

Supplemental Figure 1. Amino acid sequence comparison of plant AUG2 homologs and human HAUS2. The GenBank accession numbers are NP_565760 (At2g32980, At AUG2), NP_001061229 (Os08g0204800, Os AUG2), XP_001754674 (Pp AUG2), and NP_060567 (HAUS2).

(A) Sequence identity and similarity among At AUG2, Os AUG2, Pp AUG2 and HAUS2. Plant AUG2 homologs are compared to the human HAUS2 protein. The plant species are *A. thaliana* (At), the rice *Oryza sativa* (Os), the moss *Physcomitrella patens* (Pp).

(B) Schematic diagram of At AUG2 and HAUS2. Coiled-coil motifs are indicated in blue. Basic regions were indicated with red bars and theoretical pI values.

(C) Multiple sequence alignment of plant AUG2 homologs and human HAUS2. Conserved (identical and similar) residues among all proteins are boxed in black and those partially conserved in gray.

A

		Identity (%)			
		At AUG4	Os AUG4	Pp AUG4	HAUS4
Similarity (%)	At AUG4		61.0	56.2	19.0
	Os AUG4	72.6		56.0	19.3
	Pp AUG4	73.5	70.1		20.4
	HAUS4	36.5	34.3	36.1	

B

```

AtAUG4 : MYKALQGFAQNLPAADVNGLLDQLERHCLAPFGSLVTRKSVYSDFQIAREEMSERIRYLEAMAIYCEAVANVEEYQCALS--VANHGGLRDVCGLYPQL : 96
OsAUG4 : NSKFAAA--SLPPPPEVAHLVDQLQRHHLAPPASLLSSCAHSDLLQAREEVASERARYLEALAVYEAATANVEEYQFAISTGVANAG-----K : 88
PpAUG4 : MVKMLLPDPATALGQQCSALLDQLERHCLAPASLVSKDANLDLLQAREEMARERARYLEALAVYCEAVAVVEEYQFALS--IANVGGIRDLLNTVFDQL : 98
HAUS4 : NASGDFCSPGEG--MEILCCWCSKQLPFCNLSKEDLLQNEYESKLLLNLSLHVLESGLSLTLAKEQIQWKEVRLHKTTLWR----- : 80

AtAUG4 : GLKNSQVMELELHRLVVAEPAACKLRLLPLSDGSEIHBEETKWSILSRSSLDSEASTFLLSSTNSVNYANSANSVAG-----GISLSAVDTEVGG : 190
OsAUG4 : KUNCSEQVMELELHRLVVAEPAACKLRLLPLSDGSDVHBEETKLSLRSSEFDSMTSAAPSSSISTSYNNYSTASAATVAAAPCTGGSEFVPEPGVGG : 188
PpAUG4 : GIRSSEQVMDALEQRLVVAETQRLRLPLASKQCDLHEDDNEEWGNVSRSEDSSTTSLSLSTIISVHTTASATASIAS----GGKEPEFVPEPGVGG : 194
HAUS4 : ---S--EILHRVIGQLVVDYYVKIQDTNVVSEKKEEPLERLLVTELMRLLGFSQERE--PP----- : 138

AtAUG4 : VVNRFLGITPAVLSYVQLQN-TISMDADYCMFLAREIEGRLEKCKDADDAIVD--T-DSSVGNRNSCARLPERVFFIIEEIRDEFAATREDIYSAERK : 287
OsAUG4 : VEDRELGITSDVLYVQCQPPAMVDVYQRLAREIEARTEKCKTADADLAMD--ERSSSISQISSARLPERVKLIIEEIRKPEALILDILASMRK : 287
PpAUG4 : VVNRFLGITPAVLRCTHLIRVFPADNTQYCMFLIEIEBARLAKCKDRVSAETD--E-TGVADSAGPILRLPERVKIADIEBAEPAALIEHLIYAAERK : 292
HAUS4 : ----LGLERDLELMP----LSELFVWMRARIQCEVEECLKCKFTLLCYLDFNSDADESEVKAAKVVKIABVVLVGECCCGDAKSQQKQCMLLLRK : 230

AtAUG4 : FAEYYNVLEQILGVLLKLVKDKLEHCKVNEVCKVNIQRCETMNRKLRVLENVLLLETYTPDSTSALEHNTFNMLVEMTEPASAANKAVTFLREYQGV : 387
OsAUG4 : FAEYYNVLEQILGVLLKLVKDKLEHCKVNEVCKVNIQRCETMNRKLRVLENVLLLETYTPDSTSALEHNTFNMLVEMTEPASAANKAVTFLREYQGV : 387
PpAUG4 : FSEYYNVLEQILGVLLKLVKDKLEHCKVNEVCKVNIQRCETMNRKLRVLENVLLLETYTPDSTSALEHNTFNMLVEMTEPASAANKAVTFLREYQGV : 392
HAUS4 : SFAISQVLLRCLLLELRLQEHRLKTCSELRNNAVYEVKCGAMILKLRMEELKILSDTYTVERVEVHRIIDRLIECAIHLQEQDMENSQVLSNYEVL : 330

AtAUG4 : DPEFDLIRROYHLEIKKLENCQWTECVEMDLRSHD----- : 423
OsAUG4 : DPEFDLIRROYHLEIKKLENCQWTECVEMDLRPHDHADV : 428
PpAUG4 : DQDFDLEIRRYHLEIKKLENCQWTECVEMDLRSHD : 433
HAUS4 : GEPFDLIRVKEYTVLQKATENKRFPAIQEFSKVVYR----- : 363
    
```

Supplemental Figure 2. Sequence comparison of plant AUG4 homologs and human HAUS4. The GenBank accession numbers are AEE32582 (At1g507110, At AUG4), EAZ21518 (OsJ_05142, Os AUG4), XP_001768748 (Pp AUG4), and NP_060285 (HAUS4).

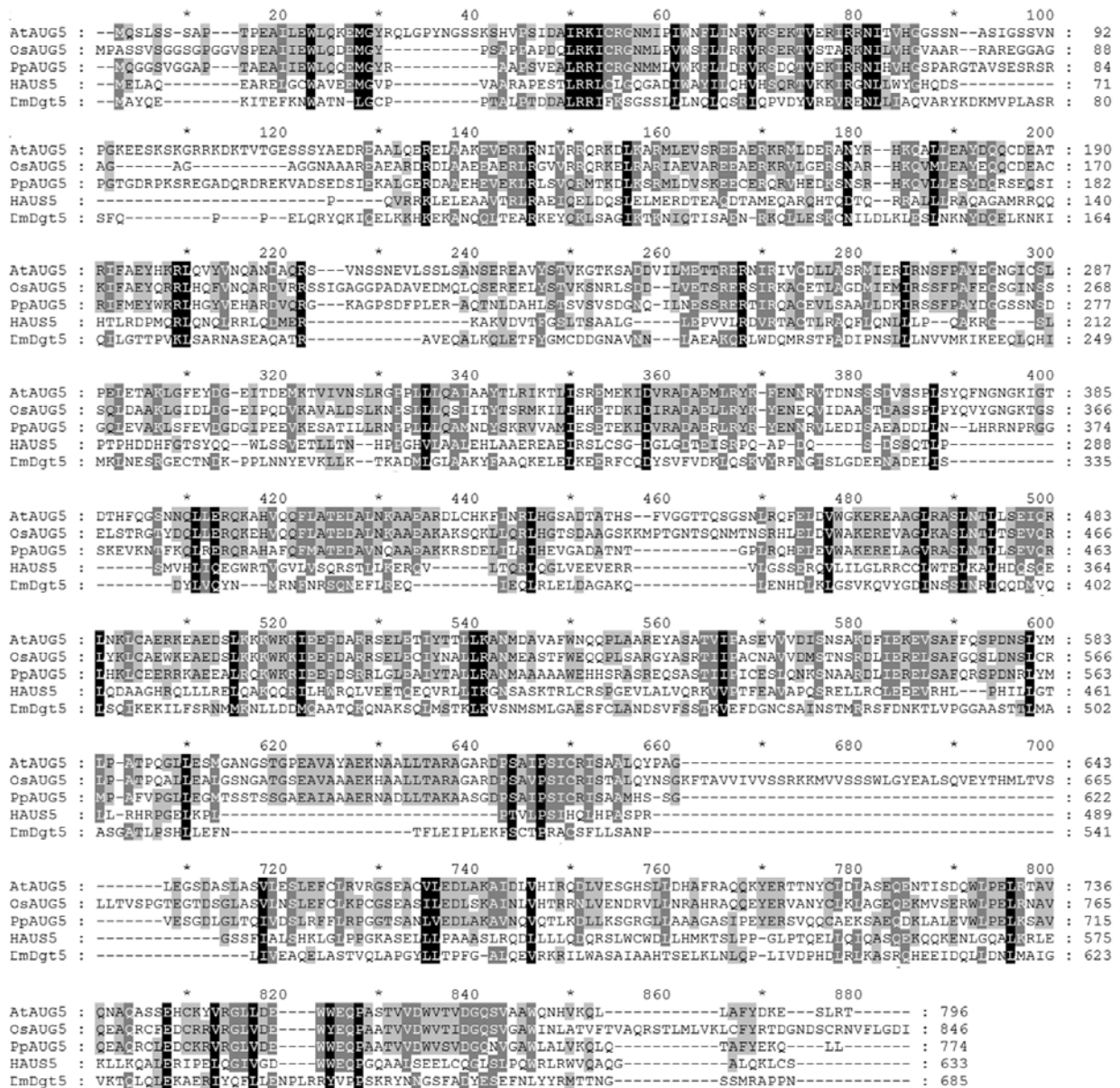
(A) Sequence identity and similarity among At AUG4, Os AUG4, Pp AUG4 and human HAUS4.

