

Supplementary Materials

Supplementary Table S1: Primers used in this study.

Primer name	Primer sequence (from 5' to 3')
CyfaAG1F	GTCTTCTCAGTCAGGAAAC
CyfaAG1R	GGACTTGAGGAAACTCATC
3RGSPAG2F	ATGGGGAGGGGGAAGATAGAGAT
CyfaAG2F	AGTCGACTATGATGGAGCCAA
CyfaAG2R	ATCTCCATCAATGCAACTCTC
pAG1SP1	TGCATATTCATAAAGGCGACACGGC
pAG1SP2	CGACCTCAGCATCACAGAGAACA
pAG1SP3	TCTCTTGATCTCTATCTTCCCCCTCC
pAG1SP4	GAACCACCTCTTATTTACACTTCGAG
pAG1SP5	CTCAAAGCAAGCAGCAATGGCCTCA
pAG1SP6	GCCTGAGCTGCACTCACACTAATAT
pAG2SP1	GAGGCTTCTTGTCATGTAATACTGCGC
pAG2SP2	CCTTCACACTGTTATTGGCATAAC
pAG2SP3	TACAGAAGGTGACTTGCCTGTTT
pAG2SP4	TTGTGCTTGCTGCGCTTCTTCTCC
pAG2SP5	TTAGATGATGGGTGGGCACTAGAG
pAG2SP6	TGGCGTTTGAATACGACGTTGGAC
pAG2SP7	GTTTGAAAGGGCAGCCATGACAG
pAG2SP8	CTAGTTTCACCCACATTCTCGTCG
pAG2SP9	CTTGCAAGTTTACATGGATTAGACC
5RAG1GSP1	ATGCTGATGCTGCTGTGCTC
5RAG1GSP2	CTACGCAGGTACATGTTATCAGTTTGG
5RAG1GSP3	GCATCACCCAGTAAGTTCCTGTTG
5RAG2GSP1	GTTTATGTGTGGCTGCTGT
5RAG2GSP2	CGGAGGTACATGTTGTCGTTTTGCAGT
5RAG2GSP3	CCCATCAGATTCCTGTTTGAGTTC
TpCyfaAG1F	ATGATTACGAATTC <u>GAGCT</u> CCCACCATTTTAATGTTATAGAAA
TpCyfaAG1F1	ATGATTACGAATTC <u>GAGCT</u> CATAGAAATTATATGAGAACTTCA
TpCyfaAG1F2	ATGATTACGAATTC <u>GAGCT</u> CAGATCAATGGTAGTAGCCAGTTA
TpCyfaAG1R	TCTGCAGGTCGACT <u>TCTAGAG</u> TTCCTTCCAACAGGAAAAATCAAC
TpCyfaAG2F	ATGATTACGAATTC <u>GAGCT</u> CGTCGAGTTTGGAGTTATAGTTTTAAG
TpCyfaAG2F1	ATGATTACGAATTC <u>GAGCT</u> CGAGTTTTCCTAGCAAACATGAT
TpCyfaAG2F	ATGATTACGAATTC <u>GAGCT</u> CGCTTCAAGACTTATCAGCTTAA
TpCyfaAG2R	TCTGCAGGTCGACT <u>TCTAGA</u> AGTCGACTCCGTTGGTCCCTCC
qGUSF	GTTCTGCGACGCTCACACCGATA
qGUSR	CAGCCATGCACACTGATACTCTTC
qActinF	GACCGTATGAGCAAAGAGATC
qActinR	CACATCTGTTGGAAGGTGCT

qCyfaAG1F	CCTGCGTAGTAAGATAGCTGACAATG
qCyfaAG1R	GCAGTCTGTTGCTGGTGAGAATAATG
qCyfaAG2F	GGGAGATGGAAGCTGCAAAACGAC
qCyfaAG2R	GCTGTTGGAGAGAATAGTGATGGCTG
qCyfaactinF	AAGACTTACACCAAGCCGAAGAAGATC
qCyfaactinR	CCAGCTCCACAGGTTGCGTTAG

Supplementary Table S2: Information on Sequences selected for alignments and phylogenetic analyses from NCBI GenBank.

