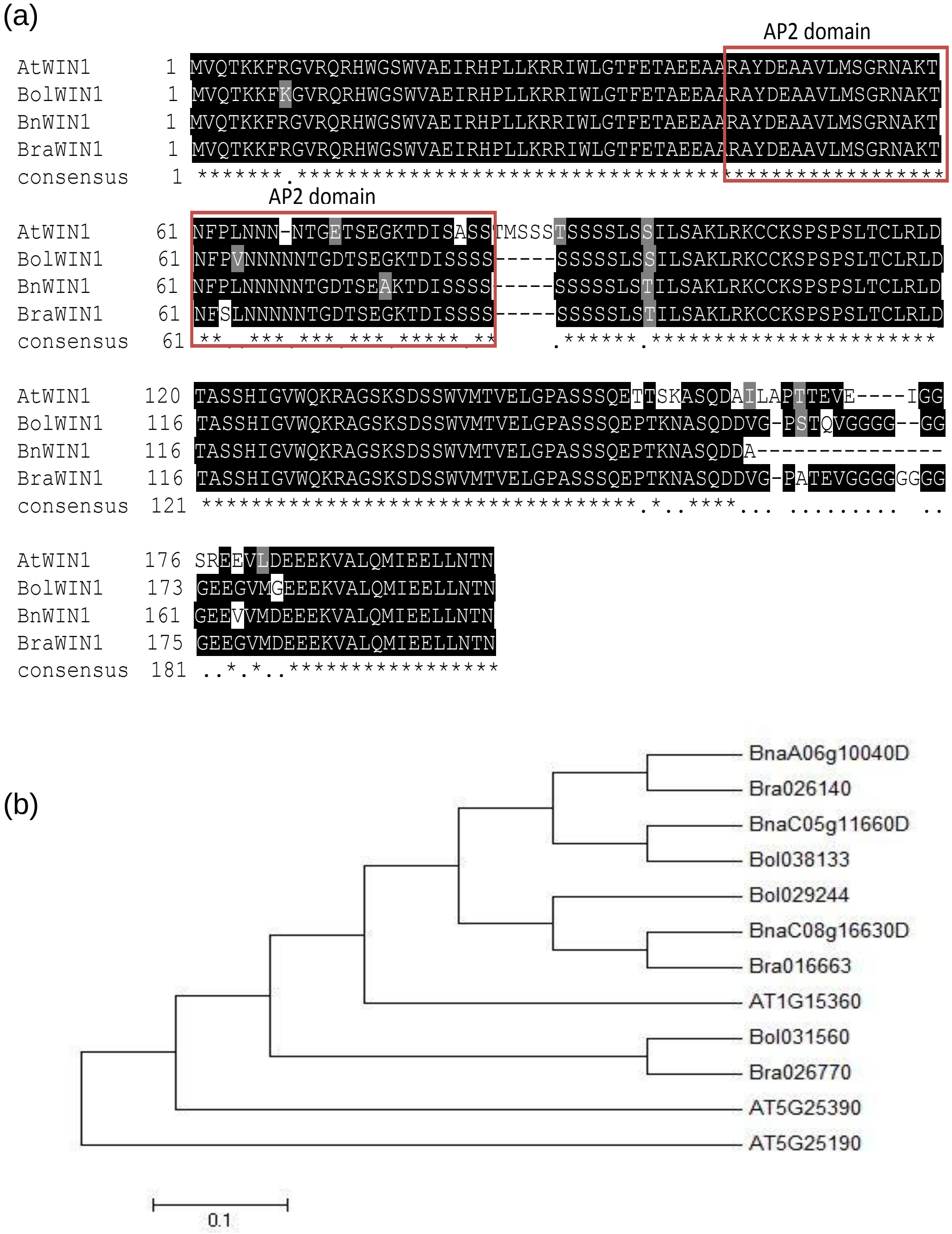

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AtWIN1       1 MVQTKKFRGVRQRHWGSWVAEIRHPLLKRRIWLGTFETAEEAARAYDEAAVLMSGRNAKT
BolWIN1      1 MVQTKKFKGVRQRHWGSWVAEIRHPLLKRRIWLGTFETAEEAARAYDEAAVLMSGRNAKT
BnWIN1       1 MVQTKKFRGVRQRHWGSWVAEIRHPLLKRRIWLGTFETAEEAARAYDEAAVLMSGRNAKT
BraWIN1      1 MVQTKKFRGVRQRHWGSWVAEIRHPLLKRRIWLGTFETAEEAARAYDEAAVLMSGRNAKT
consensus    1 *******.****************************************************

AtWIN1      61 NFPLNNN-NTGETSEGKTDISASSTMSSSTSSSSLSSILSAKLRKCCKSPSPSLTCLRLD
BolWIN1     61 NFPVNNNNNTGDTSEGKTDISSSS-----SSSSSLSSILSAKLRKCCKSPSPSLTCLRLD
BnWIN1      61 NFPLNNNNNTGDTSEAKTDISSSS-----SSSSSLSTILSAKLRKCCKSPSPSLTCLRLD
BraWIN1     61 NFSLNNNNNTGDTSEGKTDISSSS-----SSSSSLSTILSAKLRKCCKSPSPSLTCLRLD
consensus   61 ** . *** *** *** ***** **     .******.**********************