(B) Multiple sequence alignment of plant AUG4 homologs and human HAUS4.

A

		Identity (%)				
		At AUG5	Os AUG5	Pp AUG5	HAUS5	Dm Dgt5
Similarity (%)	At AUG5		54.0	48.7	18.7	18.2
	Os AUG5	66.7		44.2	19.8	13.1
	Pp AUG5	67.1	61.6		19.5	18.4
	HAUS5	31.2	32.7	34.8		17.5
	Dm Dgt5	34.7	24.3	34.7	32.1	

B



Supplemental Figure 3. Sequence comparison of plant AUG5 homologs, human HAUS5 and *Drosophila melanogaster* (fly) Dgt5. The GenBank accession

Supplemental Data. Hotta et al. Plant Cell. (2012). 10.1105/tpc.112.096610

numbers are AED94368 (At5g38880, At AUG5), EEE69629 (OsJ_29218, Os AUG5), XP_001756819 (Pp AUG5), NP_056117 (HAUS5), and NP_610785 (Dm Dgt5).

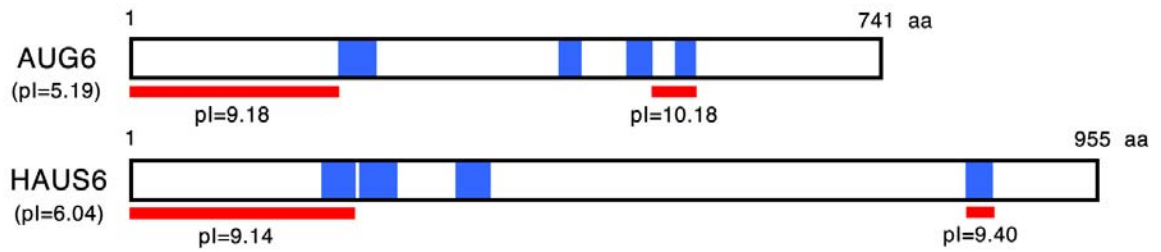
(A) Sequence identity and similarity among At AUG5, Os AUG5, Pp AUG5, human HAUS5 and Dm Dgt5.

(B) Multiple sequence alignment of plant AUG5 homologs, human HAUS5 and Dm Dgt5.

A

		Identity (%)				
		At AUG6	Os AUG6	Pp AUG6	HAUS6	Dm Dgt6
Similarity (%)	AtAUG6		59.9	32.9	15.0	19.0
	Os AUG6	72.2		34.5	16.3	18.0
	Pp AUG6	45.3	46.8		13.4	16.2
	HAUS6	26.8	26.4	24.6		16.1
	Dm Dgt6	32.2	31.1	26.0	26.3	

B



C

```

*          *          *          *          *
AtAUG6 : -----*-----20-----*-----40-----*-----60-----*-----80-----*-----100-----: -
OsAUG6 : -----*-----20-----*-----40-----*-----60-----*-----80-----*-----100-----: -
PpAUG6 : MFWSFGTRREFFYQTHFVSDLFGCTGFWRSAFVSHKGRSLADLDVDEQWTMRSPDLSDSSNLRGFKRCVKLRNYCPDREGFCVREAAFLICNMVFCFKLK : 100
HAUS6 : -----*-----20-----*-----40-----*-----60-----*-----80-----*-----100-----: -
LmDgt6 : -----*-----20-----*-----40-----*-----60-----*-----80-----*-----100-----: -

*          *          *          *          *
AtAUG6 : -----*-----120-----*-----140-----*-----160-----*-----180-----*-----200-----: 62
OsAUG6 : -----*-----120-----*-----140-----*-----160-----*-----180-----*-----200-----: 63
PpAUG6 : KGLKIQFLQAHCKKMDALLKEKDREREKENADRDREREREKEREGD-VGAAAYTNCILICGDPNVLC---PGACMRAGLFRHSNPRLGECLNIFIMC : 195
HAUS6 : -----*-----120-----*-----140-----*-----160-----*-----180-----*-----200-----: 63
LmDgt6 : -----*-----120-----*-----140-----*-----160-----*-----180-----*-----200-----: 63

*          *          *          *          *
AtAUG6 : -----*-----220-----*-----240-----*-----260-----*-----280-----*-----300-----: 162
OsAUG6 : -----*-----220-----*-----240-----*-----260-----*-----280-----*-----300-----: 163
PpAUG6 : AIRGPNLSAKDAGWPIFAAQSREFRKVVQGLINELGCGALPRNSRVSSATCCGRFVELLWHLHSAHATREVERRTFPADVASNPLPASLDELVC : 295
HAUS6 : VLD-QSLKKEVRFKQWEFECKSDTFRKHCCCEWIKRISGCGSSFPQVQGLFPLSPGGKFFIHLMYHFAFVAMKYKSNKSNSSHFFVETFNKFDLL : 162
LmDgt6 : ILD-PAEFRS--RFFWPTLRKSEANFRSSTVEYIKHNEKHCHHWAKISYLVMPGCRFNFLEFVGFVQETIQREK-SGLEAGTPNVS---- : 155

*          *          *          *          *
AtAUG6 : S-----HAAALLPVTKARIVLERRRFLKNMETAVQRCAMWSNLAHMTAEFR--GLCAEAYICCEIEKLNDRNKKVQEGEWDDLVSSSS---Q : 248
OsAUG6 : L-----HAAALLPVTKARIALERRRFLKNANIAVQRCQTWSNLAHMTAEFR--SLCAEAYICCEIEKLDNRNKKKLEGEWDERISSSSG---Q : 250
PpAUG6 : EN-----TRPVSLAVTKARIALERRRFLKNMETAVQRCQTSWSNLAHMTAEFR--ALCAEAYICCEIEKIQESSYPNVSDDSAVSDETEGFVNS--I : 384
HAUS6 : HKCIARCHEFARSRFLQLLQDCVTCRYQENQLSKQVNRNLRSECIENIHKRMEPYDDHNSNEKTKQKVRSTWASVNETLMLFEKEREVVSVLSLV : 262
LmDgt6 : L-----AKVMRQNAVMTAEAS-----SYVVNIE-----ENTLIRDKTKLIRRMADLSADMVPEEQIADDG----FL : 215

*          *          *          *          *
AtAUG6 : NSHLVS--KARRFVNDSTYARKGQ-----HEVLASGFEDLTAHREHRYRISGSALLAAMQ-----SSQVPRADLISAH----- : 315
OsAUG6 : NSHLVS--KARRFVNDSTYARKGQ-----HEVLASGFEDLTAHREHRYRISGSALLAAMQ-----SSSVPHSELSAR----- : 317
PpAUG6 : SAGFVI--RASQLKGCILSHSER-----VAELASGFEDLTAHREHRYRIDGAVLRARVVLGVSVNLFPVSSSCSTADYDSQ----- : 459
HAUS6 : NYALDGTNVATNPRPDIIDRIEKQMFQLHIGNVYEAGKINLTVICILNRYLVMRYRCCQADQARLTVLHYLEKETFKQKERLSLTKHMYRYRKDDL : 362
LmDgt6 : DEFEAT--APLQVERVITQPTER-----KFDLBSLCGLKEAIDLQFQCAENNSKBEVEK-----AURGRM----- : 276

*          *          *          *          *
AtAUG6 : -----*-----520-----*-----540-----*-----560-----*-----580-----*-----600-----: 340
OsAUG6 : -----*-----520-----*-----540-----*-----560-----*-----580-----*-----600-----: 330
PpAUG6 : -----*-----520-----*-----540-----*-----560-----*-----580-----*-----600-----: 484
HAUS6 : TTIRHSVVEKQGEWHKKWKEFLGLSPFLIKGWTPSVDLLPMSPLSFPASEEYVAKSILCQYPASLPDAHKQHNQENGCRGSDTIGALHLDLANSPAS : 462
LmDgt6 : -----*-----520-----*-----540-----*-----560-----*-----580-----*-----600-----: 296

*          *          *          *          *
AtAUG6 : LVDSEFETASSQASDETHSR-----VDRGGRIN-QTVLVAEVRRTTHAQRRHKQSL-----LAKANDCGDDELIRASDGGT-----S : 415
OsAUG6 : -----*-----620-----*-----640-----*-----660-----*-----680-----*-----700-----: 401
PpAUG6 : ITRRWTHALQTVHKQTRLLVEAVEHVIVADLLEKLN-LKNYIVAVRQKFKIISLYLRVLLGIIISGLVLKASNNCAGCEEMMESHGEE-----S : 578
HAUS6 : FTSQSVSSDRNSVIVTEK-----LTKMTPKERNEATSKKPEPEVENSTSDVAKNT-----ESSFGSLLAKKSDPFQKQDHLVVE : 543
LmDgt6 : KDALINGFNRIISGTIAEQ-----LHNDHYNESNARVTTDLQALRVES-QSEVQIN-----NLLKQNEPFSKKDK-----C : 363

*          *          *          *          *
AtAUG6 : GHVESAAITTEHQHLASFCVLLNCKEVSATQKSECTEAMNSLPPPTLPPVTRSNQCASSLLCSGSGRIMECVSNDIAETSTMSNVCKEYVSS : 515
OsAUG6 : THADSLTALIAHRRQHLVSHCGLLNCKEAIKAMQCSHADLSEVNSVSS--NPMDRISRLSPVQNSGFGRAE--SSSEIEMSTSKLSTHDKAGS : 498
PpAUG6 : VHVHSHRTLICEHKQHFSSLSRSLKNCLEASMPGMEAAITLIRVBCPDMTMAASRAQNALIVTSKTSHWVATSRLEDLEQSALEFINNSAMPLELTPS : 678
HAUS6 : VARAVSDPQLSEKGEIKLBEELISGNSNPLTRNCPRTPEINITEIRSSWRKAIEEMENRKEPIQMDAHRVLPESFVHLNQRFSMADFLLEP : 643
LmDgt6 : SANAGSARVQTLQPATPRFESVSSK-----FVS-----TPPIRIDMGGGGGRNAP---VRLALCGDFNQRQFDALNSLAPAPPRARRKALDGS : 449

*          *          *          *          *
AtAUG6 : FTTRKPLQLFSSPSSSGKGGCKRQTVASQVNRKESLSEKNSIDQAL-SNARPD-----*-----820-----*-----840-----*-----860-----*-----880-----*-----900-----: 569
OsAUG6 : PAUKRPLFLSLAPSSSGKGTCAKRNALGRQP-SCEILSEKTLPLPS--TKDET-----*-----820-----*-----840-----*-----860-----*-----880-----*-----900-----: 551
PpAUG6 : PAUKRPL--YTSANGVSTFSKAASG--SSMP-SIDVLCGEGLENG--IVWN-----*-----820-----*-----840-----*-----860-----*-----880-----*-----900-----: 726
HAUS6 : TVSDFG--QSHLEEKVISDCCVPPKHVLTSHDEPPTCNQDILLNKVICHQDLECLAFKLTSETSRMETFSPAAGNRIDVGGSEEFMILDLHLE : 740
LmDgt6 : TCGDIN--G-ILNRSKINDPMLRTHKNTSKAAPANLSSIG-----SK-----*-----820-----*-----840-----*-----860-----*-----880-----*-----900-----: 494

*          *          *          *          *
AtAUG6 : -----*-----920-----*-----940-----*-----960-----*-----980-----*-----1000-----: 645
OsAUG6 : -----*-----920-----*-----940-----*-----960-----*-----980-----*-----1000-----: 627
PpAUG6 : -----*-----920-----*-----940-----*-----960-----*-----980-----*-----1000-----: 803
HAUS6 : VSCNKPSTNKTMLWNSFGISGISSKSPDNDFCILHETPEEVGHLSFNSSSEANFKLEPNSPMHGTLLEDVVGGRCPTTPEDFNLQALRSRYEAL : 840
LmDgt6 : -----*-----920-----*-----940-----*-----960-----*-----980-----*-----1000-----: 559

*          *          *          *          *
AtAUG6 : PSFLEPNVPDSFAPSK--YSDLPDYDLDLSD--FKDYDNGGFLSAGS--NSVASDAQCSFYDIDDQVFSFPTLNDSS---LLSDAYEDLVAHT : 731
OsAUG6 : MKESDLHFN--VDSF--MHATVYSSKLN-----GHDDRTVTSLLDP-----VSGGHQSFITDLDLQVFSFPLLETS---LFCDAYEDLVAHT : 707
PpAUG6 : PTFPSENDRDVEEK--NGYVADPCNFVRGVPMSRKGILGRQHERSSWKSPhDLPQRTSELVHDFQPTSSSLFDCNSFDRTEFGDTYDNLVAAP : 900
HAUS6 : KRSKSKREESVLSNSGTPRHRKPELSPTPQN--VQDTEFLFLDCLDHL--TEHKPSLRISIGERKRSPLKFSFV--EQLRRTIACSGSD : 931
LmDgt6 : IKVIEVSRNVLNIST--PSGRIDAVPHTES--HQQDVAP--R--QLN--DRTINDSLQ-----LDFDFNEND--KNAENVSHKFDQDC : 635

*
AtAUG6 : S--ETEAALVEH----- : 741
OsAUG6 : S--ETATALVEH----- : 717
PpAUG6 : T--DLSAFMSIGDRRETRAI-- : 919
HAUS6 : PNLKEDLILNKSLDAKEPPSDLTR : 955
LmDgt6 : G--GSDLLQNSDSVLYK--DIIF : 654

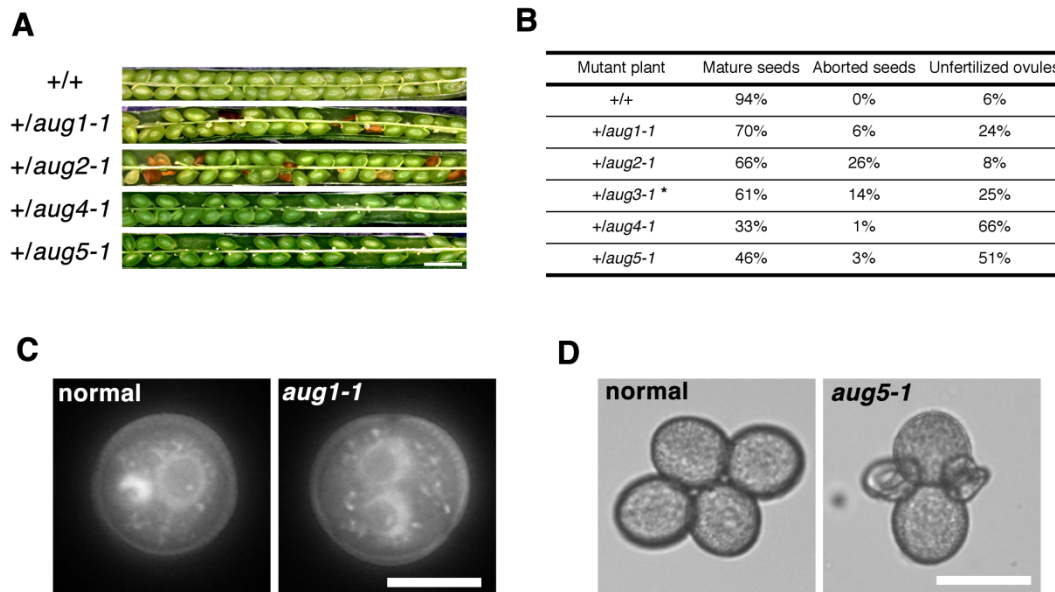
```

