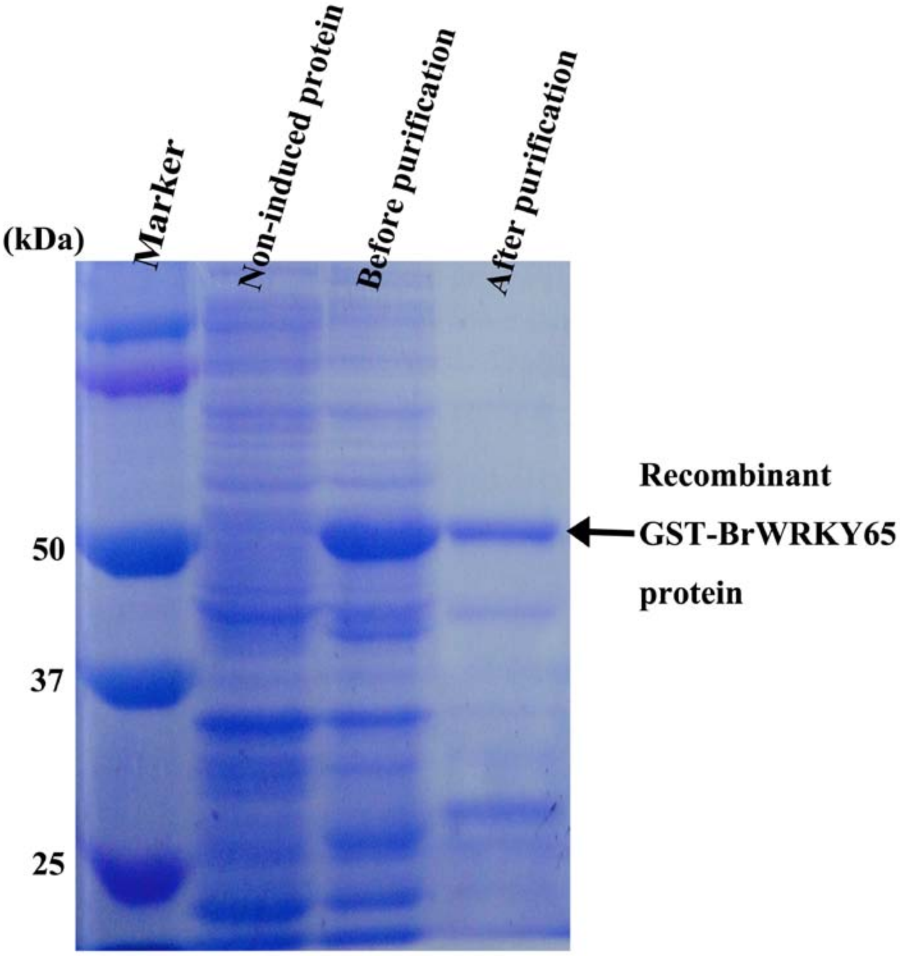

Figure S1. SDS-PAGE gel stained with coomassie blue demonstrating affinity purification of the recombinant GST-BrWRKY65 protein used for the EMSA assay.

Table S1. Summary of primers used in this study.

