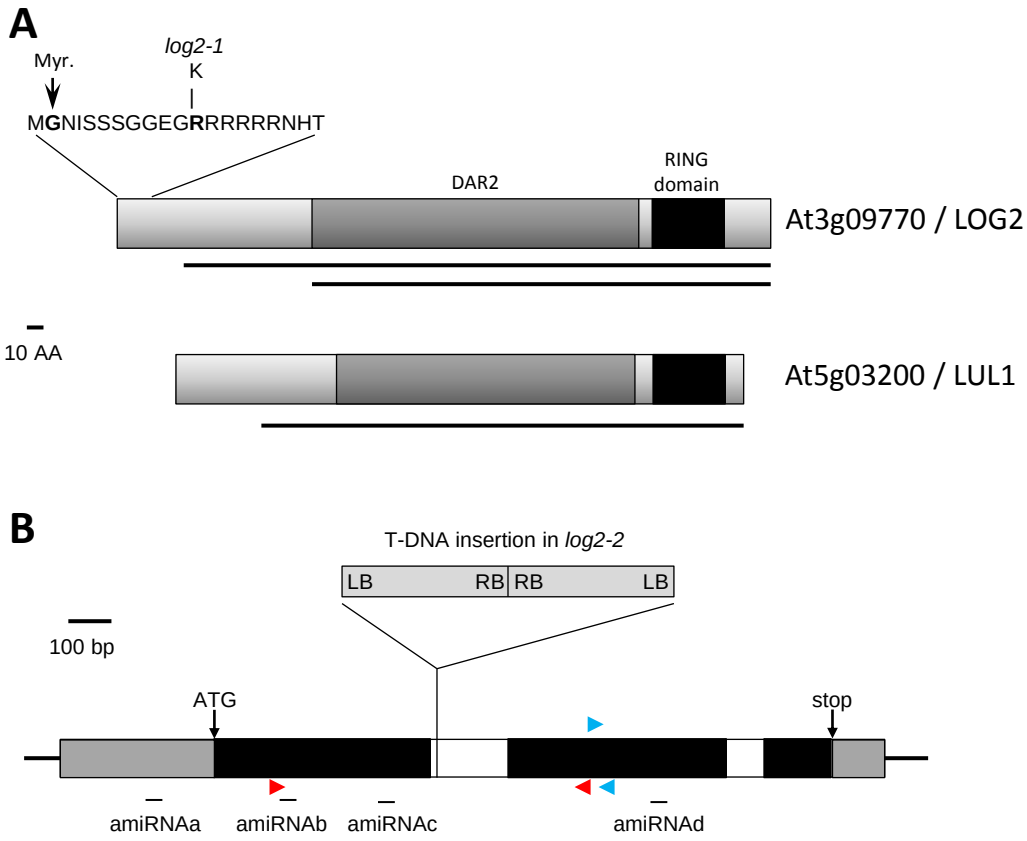
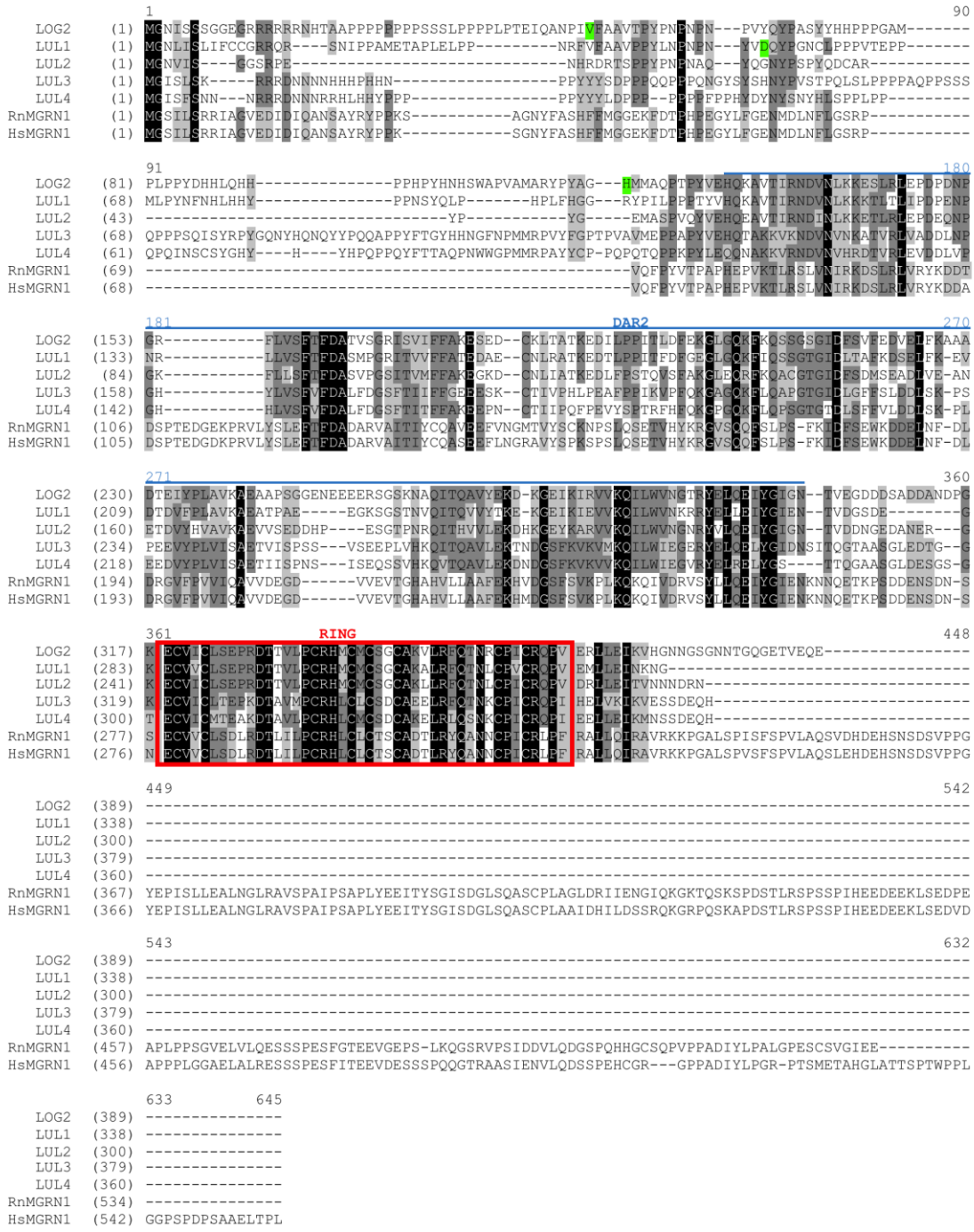