Supplemental Figure 4. Sequence comparison of plant AUG6 homologs, human HAUS6 and Dm Dgt6. The GenBank accession numbers are NP_568585 (At5g40740, At AUG6), NP_001046716(Os02g0329300, Os AUG6), XP_001773092 (Pp AUG6), NP_060115 (HAUS6), and AAF56860 (Dm Dgt6).

(A) Sequence identity and similarity among At AUG6, Os AUG6, Pp AUG6, HAUS6 and Dm Dgt6.

(B) Schematic diagram of At AUG6 and HAUS6. Coiled-coil motifs were indicated in blue. Basic regions are indicated with red bars and theoretical pI values.

(C) Multiple sequence alignment of plant AUG6 homologs, HAUS6 and Dm Dgt6.



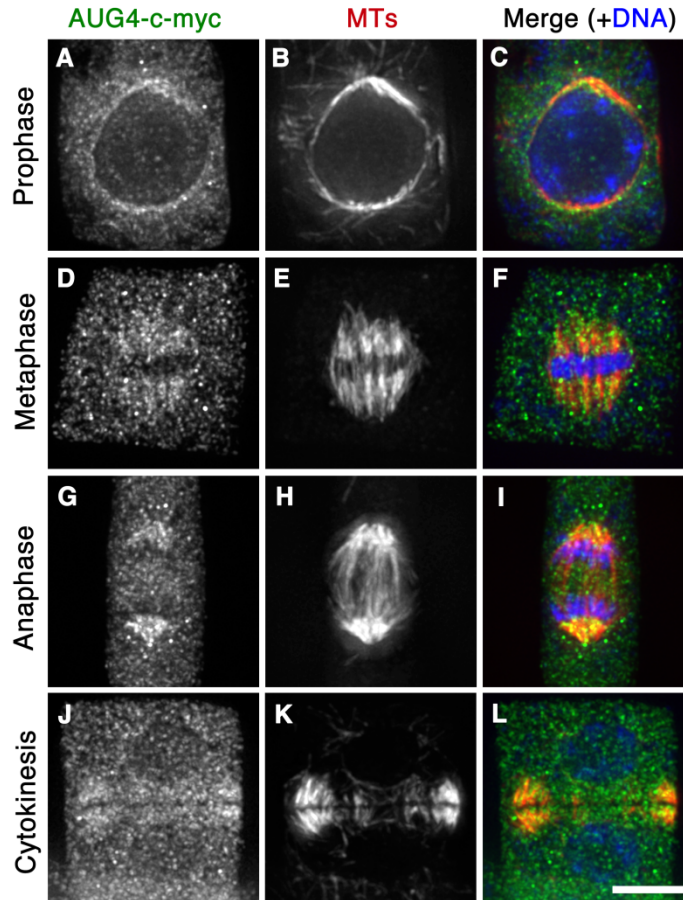
Supplemental Figure 5. Phenotypes caused by the *aug1-1*, *aug2-1*, *aug4-1* and *aug5-1* mutations.

(A) Defects in developing fruits/siliques in the mutants. Compared to the siliques produced by the +/+ (WT) control plant, heterozygous *aug1-1*, *aug2-1*, *aug4-1* and *aug5-1* mutants contain white unfertilized ovules and brown aborted seeds. Bar = 1 mm.