Taxon and species	Protein name	Accession numbers	Lineage
Magnoliaceae			
<i>Nymphaea tetragona</i>	MsAG	ALF02827.1	AG
<i>Magnolia wufengensis</i>	MawuAG1	QDF82834.1	AG
	MawuAG2	QDF82835.1	AG
	MawuSTK	QDF82836.1	D
Liliaceae			
<i>Lilium longiflorum</i>	LMADS10	AIJ29174.1	AG
	LMADS2	AAS01766.1	AGL11
Orchidaceae			
<i>Cymbidium ensifolium</i>	CeMADS1	ADP00515.1	AG
	CeMADS2	ADP00516.1	AG
<i>Cymbidium faberi</i>	CyfaAG1	QDF44723.1	AG
	CyfaAG2	QDF44724.1	AG
	CfSTK	QDF44725.1	D
<i>Cymbidium sinense</i>	CsAG1	AVP27263.1	AG
	CsAG2	AVP27264.1	AG
<i>Dendrobium thyrsiflorum</i>	DthyrAG1	AAY86364.1	AG
	DthyrAG2	AAY86365.1	D
<i>Dendrobium hybrid cultivar</i>	DOAG1	AXB26295.1	AG
	DOAG2	AXB26296.1	D
<i>Oncidium hybrid</i>	OMADS2	AIJ29175.1	AGL11
	OMADS4	AIJ29176.1	AG
Asparagaceae			
<i>Hyacinthus orientalis</i>	HAG1	AAD19360.2	AG
Gramineae			
<i>Zea mays</i>	ZAG1	AAA02933.1	AG
	ZMM2	AAB81103.1	AG
	ZMM23	CAD23413.1	AG

	<i>Oryza sativa</i>	OsMADS3	Q40704.1	AG
		OsMADS58	BAE54300.1	AG
		OsMADS13	Q2QW53.2	AG
Eupteleaceae	<i>Euptelea pleiosperma</i>	EUplAG1	ADC79698.1	AG
		EUplAG2	ADC79699.1	AG
Lardizabalaceae	<i>Akebia trifoliata</i>	AktAG1	AAT46102.1	AG
		AktAG2	AAT46096.1	AGL11
Altingiaceae	<i>Liquidambar formosana</i>	LAG	AAD38119.1	PLE
Vitaceae	<i>Vitis vinifera</i>	Vvmads1	AAK58564.1	PLE
Fabaceae	<i>Medicago truncatula</i>	MtAGa	AIT11837.1	euAG
		MtAGb	AIT11838.1	euAG
		MtSHP	AFU81372.1	PLE
Rosaceae	<i>Prunus persica</i>	PpMADS4	AAU29513.1	euAG
		PPERSTK	ABQ85556.1	D/AGL11
		PPERSHP	ABG75908.1	PLE
	<i>Prunus lannesiana</i>	PrseAG	ADK95058.1	euAG
		PrseSTK	ADD91578.1	AGL11/D
		PrseSHP	ADG45819.1	PLE
	<i>Geum rupestre</i>	TrAG	ABB59994.1	euAG
		TrSHP	ABB59995.1	PLE
	<i>Rosa rugosa</i>	MASAKO D1	BAA90743.1	PLE
		MASAKO C1	BAA90744.1	euAG
Cucurbitaceae	<i>Momordica dioica</i>	MdMADS07	AXR70629.1	euAG
		MdMADS08	AXR70630.1	D
	<i>Cucumis sativus</i>	CUM1	AAC08528.1	euAG
		CUM10	AAC08529.1	AGL11/D
Salicaceae	<i>Populus trichocarpa</i>	PTAG1	AAC06237.1	euAG
		PTAG2	AAC06238.1	euAG
	<i>Populus alba</i>	PaAG1	AZR37458.1	euAG

Brassicaceae	<i>Arabidopsis thaliana</i>	PaAG2	AZR37457.1	euAG
		AG	P17839.2	euAG
		SHP1	OAP06129.1	PLE
		SHP2	AAU82057.1	PLE
		STK	OA098566.1	D
Polygonaceae	<i>Fagopyrum esculentum</i>	FaesAG	AFO83615.1	euAG
		FaesSTK	QLC27650.1	D
Primulaceae	<i>Cyclamen persicum</i>	CpAG1	BAK18552.1	euAG
		CpAG2	BAK18553.1	euAG
		CpSTK	BAK09621.1	STK
Theaceae	<i>Camellia japonica</i>	CjAG	AIP87050.1	euAG
Actinidiaceae	<i>Actinidia argute</i>	AcarAG	ADU15476.1	euAG
Rubiaceae	<i>Coffea arabica</i>	CaAG	AHW58037.1	euAG
Gentianaceae	<i>Gentiana scabra</i>	GsAG1	BAS04480.1	PLE
		GsAG2	BAS04484.1	PLE
		GsSTK1	BAS04473.1	D
Solanaceae	<i>Nicotiana benthamiana</i>	NbAG	AFK13159.1	euAG
		NbSHP	AFK13160.1	PLE
	<i>Solanum lycopersicum</i>	TAG1	AAA34197.1	euAG
		TAGL11	AAM33102.2	AGL11/D
		TAGL1	AAM33101.2	PLE
	<i>Petunia hybrida</i>	pMADS3	CAA51417.1	euAG
		FBP7	CAA57311.1	D
		FBP11	CAA57445.1	D
		FBP6	CAA48635.1	PLE
Plantaginaceae	<i>Antirrhinum majus</i>	FAR	BAI68392.1	euAG
		PLE	BAI68391.1	PLE
Oleaceae	<i>Fraxinus pennsylvanica</i>	FpAG	AFP99884.1	euAG

