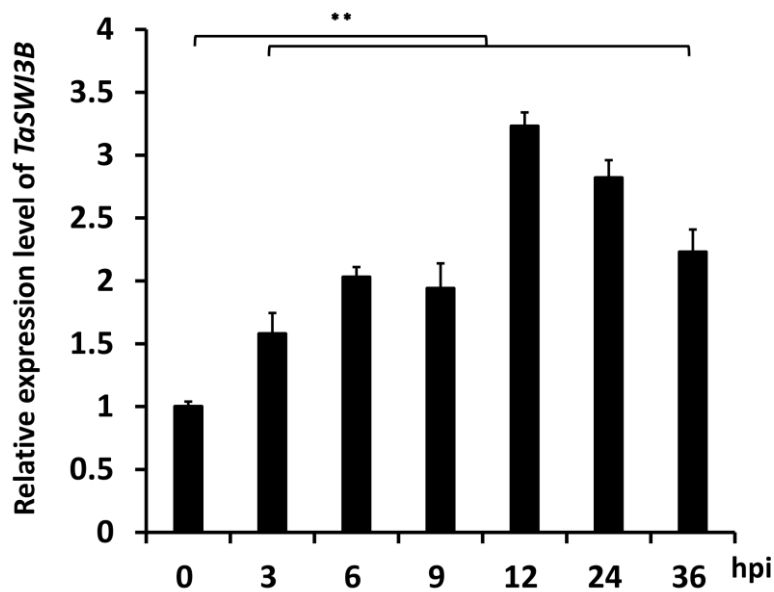




Supplementary Figure S2 Alignment of nucleotide sequences at the coding regions of allelic *TaSWI3B-6A*, *TaSWI3B-6B*, and *TaSWI3B-6D* genes. Regions chosen for the RT-qPCR and BSMV-VIGS are underlined in blue and green, respectively.



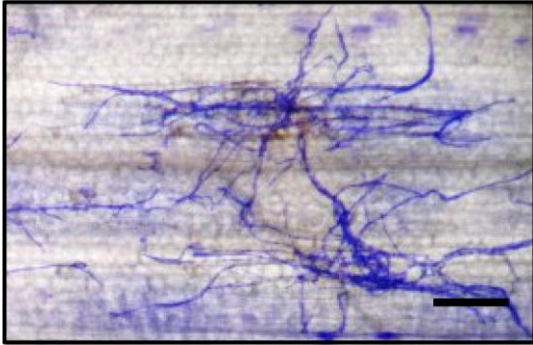
Supplementary Figure S3 RT-qPCR analysis of *TaSWI3B* expression levels in wheat leaves under *B.g. tritici* infection.

Results table

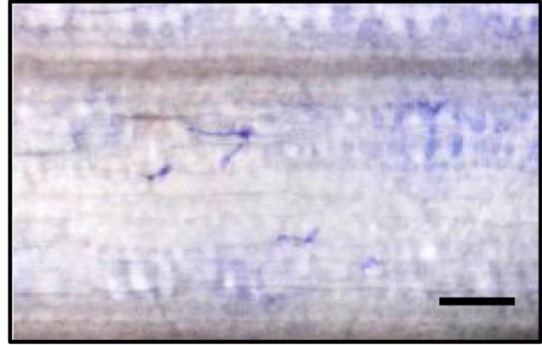
Genomic Location	Overlapping Gene(s)	Orientation	Length	Score	E-val	%ID
6A:17211802-17212003 (Sequence)	TraesCS6A02G157800	Reverse	204 (Sequence)	204	5.3e-110	100.0 (Alignment)
6B:231344825-231348628 (Sequence)	TraesCS6B02G195400	Reverse	204 (Sequence)	192	7.6e-103	98.5 (Alignment)
6D:133205969-133207172 (Sequence)	TraesCS6D02G156700	Reverse	204 (Sequence)	188	1.9e-100	98.0 (Alignment)
6A:172112089-172112186 (Sequence)	TraesCS6A02G157800	Reverse	98 (Sequence)	98	9.5e-47	100.0 (Alignment)
6D:133207284-133207381 (Sequence)	TraesCS6D02G156700	Reverse	98 (Sequence)	94	2.3e-44	99.0 (Alignment)
6B:231348712-231348809 (Sequence)	TraesCS6B02G195400	Reverse	98 (Sequence)	90	5.6e-42	98.0 (Alignment)
2B:368715717-368715737 (Sequence)		Reverse	21 (Sequence)	21	0.84	100.0 (Alignment)
2B:60955524-60955544 (Sequence)		Forward	21 (Sequence)	21	0.84	100.0 (Alignment)
1A:90986139-90986159 (Sequence)		Forward	21 (Sequence)	21	0.84	100.0 (Alignment)
1A:41095991-41095991 (Sequence)		Forward	21 (Sequence)	21	0.84	100.0 (Alignment)
2D:18136680-18136799 (Sequence)		Forward	21 (Sequence)	21	0.84	100.0 (Alignment)
2D:495299625-495299645 (Sequence)		Forward	21 (Sequence)	21	0.84	100.0 (Alignment)
6D:389657974-389657994 (Sequence)		Forward	21 (Sequence)	21	0.84	100.0 (Alignment)
6B:671623232-671623252 (Sequence)		Forward	21 (Sequence)	21	0.84	100.0 (Alignment)
1B:538862808-538862828 (Sequence)		Forward	21 (Sequence)	21	0.84	100.0 (Alignment)
3A:634334046-634334070 (Sequence)		Reverse	25 (Sequence)	21	0.84	96.0 (Alignment)
3A:420892278-420892298 (Sequence)		Forward	21 (Sequence)	21	0.84	100.0 (Alignment)
7A:248309523-248309547 (Sequence)		Forward	25 (Sequence)	21	0.84	96.0 (Alignment)
3B:84930028-84930048 (Sequence)		Reverse	21 (Sequence)	21	0.84	100.0 (Alignment)
7B:331263949-331263969 (Sequence)		Forward	21 (Sequence)	21	0.84	100.0 (Alignment)
1A:591224096-591224119 (Sequence)		Reverse	24 (Sequence)	20	3.3	95.8 (Alignment)
6A:187550906-187550929 (Sequence)		Reverse	20 (Sequence)	20	3.3	100.0 (Alignment)
6A:159424330-159424349 (Sequence)		Forward	20 (Sequence)	20	3.3	100.0 (Alignment)
6A:159565835-159565854 (Sequence)		Forward	20 (Sequence)	20	3.3	100.0 (Alignment)
1D:353458036-353458055 (Sequence)		Reverse	20 (Sequence)	20	3.3	100.0 (Alignment)
6B:222883030-222883049 (Sequence)		Reverse	20 (Sequence)	20	3.3	100.0 (Alignment)
1B:611527996-611528015 (Sequence)		Forward	20 (Sequence)	20	3.3	100.0 (Alignment)
4A:725029943-725029962 (Sequence)		Forward	20 (Sequence)	20	3.3	100.0 (Alignment)
7A:374163218-374163237 (Sequence)		Forward	20 (Sequence)	20	3.3	100.0 (Alignment)
7A:675765859-675765878 (Sequence)		Forward	20 (Sequence)	20	3.3	100.0 (Alignment)

Supplementary Figure S4 Whole genome searching of allohexaploid bread wheat using the fragments chosen for *TaSWI3B* silencing by BSMV-VIGS method in this study.

BSMV- γ



BSMV-*TaSWI3B*



Supplementary Figure S5 Powdery mildew microcolony formation on wheat plants infected with BSMV- γ and BSMV-*TaSWI3B*. Bar, 150 μ m.