(B) Percentages of normal seeds, unfertilized ovules (white), and aborted seeds (brown) in siliques produced by the control (+/+) and heterozygous mutants.

(C) DNA staining of control and defective pollen grains produced by an +/*aug1-1* plant. A control pollen grain after mitosis I contains a brightly stained generative nucleus and a less bright vegetative nucleus (left panel). A defective pollen grain contains two identically stained nuclei resembling the vegetative nucleus (right panel). Bar = 10 μ m.

(D) Attached tetrad pollen grains produced by the +/*aug5-1* *qrt/qrt* plant. A normal tetrad contains fully enlarged four pollen grains attached together (left panel). A tetrad produced by the +/*aug5-1* *qrt/qrt* plant contains two enlarged pollen grains and two shrunken pollen grains (right panel). Some attached tetrads contained three enlarged pollen grains. Bar = 30 μ m.



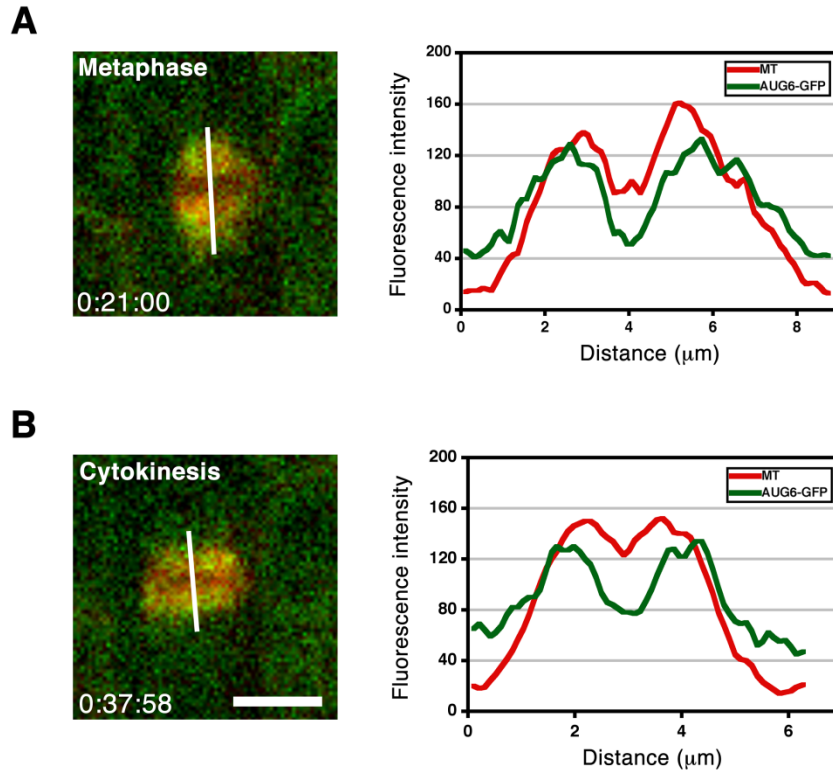
Supplemental Figure 6. Localization of AUG4-c-myc in mitotic root cells. In merged images, AUG4 is pseudocolored in green, MTs in red, and DNA in blue. Bar = 5 μ m.

(A-C) AUG4-c-myc signal appears along MTs of prophase spindle on the nuclear envelope.

(D-F) AUG4-c-myc localizes along kinetochore fiber MTs in the metaphase spindle.

(G-I) AUG4-c-myc signal is enhanced on the shortening kinetochore fiber MTs during anaphase.

(J-L) AUG4-c-myc signal decorates phragmoplast MTs.



Supplemental Figure 7. Measurement of the fluorescence intensity of AUG6-GFP in the metaphase spindle and phragmoplast shown in Figure 3M.

(A) and (B) The fluorescence intensities of AUG6-GFP and mCherry-TUB6 are measured in the spindle (A) and phragmoplast (B) along white lines indicated in the left panels. Both graphs on the right show that the AUG6-GFP signal is biased toward minus ends of MTs. Bars = 5 μm .

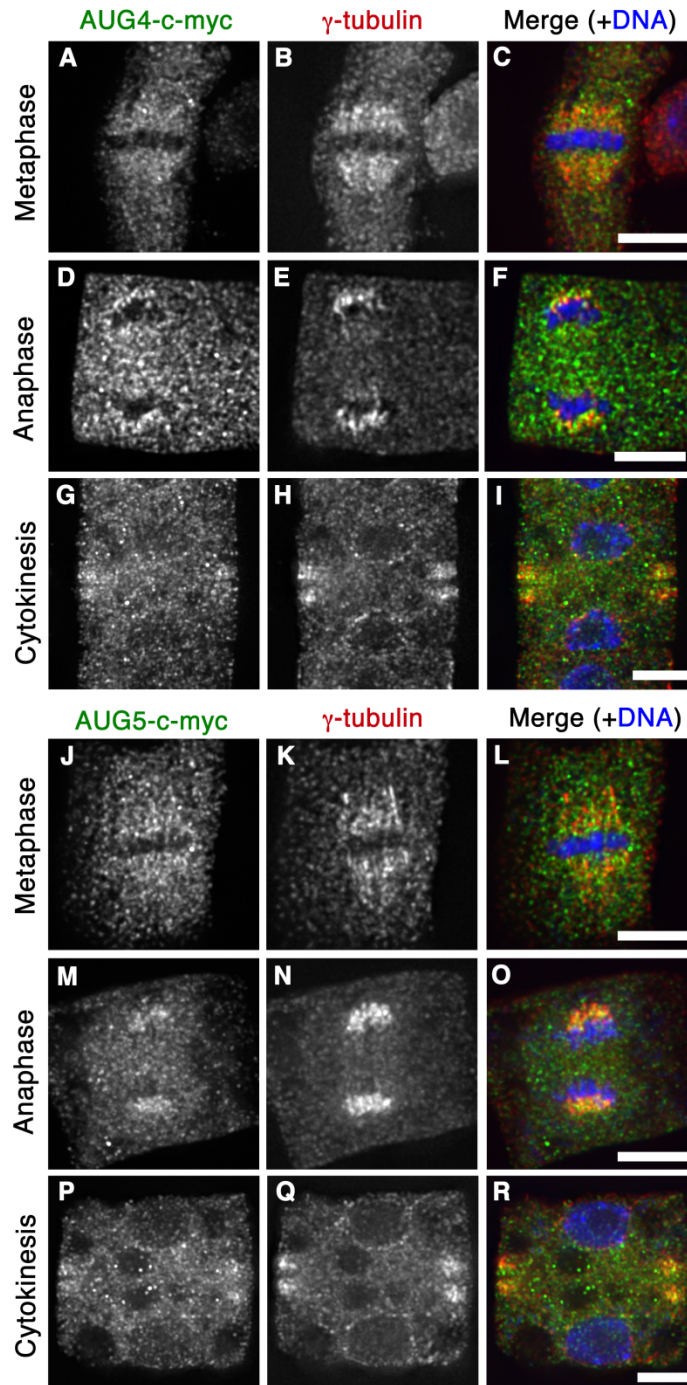
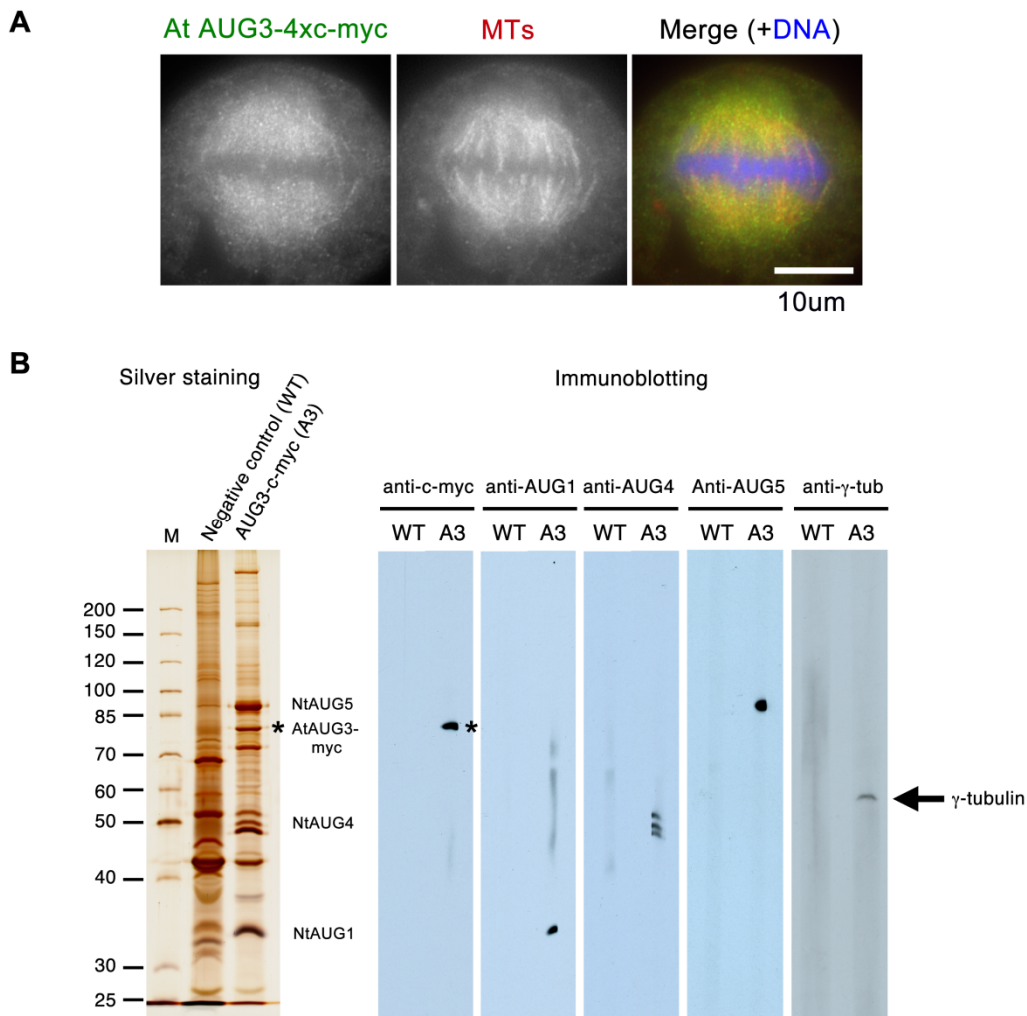


Figure 8. Dual localizations of AUG4/AUG5 and γ -tubulin. In the merged images, AUG4 or AUG5 are shown in green, γ -tubulin in red and DNA in blue. Bars = 5 μ m.

