Supplementary Table S1. Gene-specific primer sequences used in qRT-PCR

Locus name	Name	Primer name	Primer sequence (5′→3′)	Encoded protein	Product size (bp)
Glyma.01G014800	GmMYB4	Glyma.01G014800_qRT_Fw	CCAGCACCATCATCTCCCTC	MYB TF	71
		Glyma.01G014800_qRT_Rv	AGCCAGTGTTGGTGTTGGAA		
Glyma.03G123400	GmMYB77	Glyma.03G123400_qRT_Fw	AATTGGCGGTTTCATGGTGC	MYB TF	62
		Glyma.03G123400_qRT_Rv	ATCCAGCCATGACCAATCCC		
Glyma.04G042300	GmMYB102	Glyma.04G042300_qRT_Fw	GAAGACGAGGCGATCCTGAA	MYB TF	188
		Glyma.04G042300_qRT_Rv	TTGACTACCCGAAACGGTGG		
Glyma.05G032200	GmMYB176	Glyma05g032200_qRT_Fw	GCCAGCCATGCTCAGAAGTA	MYB TF	180
		Glyma05g032200_qRT_Rv	AGTTTCAGCAGGGAACACGG		
Glyma.05G051700	GmMYB128	Glyma.05G051700_qRT_Fw	AGCTGCAGCATCTTCTCAGG	MYB TF	60
		Glyma.05G051700_qRT_Rv	CCAGGTTGTGGCAAATGCTC		
Glyma.07G132400	GmMYB202	Glyma.07G132400_qRT_Fw	TGGAATCTGGTGTCTCAGCG	MYB TF	168
		Glyma.07G132400_qRT_Rv	CTTCCACTTGTTGCCGTGTG		
Glyma.09G017300	GmMYB250	Glyma.09G017300_qRT_Fw	TCAGGACTTGCATGAACGCT	MYB TF	187
		Glyma.09G017300_qRT_Rv	ATCTTTGCATCCTTCGCCCA		
Glyma.10G010300	GmMYB280	Glyma.10G010300_qRT_Fw	GCGGCGTGGAAATATCACAC	MYB TF	60
		Glyma.10G010300_qRT_Rv	CAGCGAGAGTGAAGGTCGAG		
Glyma.13G294300	GmMYB399	Glyma.13G294300_qRT_Fw	CCCTCCCTCTTGTGCTTGAG	MYB TF	69
		Glyma.13G294300_qRT_Rv	CCATCACACCTCGCGTAAGA		
Glyma.14G086500	GmMYB415	Glyma.14G086500_qRT_Fw	CCAAGTTCGGCAACAAGTGG	MYB TF	116
		Glyma.14G086500_qRT_Rv	GTCACTAACGGCGGAGGATT		
Glyma.16G093600	GmMYB467	Glyma.16G093600_qRT_Fw	AAAGAAGCCCCAGCCCATAC	MYB TF	88
		Glyma.16G093600_qRT_Rv	CCGCTTAAGGGCATACCACT		
Glyma.17G237900	GmMYB502	Glyma.17G237900_qRT_Fw	TCCGATTTGAGCGATCCGAG	MYB TF	100
		Glyma.17G237900_qRT_Rv	GATCGCAAGCAGAAGAAGCG		
Glyma.18G181300	GmMYB522	Glyma.18G181300_qRT_Fw	TGTCTGAGTTGGTGGAGTGC	MYB TF	72
		Glyma.18G181300_qRT_Rv	CCTCCTTCTTATGTCCGGCC		
Glyma.03G181700	GmPAL1	*Glyma.03G181700*_qRT_Fw	AGCAACACAACCAGGATGTCAA	Phenylalanine ammonia-lyase 1	120
		*Glyma.03G181700*_qRT_Rv	CAATTGCTTGGCAAAGTGCA		
Glyma.02G236500	GmC4H	*Glyma.02G236500*_qRT_Fw	AGGCGAGATCAACGAAGACAAC	Cinnamic acid 4-hydroxylase	109
		*Glyma.02G236500*_qRT_Rv	GTTCACAAGCTCAGCAATGCC		