Supplemental Fig. S1. Structure of LOG2 and LUL1 proteins, *LOG2* gene, and multiple sequence alignment of LOG2, LULs and MGRN proteins.

A. Schematic of LOG2 and LUL1 proteins identified by the yeast-two-hybrid screening. The lines below each diagram represent the parts encoded by the plasmids isolated from the yeast-two-hybrid screening. The amino sequence at the N-terminus is shown for LOG2 with position of the *log2-1* mutation indicated. Myr, predicted myristoylation site; DAR2 (Domain Associated with RING #2), also found in mammalian MGRN1.

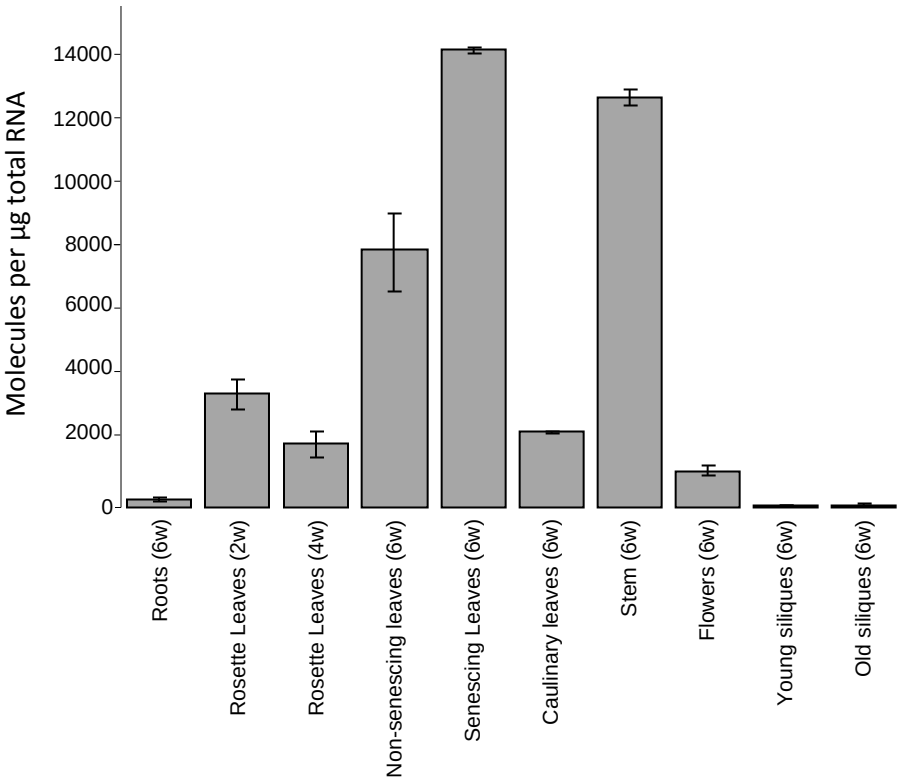
B. Representation of *LOG2* gene. Coding exons, introns and predicted UTRs are designated with black boxes, white boxes, and grey boxes, respectively. The position of the amiRNAs are indicated with black lines under the diagram. Arrowheads represent the oligonucleotides used for quantitative (blue) and semi-quantitative (red) PCR. LB and RB, left and right border of T-DNAs. The position of T-DNA insertion (SAIL_729 _A08 ,between 519 and 533 bp downstream from LOG2 ATG) was verified by sequencing border PCR fragments.