(A-I) AUG4-c-myc and γ -tubulin. (J-R) AUG5-c-myc and γ -tubulin. Both AUG4 and AUG5 colocalize with γ -tubulin in metaphase (A-C, J-L), anaphase (D-F, M-O), and cytokinesis (G-I, P-R).



Supplemental Figure 9. Detection of the interaction between augmin and γ -tubulin *in vivo*.

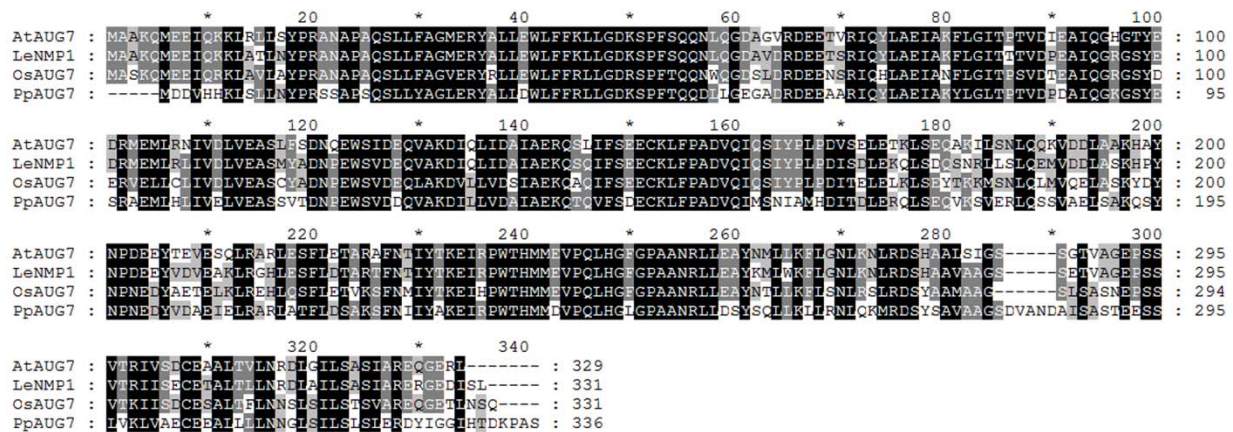
(A) At AUG3-c-myc localization inside the spindle of a BY-2 cell. AUG3 signal decorates along spindle MTs as seen in the *Arabidopsis* cells. In the merged image, AUG3 is shown in green, MTs in red, and DNA in blue. Bar = 10 μ m.

(B) At AUG3-c-myc forms a complex with tobacco augmin subunits. When At AUG3-c-myc is enriched by immuno-affinity purification from BY-2 cells expressing the protein, at least three tobacco augmin subunits can be detected by immunoblotting using anti-AUG1, anti-AUG4 and anti-AUG5 antibodies (right panel, immunoblotting). γ -Tubulin is also detected by an anti- γ -tubulin antibody (arrow). The bait, At AUG3-c-myc is marked by asterisks.

A

		Identity (%)			
		AtAUG7	LeNMP1	OsAUG7	PpAUG7
Similarity (%)	AtAUG7		83.1	71.1	57.2
	LeNMP1	90.9		72.9	60.7
	OsAUG7	85.5	88.0		59.5
	PpAUG7	76.8	77.7	77.7	

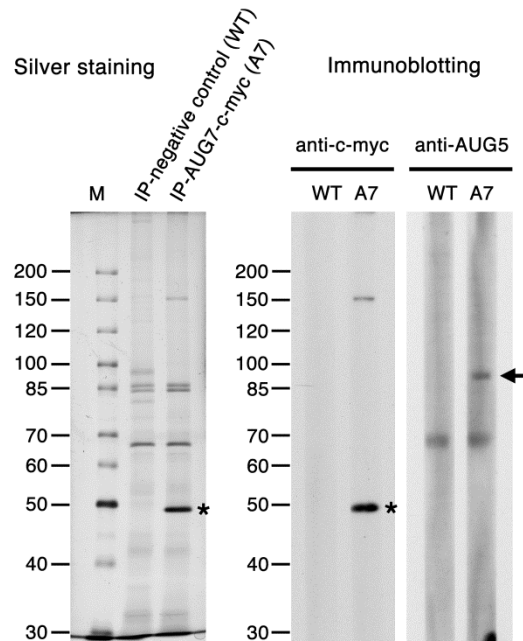
B



Supplemental Figure 10. Sequence comparison of the AUG7 homologs. The GenBank accession numbers are NP_568354 (At5g17620, At AUG7), NP_001234492 (SI NMP1), NP_001044927 (Os01g0869500, Os AUG7), and XP_001777152 (Pp AUG7).

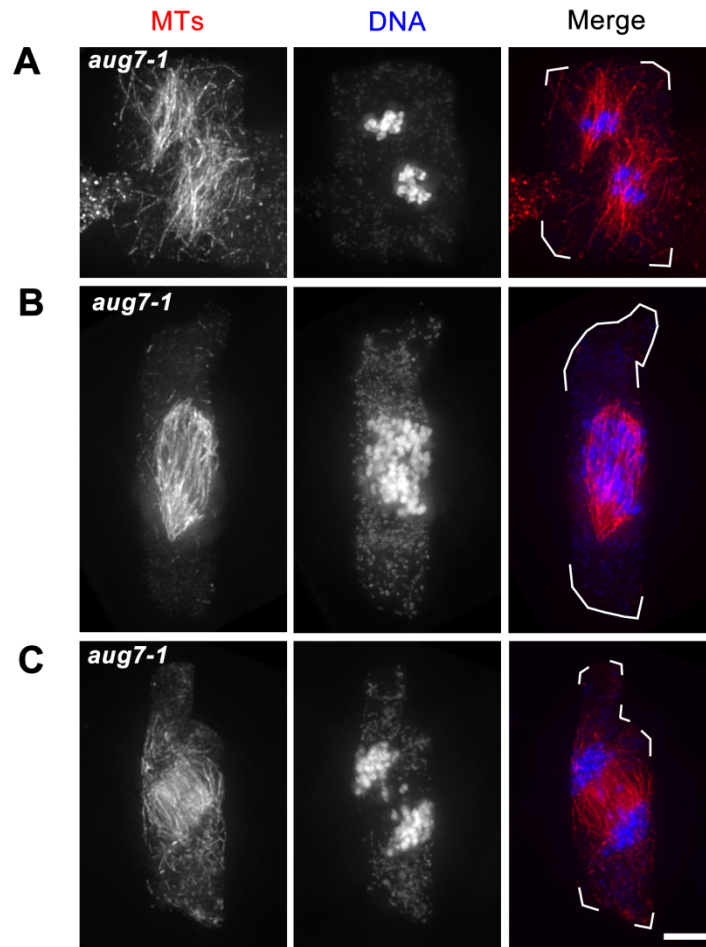
(A) Sequence identity and similarity among At AUG7, SI NMP1 (tomato AUG7 homolog), Os AUG7, Pp AUG7.

(B) Multiple sequence alignment of plant AUG7 homologs. Conserved (identical and similar) residues among all proteins are boxed in black and those partially conserved in gray. AUG7 is highly conserved in the plant kingdom.



Supplemental Figure 11. Interaction of AUG7 and AUG5 *in vivo*.

Proteins were extracted from transgenic Arabidopsis plants expressing AUG7-c-myc, and the fusion protein was enriched by anti-c-myc affinity purification (left panel, silver staining). In addition to AUG7-c-myc revealed by the anti-c-myc antibody (asterisks), AUG5 was detected by the anti-AUG5 antibody (arrow in the right panel).



Supplemental Figure 12. Dividing *aug7-1* cells with excessive numbers of chromosomes. MTs are shown in red and DNA in blue. Cell outline is indicated by white frames. Bar = 5 μ m.

(A) A cell undergoing mitosis contains two metaphase spindles.

(B) An anaphase cell with excessive number of chromosomes.

(C) Phragmoplast is formed between two reforming nuclei containing excessive number of chromosomes.

Supplemental Table 1. List of the peptides identified in the LC-MS/MS analysis corresponding to Figure 1. Sample #, as the number shown in Figure 1A; Gene ID, genetic locus identified by TAIR; # peptide, number of unique peptides; peptide sequence, sequences of unique peptides identified.