Glyma.01G232400	Gm4CL	*Glyma.01G232400*_qRT_Fw	AGGCAATGTACGTGGACAAGCT	4-Coumarate:CoA ligase	118
		*Glyma.01G232400*_qRT_Rv	TCCGAGAGGACAGAGAAGTGGA		
Glyma.08G109400	GmCHS1	*Glyma.08G109400*_qRT_Fw	AAGCGCATGTGTGATAAGTCGA	Chalcone synthase 1	112
		*Glyma.08G109400*_qRT_Rv	TTGCATCCAACGAAGGTGC		
Glyma.05G153200	GmCHS2	*Glyma.05G153200*_qRT_Fw	TATGGCACCTTCATTGGATGC	Chalcone synthase 2	1142
		*Glyma.05G153200*_qRT_Rv	GCTGGTGGTGCAAAAAATGAG		

Locus name	Name	Primer name	Primer sequence (5′→3′)	Encoded protein	Product size (bp)
Glyma.08G109300	GmCHS3	*Glyma.08G109300*_qRT_Fw	GAGATCCGTAATGCACAACGTG	Chalcone synthase 3	145
		*Glyma.08G109300*_qRT_Rv	CTTTGAGCTCGGTCATGTGCT		
Glyma.08G110700	GmCHS4	*Glyma.08G110700*_qRT_Fw	CCTTCCAAGCCACTTTGCA	Chalcone synthase 4	81
		*Glyma.08G110700*_qRT_Rv	CTGGAGCAAAGGATGAAAGTGA		
Glyma.08G109200	GmCHS5	*Glyma.08G109200*_qRT_Fw	CACTTTGCCACATTCATTCC	Chalcone synthase 5	114
		*Glyma.08G109200*_qRT_Rv	TGTGAATGAACTAATGAAGCTATAGC		
Glyma.09G075200	GmCHS6	*Glyma.09G075200*_qRT_Fw	ACCAACAGTGACCACATGAACG	Chalcone synthase 6	126
		*Glyma.09G075200*_qRT_Rv	GGCACAAACACTTGGATTCTCC		
Glyma.01G228700	GmCHS7	*Glyma.01G228700*_qRT_Fw	AACCCACCAAACCGTGTTGAT	Chalcone synthase 7	111
		*Glyma.01G228700*_qRT_Rv	CTTGTCACACATGCGCTGAAAT		
Glyma.11G011500	GmCHS8	*Glyma.11G011500*_qRT_Fw	ATGGAGCTGCTGCTGTCATTG	Chalcone synthase 8	132
		*Glyma.11G011500*_qRT_Rv	CCTCACGAAGGTGTCCATCAA		
Glyma.14G005700	GmCHR	*Glyma.14G005700*_qRT_Fw	CAAAGCCATTGGAGTCAGCAA	Chalcone reductase	106
		*Glyma.14G005700*_qRT_Rv	CCATGCAAGGTTCATCTCCACT		
Glyma.20G241500	GmCHI1A	*Glyma.20G241500*_qRT_Fw	GGCGCTGAATACTCAAAGAAGG	Chalcone isomerase 1A Type II	141
		*Glyma.20G241500*_qRT_Rv	AGAGGCACCAGGTGCAAAATT		
Glyma.20G241500	GmCHI1B	*Glyma.20G241500*_qRT_Fw	AGCTGAATTGCTCGACTCCCT	Chalcone isomerase 1B Type II	149
		*Glyma.20G241500*_qRT_Rv	CAGATTGCATATGTGCCACACA		
Glyma.07G202300	GmIFS1	*Glyma.07G202300*_qRT_Fw	AGAATTCCGTCCCGAGAGGTT	Isoflavone synthase 1	148
		*Glyma.07G202300*_qRT_Rv	TGCCATTCCTGAAGTAGCCAA		
Glyma.13G173500	GmIFS2	*Glyma.13G173500*_qRT_Fw	AATGTGCCCTGGAGTCAATCTG	Isoflavone synthase 2	121