C



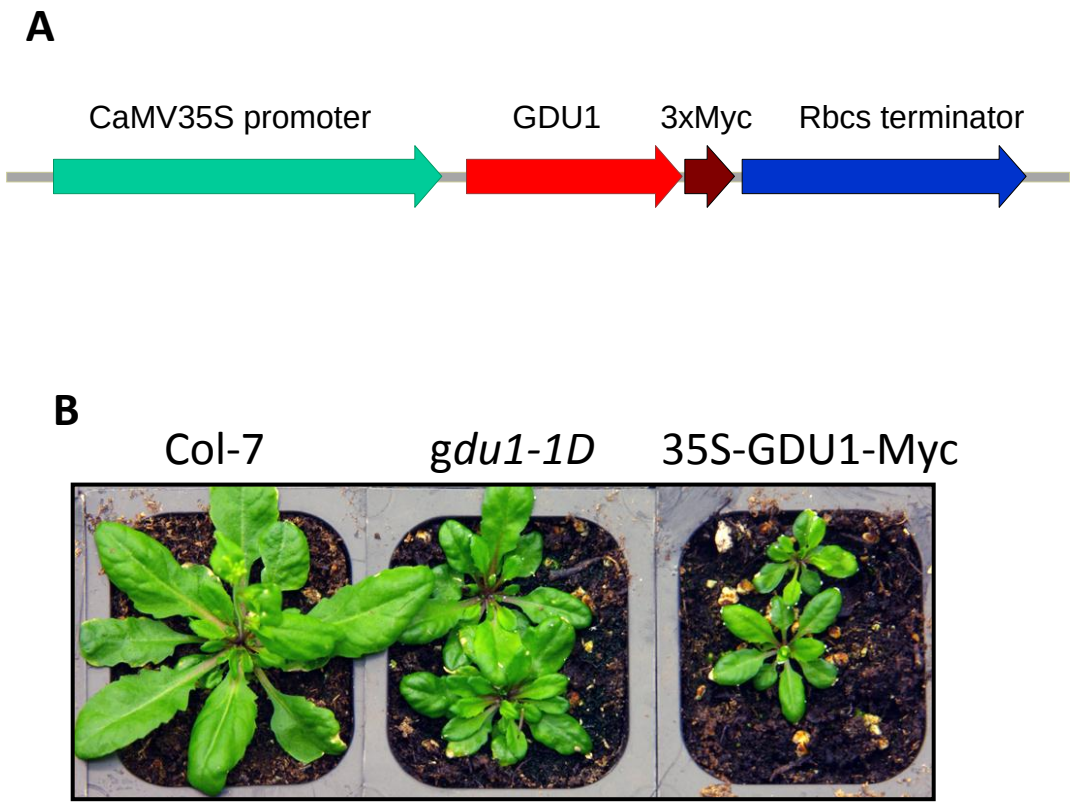
Supplemental Fig. S1 (continued). Structure of LOG2 and LUL1 proteins, *LOG2* gene, and multiple sequence alignment of LOG2, LULs and MGRN proteins.

C. Multiple sequence alignment the Arabidopsis LOG2, LULs and rat and human MGRN1 proteins (NM_001013964 and NM_001142289). The DAR2 and RING domains are indicated in blue and red, respectively. The start of the clones isolated by the yeast-two-hybrid screening are indicated in green. The sequence alignment was generated by CLUSTALX2 (**Larkin, MA** et al. (2007) Clustal W and Clustal X version 2.0. Bioinformatics, **23**:2947-2948).