Sample#	Gene ID	Gene Name	# peptides	Peptide sequence			
1	At5g38880	AUG5	50	AGARDPSAIPICR AHVQOFLATEDALNK AHVQOFLATEDALNKAAEAR AIDLWHR ANMDAVAFWVWQOPLAAR DKTVTGESSSYAEDR DPSAIPICR EAVYSTVK ELAAKEVER EVLSSLSANSE FENNRVTDNSSSDVSSPLSYQFNNGK GNMIPWFLINR GSEACVLEDLAK HKQALLEAYDQCCDEATR IFAEYHGR IGTDTHFGGSSNOLLER IRNSFPAYEGNGICSLPELETAK IVCDLLASR KEAEDSLKKK LGFEDYDGEITDEM LHGSADTATHSFPVGGTTQSGSNLR LNKLCAR LOVYVNOANDAQR MLEVSRREEAER NAALLTAR NITVHGGSSNASIGSSVNPQKEESK NSFPAYEGNGICSLPELETAK OALLEAYDQCCDEATR ODLVESGHSLLDHAFR QFELDVWGKER QKAHVQOFLATEDALNK QKAHVQOFLATEDALNKAAEAR QLGPNYSSSK QLLAFYDKESLRT RLOVYVNOANDAQR RNITVHGGSSNASIGSSVNPQKEESK RSELETIYTLLK SADDVILMETTR SADDVILMETTRER SHVPSIDAIR SVNSSNEVLSSLSANSE SVNSSNEVLSSLSANSEREAVYSTVK TAVONQAASSEHCK TIYTLLKANMDAVAFWVWQOPLAAR TVTGESSSYAEDR TVTGESSSYAEDREAALQER TVTGESSSYAEDREAALQERELAAK VRGSEACVLEDLAK VTDNSSSDVSSPLSYQFNNGK VTDNSSSDVSSPLSYQFNNGKIGTDTHFGGSSN			
				At5g48520	AUG3	10	ALIQRRRARVAATSAVSGQITAIEDLSAR KNMLGAFSLK LOTQYDLLTGSSALIQGR LSTAVEEVLEHR QWIEAQVENAK RNNQEAVFGEESIKEVR RVFVDFCNP VAATSAVSGQITAIEDLSAR VFVDFCNP VIESELOGVLSATR
				At5g40740	AUG6	6	ANGDGFILR DSQSDGSEHIFVPLSATGFSR EALLIPSSAGSSR LPQLFSSTPTSSGK VKQEGEVWDLVSSSQNSHLVSK VSASPTLKLPLFSSTPTSSGK
2	At5g48520	AUG3	10	DATLAHKAELQLR LOTQYDLLTGSSALIQGR LSTAVEEVLEHR LSTAVEEVLEHRNKREIV LVAEEGSK NLQMGVLR QLDTGPYRLVAEKG RNNQEAVFGEESIKEVR RNNQEAVFGEESIKEVR VFVDFCNP			
				At5g38880	AUG5	2	IVCDLLASR LHGSADTATHSFPVGGTTQSGSNLR
	3	At1g50710	AUG4	18	CDKLADAVDDTDSSTGNR CDKLADAVDDTDSSTGNRSSAR DVQGLYPQLGLK EKCDKLADAVDDTDSSTGNR EYQGVDPHFDIAR HCLAPDGLVTK KAVTRLREYQGVDPHFDIAR KLENMOWTHIQVEMDLK LADAVDDTDSSTGNR LADAVDDTDSSTGNRSSAR LKEKCDKLADAVDDTDSSTGNR LPLISDGGIHEEIEK LREYQGVDPHFDIAR LVVAEAAQK NSPOVYVLEHR NSPOVYVLEHRLVVAEAAQK SVYSDQLAR SVYSDQLAREEMSR		
	At5g38880	AUG5	3	IVCDLLASR NITVHGGSSNASIGSSVNPQKEESK SVNSSNEVLSSLSANSE			
4	At2g41350	AUG1	33	AKAKESNALLDYTR AKAKESNALLDYTRK ALALAIEDK ALALAIEDKKR AQKESNALLDYTR AQKESNALLDYTRK ASEYRAQAAR AWLTSQFEAVGK EEQYIQQYK ELDKMTKPVLDLTLR ELVEMAEHR ELVEMAEHRK ELVEMAEHRKELDKMTKPVLDLTLR ESNALLDYTR ESNALLDYTRK EVPNFEYTHR ILAQLEDDVVPCEOMENWK ISEVKAWLTSQFEAVGK ISHRELVEMAEHRK KELDKMTKPVLDLTLR MTKPVLDLTLR SDVTGDAAVSEAKGSSDAAR SDVTGDAAVSEAKGSSDAAR SITHLYNLATASQAK SOAATIVANDFR SOAATIVANDFRK SYQDLPPDK SYQDLPPDKALALAIEDK SYQDLPPDKALALAIEDKKR TNLEVMVAVKEEQYIQQYK TNLEVMVAVKEEQYIQQYK YEMLLNR YLEEVLSQALETNDE			
				At2g32980	AUG2	1	ITQIKDVIGNKDR

Supplemental Table 2. Transmission efficiency (TE) of *aug* mutant alleles in reciprocal crosses between heterozygous mutants (+*aug*) and WT (+/+) plants.

Mutant tested	Progeny genotype when mutant as pollen donor	TE _{male} ^b	Progeny genotype when mutant as ovule donor	TE _{female} ^b
+ <i>aug1-1</i>	20 + <i>aug</i> : 167 +/+	12% ^c	39 + <i>aug</i> : 108 +/+	36% ^c
+ <i>aug2-1</i>	54 + <i>aug</i> : 74 +/+	73% ^d	62 + <i>aug</i> : 91 +/+	68% ^d
+ <i>aug3-1</i> ^a	61 + <i>aug</i> : 102 +/+	60% ^c	49 + <i>aug</i> : 131 +/+	37% ^c
+ <i>aug4-1</i>	14 + <i>aug</i> : 106 +/+	13% ^c	30 + <i>aug</i> : 94 +/+	32% ^c
+ <i>aug5-1</i>	75 + <i>aug</i> : 138 +/+	54% ^c	36 + <i>aug</i> : 80 +/+	45% ^c

Note:

^a Ho *et al.* (2011b)

^b TE = (number of +*aug* progeny)/(number of +/+ progeny) x 100%

^c The probability calculated by the chi-square test based on the expected TE = 100% (or 1 +*aug* : 1+/+ segregation) was smaller than 0.001.

^d The probability calculated by the chi-square test based on the expected TE = 100% (or 1 +*aug* : 1+/+ segregation) was between 0.01 and 0.1.

Supplemental Table 3. List of the peptides identified in the LC-MS/MS analysis corresponding to Figure 4. Sample #, as specific immune-purification experiments shown in Figure 4C; Gene ID, genetic locus identified by TAIR; # peptide, number of unique peptides; peptide sequence, sequences of unique peptides identified.

Sample#	Gene ID	Gene Name	# peptides	Peptide sequence
AUG3-myc IP	At2g41350	AUG1	15	ALAALAIEDK AWLTSQFEAVGK ESNALLDYTR ESNALLDYTRK EVPNFEYTHR ILAQLEDDVVPCEQSMENWK KYEOMLLNR MTKPVLDTLR SDVTGDLAAVSEAK SITHLYNLATASQAK SQAATIVANDFR SYQDLPPDKALAALAIEDK TNLEVMVAVKEEQYIQQYK TNLEVMVAVKEEQYIQQYK YLEEVLQSALETNDE
	At5g48520	AUG3	25	ALIQRRRARVAATSAVSGQITAIEDLSAR CSALIQAAADVQEOGAVDDRRDLSFLHGVR CSWVSLDDTSMNLR DATLAHKAEALELQR HADLVEEISTLYQK HADLVEEISTLYQKEEK KHADLVEEISTLYQK KHADLVEEISTLYQKEEK KNMLGAFSLK LLEGDDLDQAYDSISAFSSR LQTQYDLLTGQSSALIQR LSTAVEEVTLEHR NLQMGVGLGR NMLGAFSLK NNOEAVFGAEESIKEVR QWIEAQVENAK RLQTYDLLTGQSSALIQR RNNQEAIVFGAEESIK RVFVDFCNPFR SQVTSVEAHIFDLHSLR VAATSAVSGQITAIEDLSAR VFINHLVNLQAR VFVDFCNPFR VIESELOGYLSATR VMRQELYISK
	At1g50710	AUG4	16	CDKLADAVDDTDSSTGNR DVQGLYPQLGK EYQGVDPHFDTIAR FIIIEIERDEAALR FIIIEIERDEAALREDLYSADRK HCLAPDGLVTK KLENMQWTIHQVEMDLK LETYTPDISALHNIR LPLISDGGIEHEEIEK LREYQGVDPHFDTIAR LRLPLISDGGIEHEEIEK LVVAEAAQK NSPQVYETLEHR NYLVEATEEASAAYNK SVYSDLQLAR VLENVLLLETYTPDISALHNIR
At5g98880	AUG5	35	AGARDPSAIPSICR AHVQQFLATEDALNK AIDLVIHR ANMDAVAFWNOQPLAAR ASLNTLLSEIQR DKTYTGESSYAEDREAALQER EYASATVIPASEVVDISNSAK GSEACVLEDAK HKOALLEAYDQCCDEATR IFAEYHKR IGDTHFQGSNNOLLER IVCDLLASR LGFYDGEITDEM LHGSADTATHSVGGTTQSGSNLR LQVYVNOANDAQR NAALLTAR NITVHGGSSNASIGSSVNPKEESK NSFPAYEGNGICSLPELETAK QALLEAYDQCCDEATR ODLVESGSHLLDHAFR OKAHVQFLATEDALNK QLLAFYDKE QLLAFYDKESLRT RNITVHGGSSNASIGSSVNPKEESK RSELETIYTLK SADDVILMETTR SELETIYTLK SHVPSIDAIR SHVPSIDAIRK SVNSSNEVLSLSANSER TYITLLKNMDAVAFWNOQPLAAR TNYCLDLASEQENTISQWLPCLR TVTGESSYAEDREAALQER VRGSEACVLEDAK VTDNSSSDVSSPLSYQFNQNGK	