Assay	**Primer sequence**			**Restriction Site**
		Forward primer(5’-3’)	Reverse primer(5’-3’)	
RT-qPCR	***BrWRKY65***	CGGCACAAAGGAGACACA	TGCTTCTCTCGACTTGCTTC	
	BrNYC1	GATGTCTGGAACACCGCCTC	TTCTCACGCTTTCTCCGTCTTT	
	BrSGR1	CAAAGCTCCCAAGAACTTACACTC	AGATTCTTGTAGCTCAGGGTAACT	
	BrDIN1	GAAACTACCAACGGCGACAAGAAG	CCGGTGTCCTCACGTCCAGA	
Subcellular localization	***BrWRKY65-GFPFor***	ttctgcccaaatcgcg ATGAAGCGAGGTCTAGATAT		***NruI***
	BrWRKY65-GFPRev	tagtcataccggtcgc AAAGATCTCAACCTGTGACCCAAC		***NruI***
Fusing GST	***pGEX-4T-1-BrWRKY65-For***	ggttccgcgtggatcc ATGAAGCGAGGTCTAGATAT		***BamHI***
	pGEX-4T-1-BrWRKY65-Rev	agtcacgatgcggccgc TCAAAAGATCTCAACCTGTGA		***NotI***
Dual LUC assay	***pBD-BrWRKY65For***	tcgccgaccggtaggcct ATGAAGCGAGGTCTAGATAT		***Stu I***
	pBD-BrWRKY65Rev	aaccagagttaaaggcct AAAGATCTCAACCTGTGACCCAAC		***Stu I***
	62sk-BrWRKY65For	tagaactagtggatcc ATGAAGCGAGGTCTAGATAT		***BamHI***
	62sk-BrWRKY65Rev	cggtatcgataagctt TCAAAAGATCTCAACCTGTGACCC		***HindIII***
	0800-BrNYC1pro1For	tatagggcgaattgg GATTTAGAACAAGCCAGATCGCCA		***KpnI***
	0800-BrNYC1proRev	ttggcgtcttccatgg AGCTAAACCAGAGAGTGAGAAGAGGAG		***NcoI***
	0800-BrSGR1proFor	tatagggcgaattgg ATAGATAAGTTCCGACCGAAGCC		***KpnI***
	0800-BrSGR1proRev	ttggcgtcttccatgg CTCTGCTTCGTTTCAATATCAGTA		***NcoI***
	0800-BrDIN1proFor	tatagggcgaattgg GCAGACACTAGGCAATAAAGGCAC		***KpnI***
	0800-BrDIN1proRev	ttggcgtcttccatgg TATACAGACACAAAGCCAAAGGATA		***NcoI***

Text S1. Promoter nucleotide sequences of *BrNYC1*, *BrSGR1 and BrDIN1*. W-box (C/T)TGAC(C/T) is marked by red and boxed. Translation start site (ATG) was shown in yellow box.

BrNYC1 (XP_009139641.1) promoter
GATTTAGAACAAGCCAGATCGCCAGATTGCAGTGACGGTTGACTTGAATAAAGAAAAATGAAAAAAGCAGATAAA
TGCAAAGTTTCTAAGATGAGGATAAGAAAAACTCTCCGCAAAATTAAGAAAGACGGCCGACCTTGGAGGTGTATA
CAAAGACACCTTAGGCCAAGAGGACGAGGGACATAATTTTTTTTAGAAACTTAGCACTAGAGTAATTTTAGGCAAT
TTTGTTGTTGTTATCGAACTGCGACTCAAAGAGATTTAAGGCTTCAGATGGTTAGAACTATAGAACTCACTCACAG
CTCTTGCGACCGTAGCTTTTACAACTTGTTGTAACAATCACAACGCTCTTAAGCGGATTTGAAATAGGAGCTGTTCT
TCATTGATTTTTCTTTTCTGTTCGGACTGGATAAAAATAAATTTTCCTTCGTCTCTCCTCTTTTACTTTGATGTGTGTT
TGATACTTTGATTCAAGAGACACCACCACGTCGTCGCTGTCTCGTTGATCTTCTTCTGTTTTGTTGGTCATGCTCAC
TCTCTATTTCCAGAGAAATCAATCTTTGCAATTAAGAAGATGTTCCGGCAAAGTATTTTGAAAGGATAGAGTGTTGA
GATTTGCATAATAGTTTCTCTGATTTAAATCAGTTTAAACGAATTCAAAGCTTGTTTATGCAAGTGTTTTGACAATGA
ATGTTCTCAAATCGATTGAAACTTTTTGGAGTTTATCACATCCACAGAAGAGTTTGAACATTTATTAGAAGCGCCAA
GGAGAGTTAAGACTGGTTTTTGGGCATTGATATCACGGTAGAGAAAATAAATTGGATTGGGATTTGATCATACAGGT
CTAACTACCGAACTGCTTTCTACCTACCAAAGACTTTTTGTTTAATTTGTAAAGCCCAAAACCTTGCAATCGAAGCC
CAAAACCTTGCAATCGAAGCCCAAGGGCTAGATAGATTAAATATCCGGTTGACAAAAGAAAAACGAACTAGCTTC
CAAAGAAAAAATCGTAAACATGTTAATCGGCAAAAAAAAAAAAAAAAACAAGTGGCACGTGTCATTGTTGGGCA
AACGAGATGAGGTTGCCGTAACGTGTGGTCATCACACTTCTCTTCCTTCCTTCTTTCTTTCCACCACCTCCTTTCTT
CGTCCTCATCTCTTTCCTTCTCCGATCTATATTTAACTTCTTCGACGACTACGAAGATTAAAAATATCTAATCTTTTGT
GTTACCCACAAGAAAAGATATATATCTTTCTTTTATCTTCTTCTCTTGTACGATATTTTGCATGAGATTTTAAAACTCC
TCTTCTCACTCTCTGGTTTAGCTATG