		*Glyma.13G173500*_qRT_Rv	GGCGTCACCACCCTTCAATAT		
Glyma.01G172600	GmIFR	*Glyma.01G172600*_qRT_Fw	AGATGGAAATGTGAAAGGAGCG	Isoflavone reductase	101
		*Glyma.01G172600*_qRT_Rv	TGTGCACGGCTTTGTTCAAG		
Glyma.02G048400	GmF3H	*Glyma.02G048400*_qRT_Fw	TTACCTGGCCCAGGAGAAAAC	Flavanone 3-hydroxylase	117
		*Glyma.02G048400*_qRT_Rv	ATTCCGGCAAGAGAAATCACTG		
Glyma.14G072700	GmDFR1	*Glyma.14G072700*_qRT_Fw	TTGTTGTCGGTCCCTTTCTGA	Dihydroflavonol-4-reductase	116
		*Glyma.14G072700*_qRT_Rv	GTGGACGAATTGACCTTGCTTT		
Glyma.17G252200	GmDFR2	*Glyma.17G252200*_qRT_Fw	CCATGGATTTTGACTCCAAGGA	Dihydroflavonol-4-reductase 2	106
		*Glyma.17G252200*_qRT_Rv	CTTCGGACAGTTTTGGCCTTC		
Glyma.12G051100	GmF-box	*Glyma.12G051100*_qRT_Fw	AGATAGGGAAATGGTGCAGGT	F-box protein family	92
		*Glyma.12G051100*_qRT_Rv	CTAATGGCAATTGCAGCTCTC		
Glyma.19G052400	GmELFa	*Glyma.19G052400*_qRT_Fw	GACCTTCTTCGTTTCTCGCA	Eukaryotic elongation factor 1-alpha	195
		*Glyma.19G052400*_qRT_Rv	CGAACCTCTCAATCACACGC		
Glyma.19G147900	GmACTIN	*Glyma.19G147900*_qRT_Fw	CTTCCCTCAGCACCTTCCAA	Actin	119
		*Glyma.19G147900*_qRT_Rv	GGTCCAGCTTTCACACTCCAT		

Locus names are taken from the *Glycine max* genome assembly Wm82.a2.v1 annotated database (http://phytozome.jgi.doe.gov/) version 11.0.

Supplementary Table S2. Primers used for the construction of effector and reporter constructs

Locus name	Name	Primer name	Primer sequence (5′→3′)	Purpose	Product size (bp)
Glyma.01G014800	GmMYB4	Glyma.01G014800_Fw	CACCATGGAGCTATTCCCAGCACAACCAGACTTG	Gene cloning	1221
		Glyma.01G014800_Rv	TTAAAGTGGCTGGCCCAAGCTGAATTCCAA		
Glyma.03G123400	GmMYB77	Glyma.03G123400_Fw	CACCATGAGGGAAGAGGATTCCAATTGGTTTTCG	Gene cloning	969
		Glyma.03G123400_Rv	TCACAACCAACCATGCCAATCAGATACGCC		
Glyma.04G042300	GmMYB102	Glyma.04G042300_Fw	CACCATGGATCGGATAAAAGGGCCATGGAGTCCT	Gene cloning	828
		Glyma.04G042300_Rv	TTATTCAACCCTACCAATTCCCATCCTCTC		
Glyma.05G032200	GmMYB176	Glyma05g032200_Fw	CACCGACGATGTCTCGCGCCTC	Gene cloning	858
		Glyma05g032200_Rv	TGCTTGAGAATATGGTCCTTGC		
Glyma.05G051700	GmMYB128	Glyma.05G051700_Fw	CACCATGGGAAGGCAACCCTGCTGTGACAAACTT	Gene cloning	864