Sample#	Gene ID	Gene Name	# peptides	Peptide sequence
AUG3-myc IP (continued)	At5g40740	AUG6	2	SNGQASSLLQSQSSGR VKQEGEVWDDLVSSSQNSHLVSK
	At5g17620	AUG7	5	ANAPAGSLLFAGMER DLGILSASIAFR IVSDCEAALTVLNR LFPADYVQISYPLPDVSELETK SPFSQONLQGDAGVREDETVR
	At4g30710	AUG8	2	CPSPSVTRPTVSSSSQSVAAK RATLATAVARLHPLPAPGSRPASPFR
AUG4-myc IP	At2g41350	AUG1	25	ALAALAIEDK ALAALAIEDKK ALAALAIEDKKR AWLTSQFEAVGK DTESSFLVAMGDISLR DTESSFLVAMGDISLRK DTESSFLVAMGDISLRKTGVEEKR ELVEMAEHR ESNALLDYTR ESNALLDYTRK EVPNFEYTHR ILAQLEDDVVPCEQSMENWK KILAQLEDDVVPCEQSMENWK KYEOMLLNR MTKPVLDTLR SDVTGDLAAVSEAK SITHLYNLATASQAK SQAATIVANDFR SYQDLPPDK SYQDLPPDKALAALAIEDK TNLEVMVAVK TNLEVMVAVKEEQYIQQYK YEMLLNR YLEEVLQSALE YLEEVLQSALETNDE
	At2g32980	AUG2	8	ESFATLQELR FFEAMSAMR IADLQVELQGR IESSFDLAVHK KIADLQVELQGR LQQPSYSLDCIPVEAEYOK LSVYORKIADLQVELQGR NVAHLTHVGMOK
	At5g48520	AUG3	39	ALIQRRRARVAATSAVSGQITAIEDLSAR CSALIQAAADVQEOGAVDDRRDLSFLHGVR CSWVSLDDTSMNLR CSWVSLDDTSMNLRDLEK DATLAHKAEALELOR DGKLEGGDDLQAYDSISAFSSR DSFLHGVR HADLVEEISTLYQK HADLVEEISTLYQKEEK KHADLVEEISTLYQK KHADLVEEISTLYQKEEK KNMLGAFSLK LACQLEK LCSLVAELGYEGAGK LLEGDDLQAYDSISAF LLEGDDLQAYDSISAFSSR LLETIPCLWELAQDQTYLQGDYDLK LQTQYDLLTGQSSALIQR LSTAVEEVTLEHR NLQMGVGLGR NMLGAFSLK NNOEAVFGAEESIK NNOEAVFGAEESIKEVR QKVFINHLVNLQAR QOAILTLK QWIEAQVENAK RLQTYDLLTGQSSALIQR RNNQEAIVFGAEESIK RNNQEAIVFGAEESIKEVR RVFVDFCNPFR SIFGTSER SQVTSVEAHIFDLHSLR VAATSAVSGQITAIEDLSAR VFINHLVNLQAR VFVDFCNPFR VIESELOGYLSATR VMRQELYISK WELAQDQTYLQGDYDLK
	At1g50710	AUG4	37	AICYEAVMVEEYQQAISVANHGGR ALQGAQNLPADVNLQIDQLER AVDTRVGGVFN CDKLADAVDDTDSSTGNR DEAALREDLYSADR DEAALREDLYSADRK DVQGLYPQLGK EDLYSADRK EYQGVDPHFDTIAR FIIIEIERDEAALR

Supplemental Data. Hotta et al. Plant Cell. (2012). 10.1105/tpc.112.096610

Sample#	Gene ID	Gene Name	# peptides	Peptide sequence
AUG4-myc IP (continued)	At1g50710 (continued)	AUG4 (continued)	37	<p> FIIEIERDEAALREDLYSADR GAAQNLPADVNLIDQLER HCLAPDGSGLVTK IEEIERDEAALR KAVTFLREYQGVDPHFDTIAR KLENMOWTIHQVEMDLK LADAINVDDTDSSTGNR LADAINVDDTDSSTGNRNSSAR LENMOWTIHQVEMDLK LPADVNLIDQLER LPLISDGGGEIHEEIEK LPLISDGGGEIHEEIEKWSILSR LREYQGVDPHFDTIAR LRLPLISDGGGEIHEEIEK LVVAEAAQK NSPOVYETLEHR NYLVEATEEASAAAYNK SDGGGEIHEEIEK SPOVYETLEHR SSANSVAGGISLSAVDTRVGGVGNR STSNVNYANSANSVAGGISLSAVDTRVGGVGNR SVAGGISLSAVDTRVGGVGNR SVYSDLQLAR VKFIIIEIER VKFIIIEIERDEAALR VLENVLLLETYPDSISALHNIR YLEAMAIYCEAVMVEEYQQAISVANHGGIR </p>
	At5g38880	AUG5	53	<p> ADAEMLR AHVQOFLATEDALNK AIDLWHIR ANMDAVAFWVWQPLAAR ASLNTLLSEIQR DKITVTESSSYAEDR DPSAIPSIQR EYASATVIPASEVVDISNSAK EYASATVIPASEVVDISNSAKDFIEK GLLDEWWEQPASTVVDVDTVGGVSAVAWQNHVK GPELLLQAIAYTLR GSEACVLEDLAK GSTGPEAVAYAEK HKQALLEAYDQCCDEATR IGTDFHFQGSNNOLLER IGTDFHFQGSNNOLLEROKAHVQOF IRNSFPAYEGNGICSLPELETAK ISAAALQYPAGLEGSASLASVLESLEFCLR IVCDLLASR KIEFFDAR LGFEYDGEITDEMCK LGFEYDGEITDEMKTIVVNSLR LHGSADTATHSFVGGTQSGSNLR LOVYVNOANDAQR MLEVSRREEAER MQSLSSSAPTPEALILEWLQK NAALLTAR NITVHGGSSNASIGSSVNPQK NITVHGGSSNASIGSSVNPQKKEESK NSFPAYEGNGICSLPELETAK QALLEAYDQCCDEATR QDLVESGHSLLDHAFR QDLVESGHSLLDHAFFRAQQKYER QFELDVWQK QKAHVQOFLATEDALNK QLGPYNGSSK QLLAFYDKESLR QLLAFYDKESLRT RLQVYVNOANDAQR RSELETIYTTLLK SADDVILMETTR SELETIYTTLLK SHVPSIDAIRK SVNSSNEVLSSL SVNSSNEVLSSLANSER TAVONAQASSEHCK TIYTTLLKANMDAVAFWVWQPLAAR TTNVCLDLASEQENTISDQWLPRLR TVTGESSSYAEDR TVTGESSSYAEDREAALQER VRGSEACVLEDLAK VTDNSSDVSPLSYQFNGNGK WQNHVKQLLAFYDKESLRT </p>
	At5g40740	AUG6	21	<p> ALTSLEPSFLEPNVDFSAFQK ANDGDGPDILR DFDKVVPIFDSAQSR DSQSDGEGSEHYFVPLSATGFQR EAALLIPSSAGSSR EHYFVPLSATGFQR GLCAEEAYLQEQLEK IMEGVSNDAELTSTMSNVQLEK INQTVDAVEIQR ISGSALLAAMDQSSQVPR </p>

