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Identification and functional analysis of the *HvWRKY1* gene associated with Qingke (*Hordeum vulgare* L. var. *nudum* Hook. f.) leaf stripe disease

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Electronic Supplementary Material (ESM)

The authors are fully responsible for both the content and the formal aspects of the electronic supplementary material. No editorial adjustments were made.

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1      ATGGAGGAAGTGGAGGAGGCCAACAGGATGGCCGTGGAGAGCTGCCACAGAGTGCTCGGCTTGCTACCCAGACCCAGGGCCCGGAGCAG
1      M E E V E E A N R M A V E S C H R V L G L L T Q T Q G P E Q
91     CTCCGGAGCATAGCTCTCGGGACGGACGAAGCCTGTGCCAAGTTCAGGAAGGTGGTCTCCCTCCTCGGCAACGAGCCCTCCGGAGGAACC
31     L R S I A L G T D E A C A K F R K V V S L L G N E P S G G T
181    ACCCATCCTAGAGCCAAGTTGTGACAGGAGGACAGCCCGGGTTCCTCAGCCAGAAGGGCTTCTTGGACAACAACCCCGGTGGTG
61     T H P R A K V V S R R Q T P G F L S Q K G F L D N N T P V V
271    GTGTTGAACAGCGCACACCTTCCACAGCTCCGCGCAGGTATCCTAGAAACAGCATTTTGGATTGCGAGCCGCGCAGCCAATCGGA
91     V L N S A H P S T S S A Q V Y P R N S I L D S Q P A H P I G
361    GGGCCTCCCAAGCTGGTCCAGCCATTGTCCGCGCATTTCAGTTTGGCGATTGCTCGCGGTATAATCAGTTCCAGCACCAGCACCAGCAG
121    G P P K L V Q P L S A H F Q F G D S S R Y N Q F Q H Q H Q Q
451    CAGCAGCAGAAAGATCGGGGCCGAGATGTTCAAGAGAAGCAACAGCGGGATCAACTGAAGTTTGACAGCCCAAGTGGCAGGGCACAATG
151    Q Q Q K M R A E M F K R S N S G I N L K F D S P S G T G T M
541    TCGTCGGCAGGTCTTCATGTCGTCTTTGAGCATGGATGGCAGCGTGGCCAGCCTGGATGCCAAGTCTTCCTCGTTTCATTGATCGGC
181    S S A R S F M S S L S M D G S V A S L D A K S S S F H L I G
631    GGGCCTGCTATGAGCGACCCGGTGAACGCGCAGCAGGCTCCAAGGAGGCGGTGCTCTGGGCGTGGGAGGATGGAATGGCAAGTGTGCT
211    G P A M S D P V N A Q Q A P R R R C S G R G E D G N G K C A
721    GCAACTGGCAGGTGCCATTGTTCAAAGAGAAGCAGGAAGTTGCGGGTGAAGAGGACGATTAAAGTTCGCCCAATTAGTAACAAAATTGCT
241    A T G R C H C S K R S R K L R V K R T I K V P A I S N K I A
811    GATATACCTCCAGATGAATACTCATGGAGGAAGTATGGGCAGAAGCCAATTAAGGGTTCCTCCACCCAGGTATACTTTTATAGTGA
271    D I P P D E Y S W R K Y G Q K P I K G S P H P R Y T F Y S G
901    TTTTATAGTTGTGTAATAAAAAAAGTGCAGAACTGCTCATCTGATACTTTGAGGGTAAATTTATTTTGCTACGATTTTCTTA
301    F F Y S C V N K K K C R T A H L I L C R V N F I L L R F S L
991    CTATATTATACATTATAGAAAGTAGTCGTATGCTATAATCACCATAATGCATCAACTTTGTTGGTAA
331    L Y Y T F I E S S R D D A I I T I M H Q L C W *

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Figure S1. Analysis of the *HvWRKY1* sequence

The single line represents a WRKY domain; *indicates a termination codon

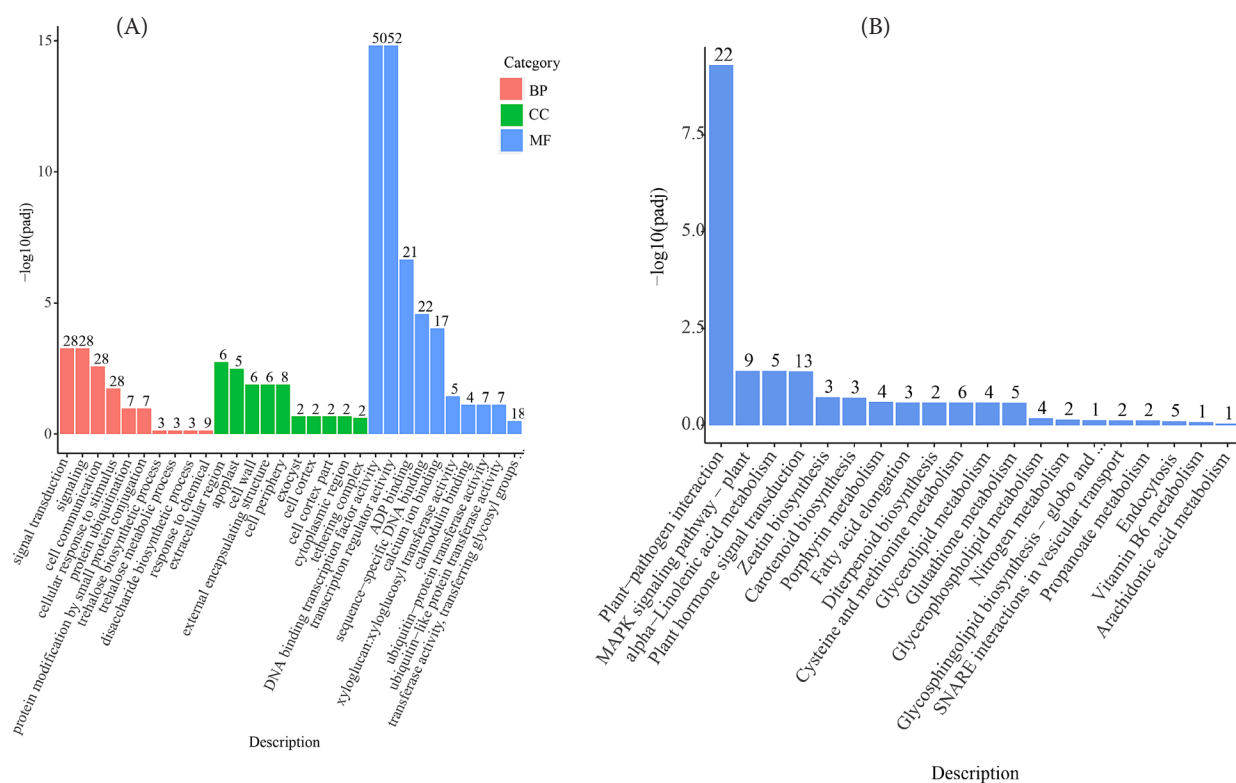


Figure S2. Gene ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment analysis of 824 differentially expressed genes (DEGs): GO enrichment bar graph; the first 30 terms of the significance analysis were selected for display; the Y axis represents the P-value, and the X axis represents the GO term (A), KEGG enrichment bar graph; the first 20 pathways of the significance analysis were selected for display; the Y axis represents the P-value and the X axis represents the top 20 pathways (B)

BP – biological process; CC – cell composition; MF – molecular function