Supplemental Figure S2: Accumulation of *LOG2* mRNA in the organs of the plant.

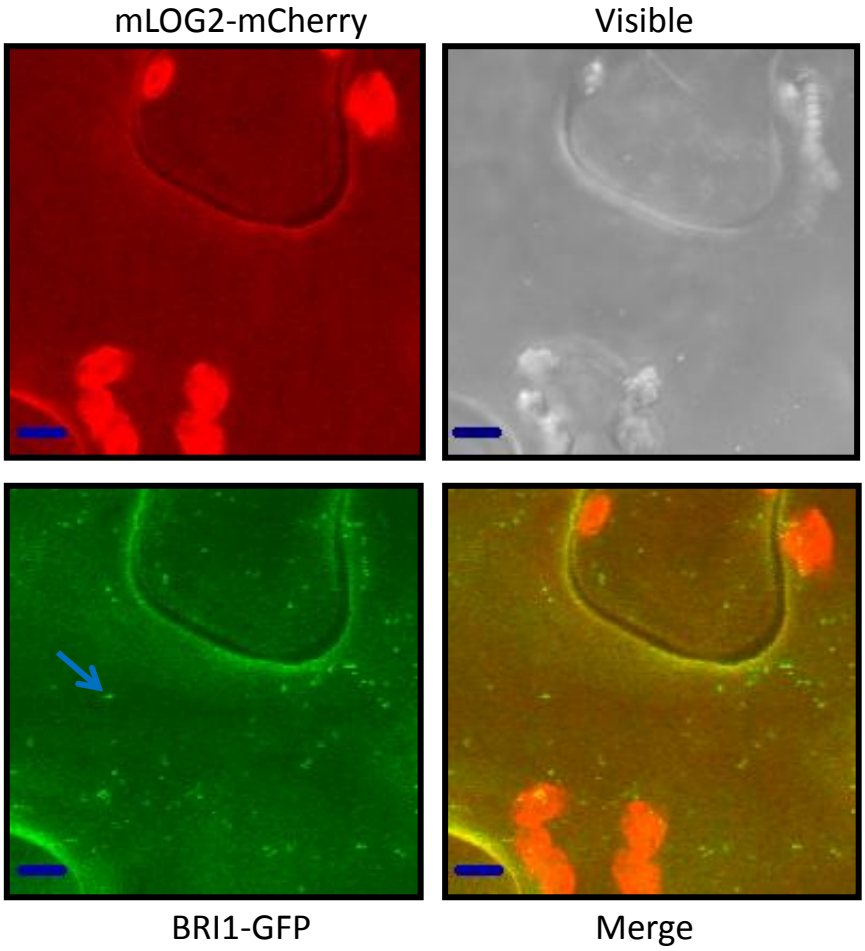
Absolute expression was determined by comparing the Ct values of the quantitative RT-PCR (qRT-PCR) performed on mRNA extracted from the various organs and the Ct values of the q-PCR performed on dilutions of a plasmid containing LOG2 coding sequence. 2w: 2-week old plants; 4w: 4-week old plants; 6w, 6-week old plants; “Flowers” correspond to the organs in the top 1 cm of the inflorescence; “Young siliques,” less than one-week old siliques; “Old siliques,” green siliques older than one week. Error bars correspond to the values of two technical replicates.



Supplemental Figure S3. Phenotype of the 35S-GDU1-Myc line.

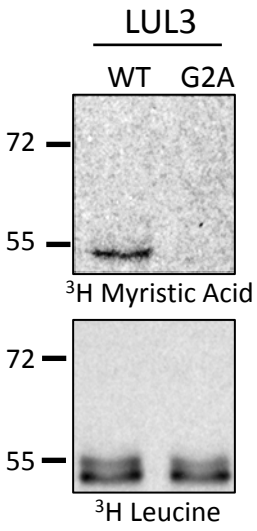
A. Schematic of the over-expression construct. This construct was inserted in Col-7 genome to generate the 35S-GDU1-Myc line.