Asteraceae	<i>Torenia fournieri</i>	TfFAR	BAG24494.1	euAG	
		TfPLE	BAG24495.1	PLE	
	<i>Chrysanthemum morifolium</i>	CAG1	BAG06959.1	euAG	
		CAG2	BAG06960.1	euAG	
		CAG3	BAG06961.1	euAG	
		<i>Gerbera hybrida</i>	GAGA1	CAA08800.1	euAG
			GAGA2	CAA08801.1	AG

The transcription start site (+1) is in bold and boxed. The start codon ATG is in bold and boxed. Putative cis-acting regulatory elements are in bold and underlined.

-1207 CCACCATTTT AATGTTATAG AAATTATATG AGAACTTCAA AAAATAACTT TTCATGT**GTC**
CArG-box POLLENILELAT52 GTGANTG10

-1147 ATGCTT**TACT** TAACC⁺AAT TATAAAATAA TTAGCACATA ATTAATATAA AACAAAGAGCA
CACTFTPPCA1

-1087 CAAGC**CACTA** TTCATTAGAT TGTATAATTT CTTCCATGAA GATAATAAAA ATCAT**TTATTT**
CACTFTPPCA1 TATABOX5

-1027 TATCCCAAAT AAGCTA**TTAT TTT**AATGTGA GAAC**TTTTGT TT**ATTTTCTA TAAGATTTAA
TATABOX5 TTTGTT motif

-967 GTGCATCCAA CTAAATAATA GAATTAAATT TTTGAAAATT TGGCTATATT TTAGATAAGT

-907 TTTTCTTTCT TAATTGATGA AACTTATAAT ACATAAGAAC TTC**TACT**ATG **AACAAA**GAAT
CACTFTPPCA1 AACAAA motif

-847 TAATAAGTGC TTTTGATCCT ACGAAAAATC GTAT**TGACATG ACCC**AAAAA TTAACT**TACT**
WRKY7IOS WRKY7IOS CACTFTPPCA1

-787 CAT**TTATCCC** AAA**ATTTATA TAAAT**GAAAT TAC**CAAT**GCTG AGATCTTAGA TAAAATCTCG
SREATMSD D2GMAUX28 CAATBOX1

-727 AT**TGAAAAATA** AAATTCTAGA GGATGTGGTC ATAGTA**CAAA TGATCATATG** ATCATTCTATA
-300ELEMENT MYCCONSENSUSAT MYCCONSENSUSAT

