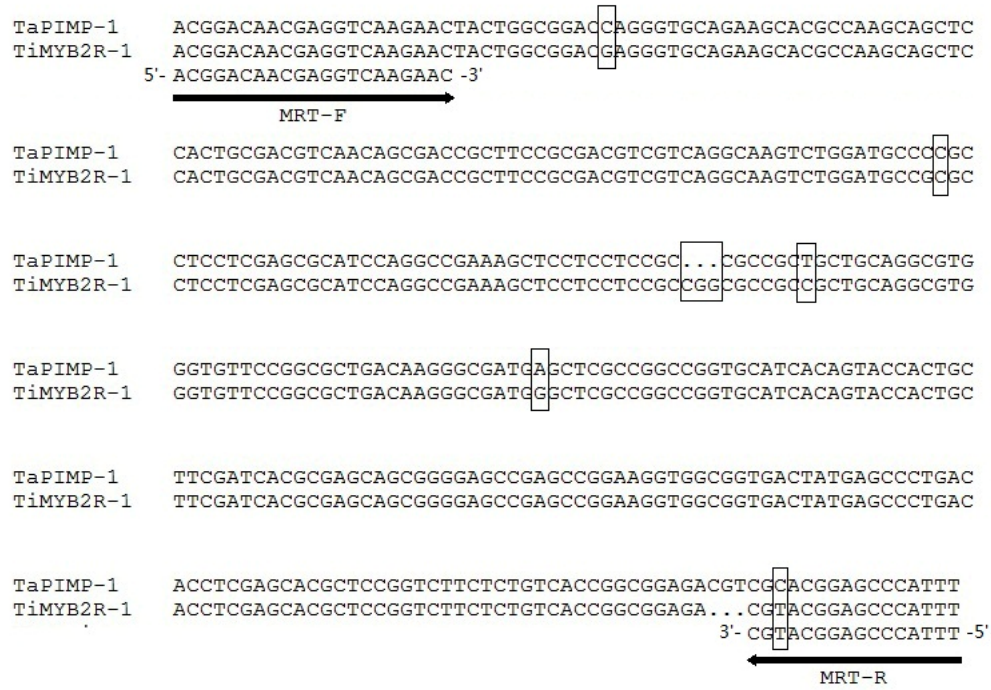


**Supplementary Figure S1.** Alignment of *TiMYB2R-1* and *TaPIMP1* sequences amplified in (Q)RT-PCR. MRT-F and MRT-R, being marked with long arrows, represent the primers for RT-PCR and Q-RT-PCR assays. The frames show the nucleotide differences between the amplified sequences of *TiMYB2R-1* and *TaPIMP1*.

Fig. S1



**Supplementary Figure S2.** The cDNA sequence and deduced amino acid sequence of TiMYB2R-1. The R2 and R3 domains are underlined with solid lines, the putative acidic domains are underlined with curve lines, and basic regions corresponding to NLS are shown by boxes.

