

Table S1 Primers used in the study

Primers	Sequence(5'-3')	objective
qTae-miR397	TCACCGGCGCTGCACACAATG	qRT-PCR
qTatubulin-F	ATCTCCAACCTCCACCAGTGTCG	qRT-PCR
qTatubulin-R	TCATCGCCCTCATCACCGTC	qRT-PCR
TaPR1-F	GAGAATGCAGACGCCCAAGC	qRT-PCR
TaPR1-R	CTGGAGCTTGCAGTCGTTGATC	qRT-PCR
TaPR2-F	AGGATGTTGCTTCCATGTTTGCCG	qRT-PCR
TaPR2-R	AAGTAGATGCGCATGCCGTTGATG	qRT-PCR
TaPR4A-F	CGTCTTCACCAAGATCGACA	qRT-PCR
TaPR4A-R	GGCAGTCGACGAACTGGTA	qRT-PCR
TaPR4B-F	CTTCACCAAGATCGACACCA	qRT-PCR
TaPR4B-R	AGCAAGCTAGCCTTTGATCG	qRT-PCR
OTaemiR397-F	<u>GGATCC</u> ACACCTCATCATACTACTAC	Make overexpression of miR397
OTaemiR397-R	<u>GGTACCA</u> ACTGAGCTCCTTCTCTCCG	Make overexpression of miR397

Note: The underlined bases are restriction enzyme sites or adaptor sequence.

Table S2 Target genes prediction

miRNA ACC.	Target Acc.	Expect	UPE	Alignment		
Using tae-miR397-5p as request						
UCACCGGCGCUGCACACAAUG	TraesCS6A02G134500.1	0.0	N/A	miRNA	21	GUAACACACGUCGCGGCCACU 1
				Target	504	CAUUGUGUGCAGCGCCGGUGA 524
UCACCGGCGCUGCACACAAUG	TraesCS7D02G230400.1	1.5	N/A	miRNA	21	GUAACACACGUCGCGGCCACU 1
				Target	287	GCUUGUGCGCGCGCCGGUGA 307
UCACCGGCGCUGCACACAAUG	TraesCS2B02G406200.1	2.5	N/A	miRNA	21	GUAACACACGUCGCGGCCACU 1
				Target	1593	GGUUGUGCGCAGUGCCGGUGC 1613
UCACCGGCGCUGCACACAAUG	TraesCS2A02G299200.1	2.5	N/A	miRNA	21	GUAACACACGUCGCGGCCACU 1
				Target	179	ACUUGUUUGCGGUGUCGGUGA 199
Using tae-miR397-X as request						
CAUUGAGUGCAGCGUUGAUGAA	TraesCS6A02G134500.1	0.0	N/A	miRNA	22	AAGUAGUUGCGACGUGAGUUAC 1
				Target	554	UUCAUCAACGCUGCACUCAAUG 575
CAUUGAGUGCAGCGUUGAUGAA	TraesCS1D02G283000.1	2.0	N/A	miRNA	22	AAGUAGUUGCGACGUGAGUUAC 1
				Target	744	CUCAUCAACGCUGCGCUCAACG 765
CAUUGAGUGCAGCGUUGAUGAA	TraesCS4A02G096400.1	2.0	N/A	miRNA	22	AAGUAGUUGCGACGUGAGUUAC 1
				Target	772	CUGAUCAACGCUGCGCUCAACG 793
CAUUGAGUGCAGCGUUGAUGAA	TraesCS4D02G208900.1	2.0	N/A	miRNA	22	AAGUAGUUGCGACGUGAGUUAC 1
				Target	767	CUGAUCAACGCUGCGCUCAACG 788

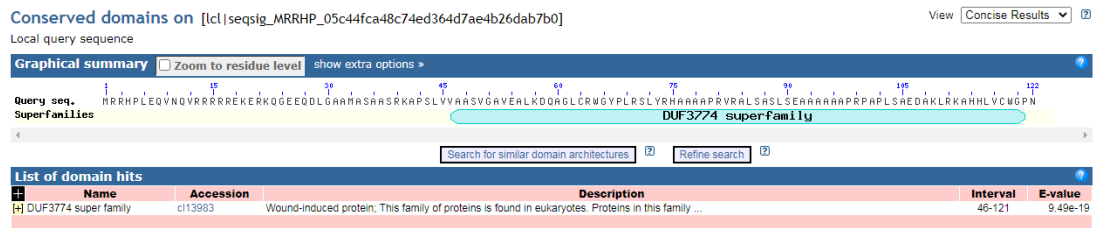


Fig S3 Prediction of conserved domain of target gene (WIP) online

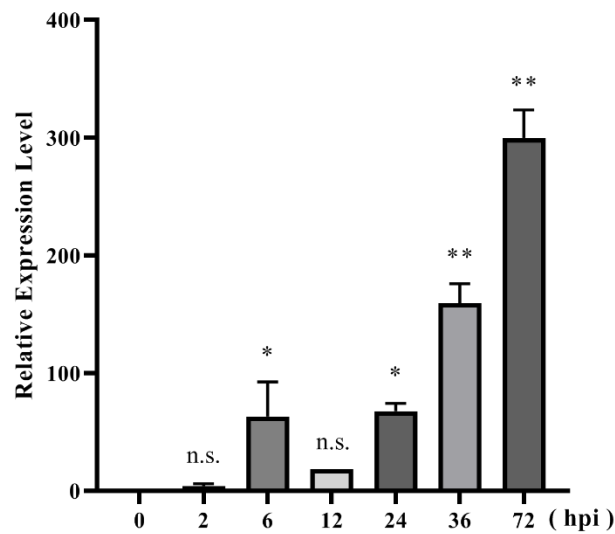


Fig S4 Expression pattern of target gene (WIP) in wheat plants after inoculation of *Bgt*

Relative expression levels are representative of the mean values of three biological replicates. Error bars represent one standard deviation (SD). The * and ** represent significant differences at levels of $P < 0.05$ and $P < 0.01$ between the control and treatment groups using Tukey's multiple comparisons test.