-667 TCATGTCCAC TAGACTAAAA AGATG**CCAAT** ATTCTTGAGC TCAAATGGCA TCGATCTAAA
CCAATBOX1

-607 GATTTACGAT GAAAAAAAGA GC**CCAAT**CAA TCTCGATCGA TCAACATGTC ATCATCAACA
CCAATBOX1

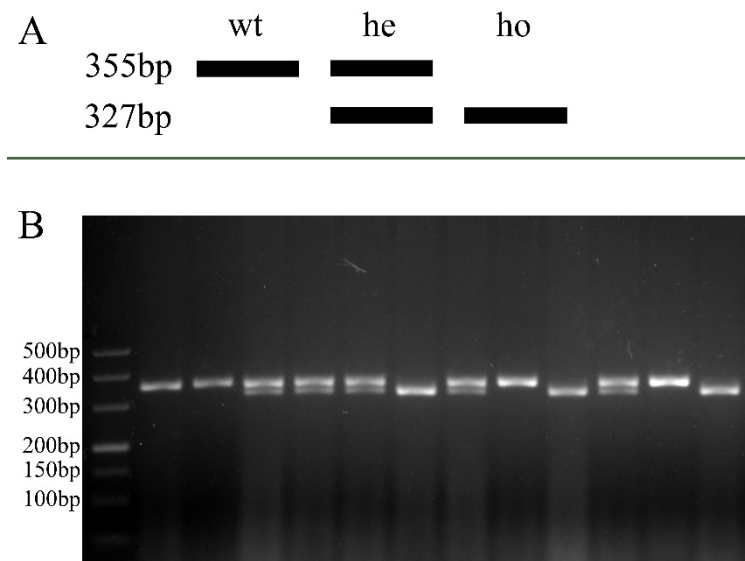
-547 TTAGAGAGAT TGGGTTGGGT CCATGGCCAG AAGTAGGGAG GAATAAATGG CACCTTAGAG

-487 CAAATT**GTGA** ACCACATTGA TCTTAAAATA AATTAGGCAG GGTAGC**CACA TG**GGAGCCAT
GTGANTG10 MYCCONSENSUSAT

-427 ATTCTCTTGT **CATATGA**AGA CAAGTAAT**TTA TCC**ATCAAAA AGAT**CAAT**TGG TAGTAGCCAG
MYCCONSENSUSAT SREATMSD CAATBOX1

-933 CTACACTAGA AATGTGAATA AATTAGAGAA TATATAAACC TATCATTTCT ATAAGTGCTA
 POLLENILELAT52
 -873 AATCTTTTCAG AAAGGTCTAA TCCATGTAAA ACTGCAAGAT TAATTATCTT CATGAATGAT
 POLLENILELAT52 ARR1AT
 -813 CCATTTACGG TAAATAAGAA GCAAGTACAC AAAGTTAAAG TAGCAACACA CA CTTAACGACG
 CACTFTPPCA1
 -753 AGAATGTGGG TGAAACTAGC CAGCTAATAT GCTTTAGAAG AAAGGACCTG TGATTGGTCCC
 GTGANTG10
 -693 AGGAGATGAT GTTGGCATTT ACGATGATCT GTCATGGCTG CCCTTTCAA CACCCACTTT
 PROXBNNAPA
 -633 GCATTGCAAG CCTGTTATAG CAAAATAAAC TATCTTTAGA GCTCACAGTT CATCTATGGT
 MYBCORE
 -573 TCTTCGATCT TAACCACAAT TAGATCTCCA AAGAATTAA GAAAATTGTA CATAATCTTA
 MYBIAT POLLENILELAT52
 -513 TATATCAAAG GCCATGTCAG CTCTAGCATC AGAAAAATTG CTTCCATGGC CTACATTATG
 POLLENILELAT52
 -453 GTGTCAAAAA ACGAATTTTA AAAATACTTA AAGCTTTATG GTTTGCAAAA GTATTTGAAT
 -300ELEMENT
 -393 TAAGAGTCAA AATATCAGAA AAAAATTAAT GAGCGGAAGA CAAAGGGCCA AGAATTGAAG
 POLLENILELAT52
 -333 AGGGAGTTGA AGGACCAATTGG CGCACTGCGT GCTTTCATCC TTCATCGTTC CTTTTGTTTT
 CAATBOX1 CACTFTPPCA1 PYRIMIDINEBOXOSRAMY1A
 -273 ATTTTTACATA GTATATTTGT TTGAGTGCAA TTCAGTCCAA CGTCGTATTC AAACGCCATT
 TATABOX5 TTTGTT motif CAATBOX1
 -213 AATAATCCCT TTCTAAAAGA CCCTTTCCCA TCTTTCTCTC TCTATCTCTT TTCTCTAGCC
 CTRMCAMV35S
 -153 CTCTTCTCTC TCTAGTGCCC ACCCATCATC TAATCCTTTG AAACCGATGG CAATGGTTGC
 CTRMCAMV35S CAATBOX1
 -93 CTGAGTTAAT AACCTGTCCT TTCATTGTAG AAAGAGAGGG AAAGCTTCAA GACTTATCAG
 POLLENILELAT52
 +1
 -33 CTTAATAACC AGCAAGTTGC TCCCCTTTCC TTCAAAGAAA ACTGGCTTTC TTTCAGGCAG
 +28 GAACCGGAGA AGAAGCGCAG CAAGCACAAC TCAATTTGCA GAGTCCGTAA ATTTAATGTT
 CAREOSREPI
 +88 TCTTCTTTCT CTTCAAAAAG TTGCAATTTT CGATTTCTGA AATTTATTTG TGGCTTTTTT
 CAATBOX1 ARR1AT TATABOX5 CArG-box
 +148 TTGTTTGTTTTGTCTGTGG AAGGACCAAC GGAGTCGACT ATG
 TTTGTT motif MYB2CONSENSUSAT

Supplementary Figure S3. Genotyping of wild-type, heterozygote and homozygous *ag-1* mutant *A. thaliana* (Landsberg erecta) plants by dCAPS.



The amplicons of transgenic lines under wild-type background were cleaved By *Afl* II to produce a fragment of 355 bp fragment, the amplicons from transgenic heterozygote *ag-1 Arabidopsis* were cleaved by *Afl* II to produce a 355 bp and a 327 bp fragments, and the amplicons from transgenic homozygous *ag-1 Arabidopsis* were cleaved by *Afl* II to produce a 327 bp fragment.