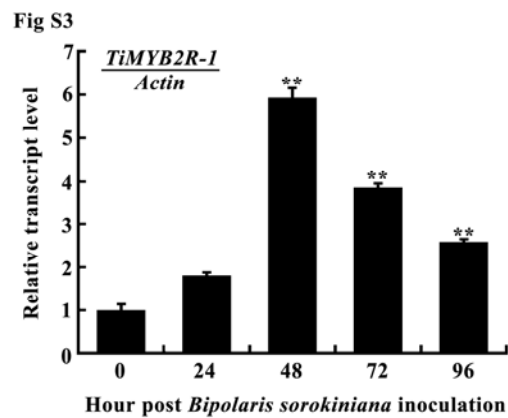
Fig S2

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1 ACTCGGTACGTCTTCCTGAAGCTTGATCGATCGAGCTCGACCTCATGGACATGGACAAG 60
1 M D M D K 5
61 GAGTACTACAAGGCCTGCATGGGCATGGAGGCGCTGCCGATGAGCCCAGCCGGTCTGTGCG 120
6 E Y Y K A C M G M E A L P M S P A G L S 25
121 GCGGTGACGACAGAGGTAGCCATGGCGCGGGCAGCGCAAGCGAGGACGAGGGCGACCTG 180
26 A V T T E V A M A A A T A S E D E G D L 45
181 AGGGGGGTCCGTGGACGGCGGAGGAGGACATGCTCCTCGTCGACTACATCTCCAAGCAC 240
46 R G G P W T A E E D M L L V D Y I S K H 65
241 GGCGAAGGGCGCTGGAAGCTCGCTCGCTCGATGCGCAGGCCTGAGGCGCACTGGGAAGAGC 300
66 G E G R W N S L A R C A G L R R T G K S 85
301 TGCCGGCTCCGGTGGCTGAAGTACCTCCGCCCTGACGTCCGACGGCGCAACATCACGCCG 360
86 C R L R W L N Y L R P D V R R G N I T P 105
361 GAGGAGCAGCTGCTGATACTGACCTGCACTCCCGGTGGGGCAACCGCTGGTCCAAGATC 420
106 E E Q L L I L D L H S R W G N R W S K I 125
421 GCGCAGCGCTCCCGGGGAGGACGGACAACGAGGTCAAGAAGTACTGGCGGACGAGGGTG 480
126 A Q R L P G R T D N E V K N Y W R T R V 145
481 CAGAAGCACGCCAAGCAGCTCCACTGCGACGTC AACAGCGACCGCTTCCGCGACGTCGTC 540
146 Q K H A K Q L H C D V N S D R F R D V V 165
541 AGGCAAGTCTGGATGCCGCGCCTCCTCGAGCGCATCCAGGCCGAAAGCTCCTCCTCCGCC 600
186 R Q V W M P R L L E R I Q A E S S S S A 185
601 GGCGCCGCGCTGCGAGCGTGGGTGTTCCGGCGCTGACAAGGGCGATGGGCTCGCCGGCC 660
186 G A A A A G V G V P A L T R A M G S P A 205
661 GGTGCATCACAGTACCACTGCTTTCGATCACGCGAGCAGCGGGAGCCGAGCCGGAAGGTG 720
206 G A S Q Y H C F D H A S S G E P S R K V 225
721 GCGGTGACTATGAGCCCTGACACCTCGAGCACGCTCCGGTCTTCTCTGTACCCGGCGGAG 780
226 A V T M S P D T S S T L R S S L S P A E 245
781 ACGTACGGAGCCCATTTCAGCGTGGGGCGCTGCCACTGCCACGGCGAACGTTGATGGC 840
246 T Y G A H F P A W G A A T A T A N V D G 265
841 TCGATGATGCAGTGGCGGGCCCGGAGTGTGGGGCCATAGGCGCGATCAGTACGTCATC 900
266 S M M Q C G G R E C G A I G G D Q Y V I 285
901 CACGGCGACAGCCTCAGCGGGAGCTGGTCGGAGCTCCTCGCGGCCACCGATATCCCGGAC 960
286 H G D S L S G S W S E L L A A T D I P D 305
961 TTTGAGTTCGGAATTTTCGACGACAACCTGTGGAACCTAGAGGACATTTACTGCTGACGA 1020
306 F E F G N F D D N L W N L E D I Y C * 323
1021 TGAACCTAACTAGAGCGC 1038

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**Supplementary Figure S3.** Transcriptional analysis of *TiMYB2R-1* in *Th. intermedium* following *B. sorokiniana* inoculation by Q-RT-PCR. The transcription of *TiMYB2R-1* was obviously induced after *B. sorokiniana* infection, and reached a peak at 48 hpi. Three biological replicates for each time point were averaged with standard error of mean indicated (SE). Asterisks indicate statistically significant variation calculated using Student's *t*-test (\*\* $P < 0.01$ ).



**Table S1 Common root rot responses of *TiMYB2R-1* transgenic and control wheat lines<sup>a</sup>**

Lines	Common root rot ( <i>Bipolaris sorokiniana</i> )	
	Infection Type	Index
O1	1.28**	25.71**
O3	1.24**	24.48**
O5	1.19**	23.75**
Null	2.81	56.29
Yangmai12	2.91	58.33

<sup>a</sup>The values derived from the average of at 30 plants each line tested in T<sub>4</sub> transgenic wheat lines and control wheat lines. Significant difference between *TiMYB2R-1* transgenic wheat lines (O1,O3 and O5) and nontransformed wheat Yangmai 12 (recipient) at \*\*p <0.01. Null indicates the segregants lacking *TiMYB2R-1*.