Sample#	Gene ID	Gene Name	# peptides	Peptide sequence
AUG4-myc IP (continued)	At5g40740 (continued)	AUG6 (continued)	21	<p> ISGSALLAAMDQSSQVPRAEILLSAHS LPQLFSSPTSSGK LWDSIMAR NSTDQALSINRPNLPTDSSSFVHNLK QEGEVWDDLVSSSSQNSHLVSK QTMASOVNKMESLSEK SNGOASSLLOSGQSGR TFPADVASNPLPSSLTDVFSHAATLLPVTK VKQEGEVWDDLVSSSSQNSHLVSK VSSLATCCGPR </p>
	At5g17620	AUG7	12	<p> AFNTIYTK ANAPAQSLLFAGMER ARLESFLETAR DIQLIDAIER DLGLSASIAR FLGITPTVDIEAIOGHGTIEDR IQYLAEIAK IVSDCEAALTVLNR LLEAYNMLLK NIVDLVEASLFDSDNQEWSIDEQVAK QSLIFSECK SPFSQOQLQGDAGVREDETVR </p>
	At4g30710	AUG8	8	<p> AESVMYIQR ASYIEDVHQLR ATLATAVAR CEDLLASTAIMQIEECSLR DHVSSLVGAISDLEANTLR KASYIEDVHQLR REEGEDAETPPPLPLSK TSFLSSSSISR </p>
AUG5-myc IP	At2g41350	AUG1	22	<p> ALAALAIEDK ALAALAIEDKK AWLTSQFEAVGK DTESSFLVAMGDILSR DTESSFLVAMGDILSRK ELVEMAEHR ELVEMAEHRK ESNALLDYTR ESNALLDYTRK EVPNFEYTHR ILAQLEDDVVPCEQSMENWK KYEMLLNR MTKVPLDILR SDVTGDLAAVSEAK SITHLYNLATASQAK SOAATVANDFR SYQDLPPDK SYQDLPPDKALAAIAEDK TNLVEMAVK TNLVEMAVKEEQYIQQYK YEMLLNR YLEEVLSALETNDE </p>
	At2g32980	AUG2	6	<p> ESFATLQELR FFEAMSAMR IADLOVELQGR IESSFDLAVHK KIADLOVELQGR LQPPYSLDCIPVEAEYQK </p>
	At5g48520	AUG3	33	<p> CSALIQAAASDVQEGAVDDR CSALIQAAASDVQEGAVDDRSLHGV CSWVSLDSTSNMLR DATLAHKALELQOR DGKLEGGDLDOAYDSISAFSSR DSFLHGV GKLEGGDLDOAYDSISAFSSR HADLVEEISTLYQK HADLVEEISTLYQKEEK KHADLVEEISTLYQK KHADLVEEISTLYQKEEK KNMLGAFSLK LCSLVAELGYEGAGK LLEGDDLDOAYDSISAFSSR LLESETIPELQWELAQLDYILOGDYDLK LOTQYDILLTQSSALIQGR LSTAVEEVTLEHR NLQMNGLVGR NMLGAFSLK NNOEAVFGAEESEK NNOEAVFGAEESEKVEYR QOAILTLK OWIEAQVENAK RLQTYDILLTQSSALIQGR RNNQOAVFGAEESEK RYVDFFCNPER SQVTSVEAIIHFDLHSLR VAATSVAHQITAIEDLSAR VFHNHVNQLAR VVDFFCNPER VIESELQGYLSATR VMRQELYISK WELAQLDYILOGDYDLK </p>

Supplemental Data. Hotta et al. Plant Cell. (2012). 10.1105/tpc.112.096610

Sample#	Gene ID	Gene Name	# peptides	Peptide sequence
AUG5-myc IP (continued)	A11g50710	AUG4	24	ALOGAAONLPADVNQLIDOLER CDKLADAIIVDDTDSSTGNR DEAALREDLYSADRK DVQGLYPQLGLK EYQGVDPHFDIAR FIIIEIERDEAALR FIIIEIERDEAALREDLYSADR HCLAPDQSLVTK KAVTRLREYQGVDPHFDIAR KLENMOWTHIQVEMDLK LADAIIVDDTDSSTGNR LENMOWTHIQVEMDLK LPLISDGGGEIHEEIEK LPLISDGGGEIHEEIEKWSILSR LREYQGVDPHFDIAR LRLPLISDGGGEIHEEIEK LVVAEAAQK NSPOVYETLEHR NYLVEATEEASAAYNK SVAGISLSAVDTDVVGGVPNR SVYSDQLLAR VKFIIIEIER VLENVLLLETYPDISALHNIR YLEAMAIYCEAVAMVEEYQQAISVANHGGIR
	A15g38880	AUG5	56	AGARDPSAIPICR AHVQQFLATEDALNK AIDLWHIR ANMDAVAFWNQOPLAAR ASEQENTISDQWLPELR ASLNTLLSEIQR DKTVTGESSSYAEDR DPSAIPICR EAVYSTVK EYASATVIPASEVVDISNSAK EYASATVIPASEVVDISNSAKDFIEK GILLDEWEPASTVVDVTVDQGSVAAWQNHVK GNMIPWNFLNR GPELLLQAIAYTLR GSEACVLEDLAK GSEACVLEDLAKAIDLH HKQALLEAYDQCDEATR IGTDTHFQGSNNQLLER IPASEVVDISNSAK IRNSFPAYEGNGICSLPELETAK ISAALQYPAGLEGSDASLASVLESLEFCLR IVCDLLASR LGFYDGEITDEMK LGFYDGEITDEMKTVIVNSLR LHGSADTATHSFVGGTQSGSNLR LQVYVNOANDAQR MQSLSSSAPTPEAILEWLQK NAALLTAR NITVHGGSSNASIGSSVNPVK NITVHGGSSNASIGSSVNPVKKEESK NSFPAYEGNGICSLPELETAK QALLEAYDQCDEATR QDLVESGHSLLDHAFR QDLVESGHSLLDHAFFRAQQKYER

Sample#	Gene ID	Gene Name	# peptides	Peptide sequence
AUG5-myc IP (continued)	A15g38880	AUG5 (continued)	56	OFELDWWGK OFELDWWGKER OKAHVQQFLATEDALNK QLGPNYGGSSK QLLAFYDKESLR RLOVYVNOANDAQR RSELETITVTLK SADDVILMETTR SELETITVTLK SFVGGTQSGSNLR SHVPSIDAIR SHVPSIDAIRK SVNNSNEVLSL SVNNSNEVLSLSANSEK TAVONACASSECHK TIYITLLKANMDAVAFWNQOPLAAR TTNYCLDLASEQENTISDQWLPELR TVTGESSSYAEDR TVTGESSSYAEDREAALQER VESGHSLLDHAFR VRGSEACVLEDLAK VTDNSSSDVSSPLSYQFNGNGK
	A15g40740	AUG6	20	ALTLSLSEPSLEPNVDPFAPSK ANDGGDPILR DFDKVWPIFSAQSR DSQSDGEGSEHYFVPLSATGFSR EAALLIPSSAGSSR EHYFVPLSATGFSR GLCAEEAYLQGELEK GLCAEEAYLQGELEKLNDR INQTVDAEVIR ISGSALLAAMDQSSQVPR ISGSALLAAMDQSSQVFPRAELLSAHSK KQOHEVLASGPIEDLHAHR LPOLFSSTPTSSGK LWDSIMAR OEGEVWDDLVSQSSQNSHLVSK QTMASQVNMESLSEK SNGQASSLQSQGSGR TFPADVASNPLPSSLTDVFSHAATLLPVTK VKOEGEVWDDLVSQSSQNSHLVSK VSSLATCCGPR
AUG5-myc IP (continued)	A15g17620	AUG7	13	ANAPAQSLFAGMER DIQLIDAIER DLGILSASIAER DSHAALSIGSSGTVAGEPSSVTR FLGITPTVDIAIQGHGTIEDR HAYNPDEEYTEVESQLR IQYLAEIAK IVSDCEAALTVLNR LFPADVQIQSIYPLPDVSELETK LLEAYNMLLK NIVDLVEASLFSNDEWSIDEQVAK QSLIFSECK SPFSQNLQGDAGVREDETVR
	A14g30710	AUG8	2	ASYIEDVHQLR ATLATAVAR

Supplemental Table 4. List of primers used in this work.

Name	Sequence
2g2LP	5'-GGTGAAGGAGGAACAATACATACAG-3'
2g1RP3	5'-GTCCTGTTTACAGAAATGAACAACCAATC-3'
TH071	5'-TTCTATTACATTGGTTGGTTTTTGTG-3'
TH072	5'-CCAATAAGTTATCATAAGGCTTCAGG-3'
1g2LP	5'-CATTGTTGATGACACTGGTAAGATC-3'
1g2RP	5'-AATACATGGAAAGAAACATGTCTGG-3'
5g2LP	5'-ATCATCTGCAGACTTAGTTCCTTTG -3'
5g2RP	5'-AGCAAATCTCATGTTCCCTTCTATTG-3'
sk18263-LP	5'-TAAAATGTCCCATCTATTTGAAAAG-3'
sk18263-RP	5'-GCCAGAGAAGAAACAATAAGTAAACC-3'
LBa1	5'-TGGTTCACGTAGTGGGCCATCG-3'
LBb1.3	5'-ATTTTGCCGATTTCCGGAAC-3'
GLB3	5'-TAGCATCTGAATTTTATAACCAATCTCGATACAC-3'
SK-L1	5'-TTCTCATCTAAGCCCCATTTGG-3'
50710-F	5'-CACCTATGTGATTAGTTAGTTTTTATATGTTAAAC-3'
50710-R	5'-TGCGCCTGCGCCGTCATGAGACTTAAGGTCCATTTCTAC-3'
38880-F	5'-CACCATCAAACAAAACCCTAGGAAGGAACCTC-3'
38880-R	5'-TGCGCCTGCGCCGTTTCGCAATGATTCTTTATCATAGAAG-3'
40740-F	5'-CACCCTTTTTGACAAAATCATGGTAGCCACTGC-3'
40740-R	5'-TGCGCCTGCGCCATGCTCCATTAAAGCGGCTTCGGTTTC-3'
17620-F	5'-CACCGTTCCTGGACTTTGCTCCTTCTCGAATATAG-3'
17620-R	5'-TGCGCCTGCGCCAAGACGCTCACCTTGCTCACGAGC-3'
Q-17620_F	5'-GGTGATAAATCACCTTTCTCACAGC-3'
Q-17620_R	5'-GGCTCGCCTCCACTAAATCAAC-3'
TH121	5'-GGAATTCTAATGAGCAGCGGAGACTGTGCTCTCTTG-3'
TH122	5'-CCCAGCTCCAAAAGAATAGCTTGTTGCTTAGCATTCC-3'
U50487_Bam5'	5'-ATATGGATCCATGGTGAAGGCACTGCAAGG-3'
U50487_Xho3'	5'-ATCGCTCGAGATCAGTCATGAGACTTAAGGTCC-3'
Xba23033F	5'-GCGGTCTAGAGATGCTTGATGAAAGAGC-3'
Hind23033R	5'-GCCGAAGCTTCTTTCTTTCCCTTCCCA-3'