		Glyma.05G051700_Rv	CTAATGCCCCTCTTCTTTCATTCCTACAGT		
Glyma.07G132400	GmMYB202	Glyma.07G132400_Fw	CACCATGAAGGATAGGCAACGTTGGAGAGCTGAA	Gene cloning	1134
		Glyma.07G132400_Rv	CTATCTTCCATTTGGTTCAGTGAGCCTTGA		
Glyma.09G017300	GmMYB250	Glyma.09G017300_Fw	CACCATGTACCCGAGGCTCATACACCCCCACGAT	Gene cloning	993
		Glyma.09G017300_Rv	CTACATGCCATACCTAGTTATTCCTTGAGG		
Glyma.10G010300	GmMYB280	Glyma.10G010300_Fw	CACCATGGATGTTAAGAAAGGTGGGTCTGTAGTA	Gene cloning	759
		Glyma.10G010300_Rv	TTATTTCATTTGGAGGTCATAAGAAAGCTG		
Glyma.13G294300	GmMYB399	Glyma.13G294300_Fw	CACCATGTTGGCGGTGTCACCTTTGAGGAGCACA	Gene cloning	1359
		Glyma.13G294300_Rv	TCAAGCACAAGAGGGAGGGATTTTGGGAAT		
Glyma.14G086500	GmMYB415	Glyma.14G086500_Fw	CACCATGGTATCATCATCGGGAAAAAGCAGAGAA	Gene cloning	870
		Glyma.14G086500_Rv	TCACTCGATGTTGCTAATTCCCATGCGCTT		
Glyma.16G093600	GmMYB467	Glyma.16G093600_Fw	CACCATGGCGACCCCCCCAAACGACGCCGCATCG	Gene cloning	963
		Glyma.16G093600_Rv	TCAGTTTTGTTGAGTAATCTTGATCCTCTT		
Glyma.17G237900	GmMYB502	Glyma.17G237900_Fw	CACCATGGATCGGGTGAAGGGTCCATGGAGCCCA	Gene cloning	855
		Glyma.17G237900_Rv	TCACTCGATGTTGCTAATTCCCATGCGCTT		
Glyma.18G181300	GmMYB522	Glyma.18G181300_Fw	CACCATGAAGGATAGGCAACGTTGGAGAGCTGAA	Gene cloning	1122
		Glyma.18G181300_Rv	CTATCTTCCATTTGGTTCAGTGAGCCTTGA		
Glyma.11G011500	GmCHS8pro	GmCHS8pro_HindIII_Fw	CCCCAAGCTTTGAGCAAGTATACCAACCAT	Transient assay	1662
		GmCHS8pro_BamHI_Rv	CTGAGGATCCCTTTCCTTCAAATTAAGTGAT		
Glyma.07G202300	GmIFS1pro	GmIFS1pro_PstI_Fw	AATCTGCAGTGACTTTGCTTGGGTGTCAA	Transient assay	1740
		GmIFS1pro_BamHI_Rv	AATGGATCCGATCTTGGCCTGAGGAAACA		
Glyma.13G173500	GmIFS2pro	GmIFS2pro_PstI_Fw	AATCTGCAGTGTACAAAGGGGAACATTTGC	Transient assay	1547
		GmIFS2pro_BamHI_Rv	AATGGATCCGTGTTCTCGTCCTTGGTTT		

Locus names are taken from the *Glycine max* genome assembly Wm82.a2.v1 annotated database (http://phytozome.jgi.doe.gov/) version 11.0.
Underlined 4 base-pai- sequences (CACC) were added for directional cloning of MYB at the 5′ end of the forward primer of pENTER/D-TOPO entry vector.
Underlined 6-base-pair sequences are the recognition sites for restriction enzymes used in plasmid construction.