AtWIN1     120 TASSHIGVWQKRAGSKSDSSWVMTVELGPASSSQETTSKASQDAILAPTTEVE----IGG
BolWIN1    116 TASSHIGVWQKRAGSKSDSSWVMTVELGPASSSQEPTKNASQDDVG-PSTQVGGGG--GG
BnWIN1     116 TASSHIGVWQKRAGSKSDSSWVMTVELGPASSSQEPTKNASQDDA---------------
BraWIN1    116 TASSHIGVWQKRAGSKSDSSWVMTVELGPASSSQEPTKNASQDDVG-PATEVGGGGGGGG
consensus  121 ***********************************.*..****... .........  ..

AtWIN1     176 SREEVLDEEEKVALQMIEELLNTN
BolWIN1    173 GEEGVMGEEEKVALQMIEELLNTN
BnWIN1     161 GEEVVMDEEEKVALQMIEELLNTN
BraWIN1    175 GEEGVMDEEEKVALQMIEELLNTN
consensus  181 ..*.*..*****************
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Supplementary Figure 1. Sequence alignment and phylogenetic analysis of WIN1 homologues from different plant species. (**a**) Sequence alignment of WIN1 homologues from *Arabidopsis thaliana* (At), *Brassica oleracea* (Bol), *Brassica napus* (Bn), and *Brassica rapa* (Bra). The red box indicates AP2 domain. (**b**) Phylogenetic analysis of homologous WIN1. The alignment and phylogenetic analysis were conducted using Clustal W and the Neighbor-Joining (NJ) method in MEGA 5 for unrooted phylogeny tree construction. The identical and conserved residues are shaded in black and gray, respectively, by Boxshade program.

Supplementary Table 1. Primers used in this study

Primer name	**Primer sequence (5’ → 3’)**	**Purpose**
RT-*Bnactin*-F	TGTTCCCTGGAATTGCTGACCGTA	Real-time PCR
RT-*Bnactin*-R	TGCGACCACCTTGATCTTCATGCT	
BnWIN1-RT-F	CCCGTCAACAACAACAACAAC	
BnWIN1-RT-R	TAGCGCTGAGGATAGAAGAGAG	
BnBCCP1-RT-F	TTCTACTCCTGCCTCTTCACCT	
BnBCCP1-RT-R	TTGCCCCTTCTGCACTTTGT	
BnLPAT5-RT-F	TTCTACTCCAGTGGCCATTTCC	
BnLPAT5-RT-R	GATTGAAATGTGTAGCGGAGGC	
BnDGAT2-RT-F	GCTGGAGAGAGAGTTGAAGGAAG	
BnDGAT2-RT-R	CGAAGACAACACAAGAAGTGGG	
BnCER1-RT-F	GGGTCTCATGAACCAAGGGG	
BnCER1-RT-R	AGCAGAGGCGATGGTGTATG	
BnKCS1-RT-F	GACCGATGGTTCTTCCTTTGTC	
BnKCS1-RT-R	TCGTCGAGAACCGCACTAC	
BnGPAT9-RT-F	TGTTGACGCCTTCTGGAATAG	
BnGPAT9-RT-R	TCCAAGTACCACACTTCACATAC	
BnLACS2-RT-F	TGTTGCTGTCGAAAACCTCG	
BnLACS2-RT-R	CTCTCGGGTACAACCACTGC	
BnKCR1-RT-F	CTCCGACTCGATTCAAGCCA	
BnKCR1-RT-R	TACGAAACCCCAGCGTTGTT	
EMSA-$P_{BnBCCP1}$-F	TTGCCTCTAAAGTATATACAACTGAACATC	Target DNA amplification
EMSA-$P_{BnBCCP1}$-R	AATCTGTTTTCTTGTTGTCGGCTATTT TTC	
EMSA-P_{DGAT2}-F	TGCGTCTGGCAGAGGATTGTCAATGTTTTT	
EMSA-P_{DGAT2}-R	GGGAAGAAGATTTTGAGTCGGTTTGGGTTT	
EMSA-P_{GPAT9}-F	GGTTTGGTCGGGCTTGCCTCTAAGGTTCAC	
EMSA-P_{GPAT9}-R	ATGCGTAAAATCAAGCCGCCGGTAGAGGTC	
EMSA-P_{LPAT5}-F	ATTGTATTCTGATTCTTTCTGTAAGTTTGC	
EMSA-P_{LPAT5}-R	AGAAAAAATGAACAGCCGACCATAATAATC	
GPAT9-OE-F	GGATCCTCTAGAATGAGCAGCACGGCAGGAA	*GPAT9*-OE cloning
GPAT9-OE-F	GAGCTCGGATCCTCACTTGTCTTCCAATCTAGC	