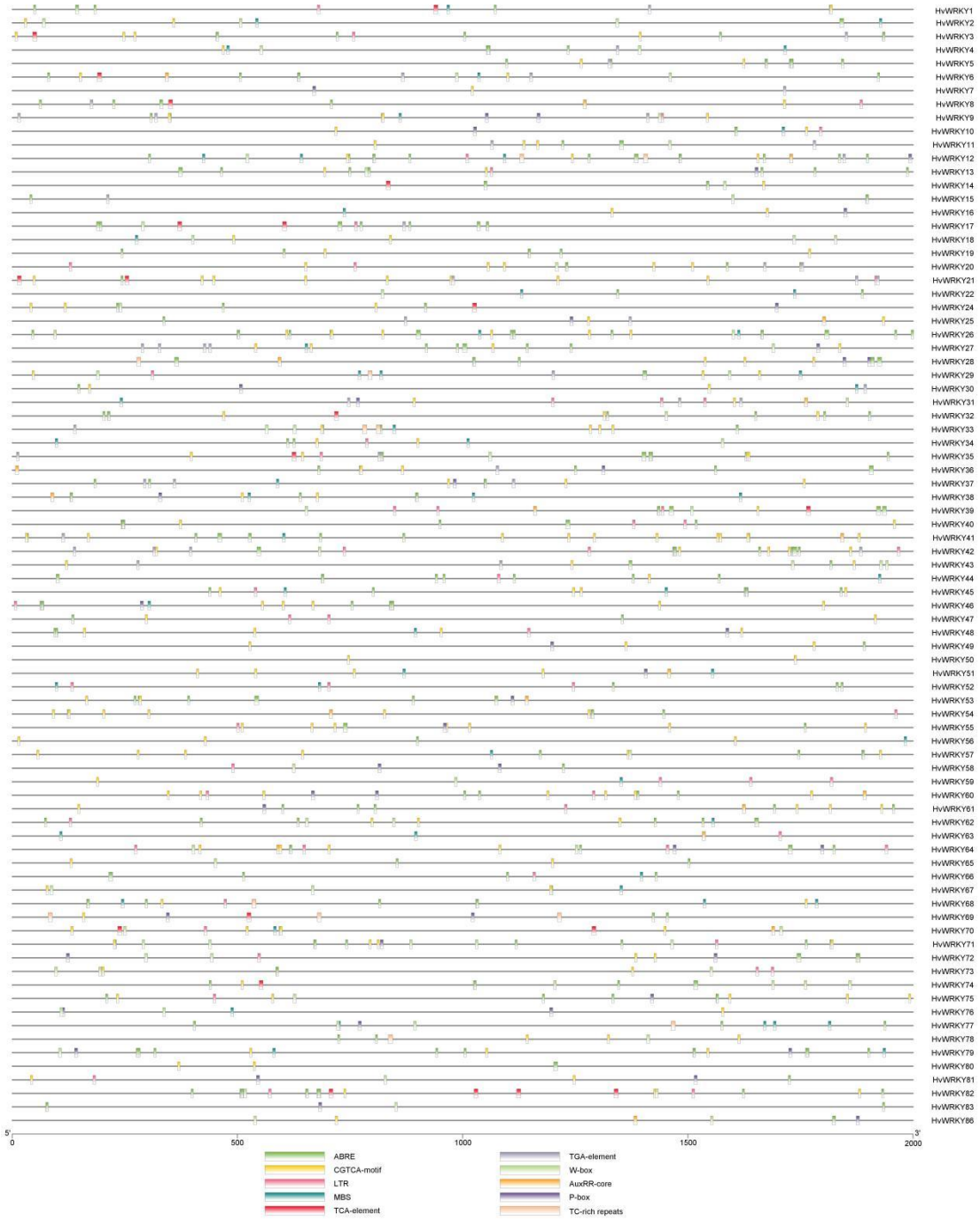

Number of Intron in Groups
Average Number
0
1
2
3
4
5
6
ab
c
a
c
c
c
bc
I
II a
II b
II c
II d
II e
III

Figure S3


HvWRKY1
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HvWRKY77
HvWRKY78
HvWRKY79
HvWRKY80
HvWRKY81
HvWRKY82
HvWRKY83
HvWRKY86
5'
0
500
1000
1500
2000
3'
ABRE
CGTCA-motif
LTR
MBS
TCA-element
TGA-element
W-box
AuxRR-core
P-box
TC-rich repeats

Table S1

Primers employed for qRT-PCR	
HvWRKY1	TCGTCGGTCCGAGTTCTTG
	CCCGTCCTCTATTCGTGGC
HvWRKY3	TCTACAGGAGCGTGAAAGCA
	ATCGGAGTCGAATTATTGGATG
HvWRKY13	CGCTCCAACATCAACAACATG
	TTGCTGGTAGCCCATCACG
HvWRKY15	GCGATGATGGTGCAGGAA
	TAGCCGTCGTCGAGGATGT
HvWRKY20	AAACCAGGGTGAAGAACGA
	TCAACCATACCAGGCGAAT
HvWRKY24	TTCTCGTGCGTCGGTCATAG
	TTTGCGTGGATGGGAAACTC
HvWRKY27	AAGCCGACAGCCACCACA
	ACCCGTCATCCAGCACCT
HvWRKY28	TGTATTTGGGCTTGCTTGG
	GCGGCTGTTGCTCCTGCTA
HvWRKY32	GTCAAGAACAGCCCGTATCCC
	AACGACCGCTCCACCCTCT
HvWRKY43	GAGGGTCAGAAATGGCAAAC
	GGGCTCCCAACAAATAAACA
HvWRKY53	TGCCCGCCATTAGCAACAA
	TGTGCTCGCCTTCGTATGT
HvWRKY55	CCAAGTCACAGCCCAAGCAA
	AAGCCTCAGCAGATTGGAAGAC

HvWRKY71	CCACCAGAGCCAATACCAGG
	CCGCTGTAGCTCCGACTCAA
HvWRKY80	GCACGCACAAGTACGACCAG
	GTGGCATCATGGGTAGTGGC
HvWRKY83	TCGACGACGGCTACAAGTGG
	CTGGCGTAGTAGACGGTGCTG
HvActin	TGGATCGGAGGGTCCATCCT
	GCACTTCCTGTGGACGATCGCTG