BrSGR1 (XP_018512704.1) promoter
ATAGATAAGTTCCGACCGAAGCCGCAACGTACAGAATTGTTTCTAAATATTCGGCGAACCGCTTGTCTCTTTGTCCC
GAAAGGTAGTGTATTATCTGATAACGAATCGAAGAGAACTCGTCAACGCTACGTTTGTGCTTTAATGAGACGACAC
ATGCCAACTCATGCAGTGAAGAAGCTGGACACCAACGTGTAACTCACAGCTTCACCTCGTCAGAGCGGATTTTGG
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ACAACAAAAAGAAAAACAAAAAGAAAAACCTAATTTTCTGGAAGATAAAGCTTAACGGAAAGCGAAAGCAAGCT
CGTTTTTTTTAAGGGCTTCCAGCTTTTGATATTGTGGGTTTTACGAACGCGCAATAATAGCGTGAGACGTTAATATAG
TTTTTCTTTTATTTAAGGATTGTATTTTCCTTCAGTCTTGTTTTTACAGATACTGATATTGAAACGAAGCAGAGATG

BrDIN1 (XP_009150416.1) promoter
GCAGACACTAGGCAATAAAGGCACGATGACCCCGAGAGCTTGGTGCTAAGGATATACAGGAAGTACGCACTAGCA
GATGCCATTGTAGTTGTGGCCGCAAATAACGCAAAACGCCCGTTGGTCTTACTGACTCCAAAGGGTAAATTCCCTT
CCCCAAGCTGTGTACTCAAAGCTGTTACTAAGCCATACATAACAAACCCAATCACTGGCAAAGGAACACCTGGAG
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TTCAAGATTATATCGCATTGAGAGTGATTCAATCAGAATCTAATCATGCCTATGAGATCAAATACCATGAATACAAAT
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AGACCTGATTAAGAACATCTGACTTCAATTAAACCAATCACACTACCATCACACACGAAAATGAAACGAGATTTAC
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GATACAGGGATAAACCTCGCCATCATCGTCGTCGTTGAACAATCGCTAATCCAACATCATCGAAAAGCTTCCCTCA
ACTTTCACTCCCTTCCGTTTCGTTAATGGGCCTAAGGCAAGGCCCATCTAGTATTAAGAGCTGGGCCTAATAAGAAA

CGTATAGTAGCATCTAATCCGAGTCAGCAAGTTATCCATATTACGACTTACGAGGTAACCGAGTTGGACTTATCAAC
TGATATCCATACTCCGCATGGCTTACATGTTGGACTCGGATAGATCTTCTAGAACTGGCTGACGTGTCAGTAGTTCC
ATATCCTTTGGCTTTGTGTCTGTATATATATACATAACATGCACGAGAAGTATAACTCAAAGTATCTACAAACACAAG
AATAAAAAATG