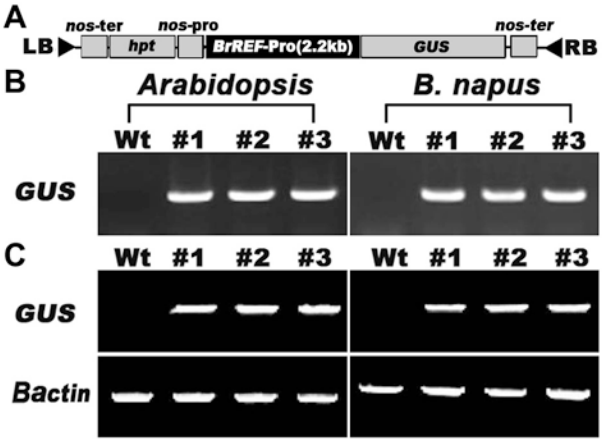
Supplemental Table 1. Oligonucleotide primers used in RT-PCR and genomic DNA PCR.

Target	Primer sequences	Expected size (bp)
BrREF gene	5'-ATGGCTGAAGATGAGATTATAGTC-3'	675
	5'- TCACTAGTGGGCTCGACAGTGATC-3'	
BrREF-Promoter	5'-TGGCACCTATAAGGAGAGAAATGTC-3'	2168
	5'- GACTATAATCTCATCTTCAGCCAT-3	
GUS	5'-AGGCCAGCGTATCGTGCTG-3'	1282
	5'-TCCACGCCGTATTCGGTGATG-3'	
Bactin	5'-TGGCATCACACTTTTCTACAA-3'	515
	5'-CAACGGAATCTCTCAGCTCC-3'	
AtActin (At3g18780)	5′-ATGGCTGAGGCTGATGATATTCAA-3′	1220
	5′-TTAGAAACATTTTCTGTGAACGATT-3′	

Supplemental Table 2. Pairwise sequence identity values for REF proteins .

	Pairwise % identity				
	BrREF	AtREF	PaRSP	RcSRPP	HbSRPP
BrREF	-	85.3	46.7	55.1	49.2
AtREF		-	45.4	55.1	45.4
PaRSP			-	56.0	51.0
RcSRPP				-	51.5
HbSRPP					-

*Accession numbers of sources from GenBank database are as follows: *Arabidopsis thaliana*, AtREF (NP_182299); *Brassica rapa*, BrREF (KJ489412); *Hevea brasiliensis*, HbSRPP (AAC82355); *Parthenium argentatum*, PaRSP (AAQ11374); *Ricinus communis*, RcSRPP (EEF30521).



Supplemental Fig. 1. *GUS* gene expression in transgenic *Arabidopsis* and *B. napus.* (A) Structure of the *BrREF* promoter-*GUS* construct used for *Arabidopsis* and *B. napus* transformation. The hygromycin phosphotransferase

gene (*hpt*), with a nopaline synthase gene promoter (*nos*-pro) and 3' terminator (*nos*-ter), served as the selectable marker for *Arabidopsis* and *B. napus* transformation. *GUS* expression was driven by the *BrREF* promoter. Left and right T-DNA borders are indicated by LB and RB, respectively. (B) PCR analysis of genomic DNA isolated from control and transgenic plants. The presence of the *GUS* gene was verified by PCR amplification using gene-specific primers. (C) Semi-quantitative RT-PCR to detect *GUS* gene expression in transgenic plants. *Bactin* gene expression was used as a quantitative control. Lanes: Wt, untransformed wild-type; lanes #1-3, selected transgenic lines 1, 2, and 3.