B. Phenotype of 4-week old 35S-GDU1-Myc line, compared to *gdu1-1D* and the parent (Col-7).



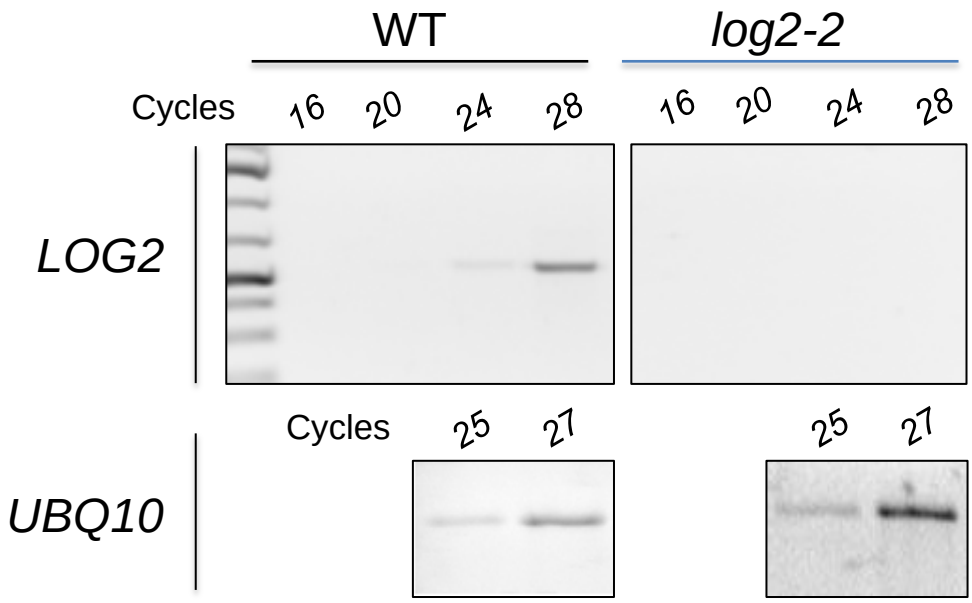
Supplemental Figure S4. Co-localization of mLOG2 and BRI1 in *N. benthamiana* epidermis cells

mLOG2-mCherry and BRI1-GFP (**Friedrichsen DM, Joazeiro CA, Li J, Hunter T, Chory J** (2000) Plant Physiol. **123**: 1247-1256) were co-infiltrated in *N. benthamiana* epidermis cells and observed by confocal microscopy. The bright dots in the green channel (arrow) correspond to endosomes, since the BRI1 protein has been shown to localize at the plasma membrane and endosomal compartments (**Geldner N, Hyman DL, Wang X, Schumacher K, Chory J** (2007) Genes Dev. **21**: 1598-1602). Maximal projections of optical sections of the abaxial side of the cell. Bar = 5 µm.



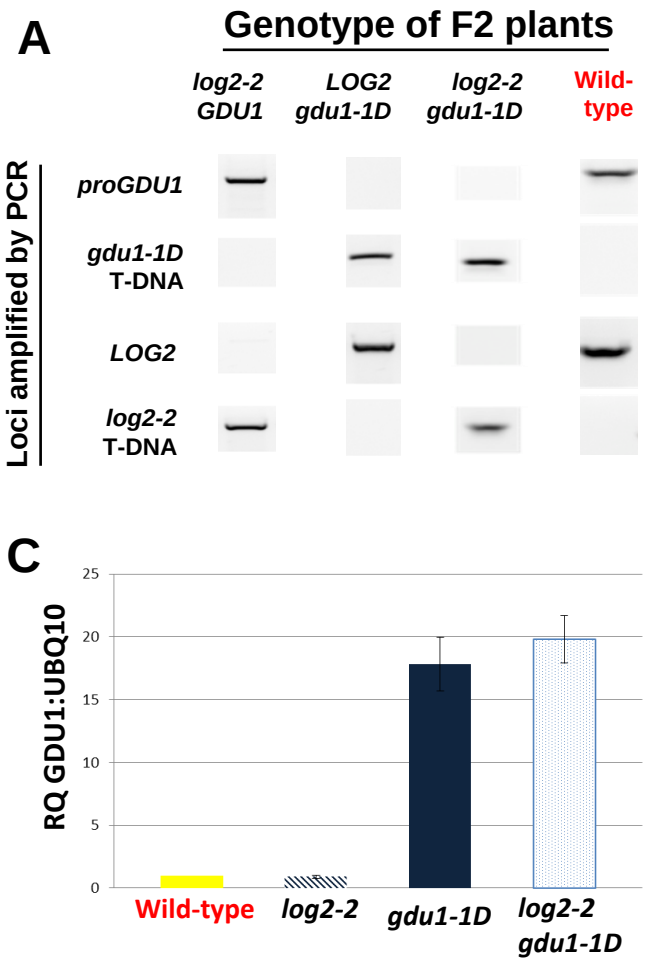
Supplemental Figure S5. LUL3 can be myristoylated *in vitro*.

LUL3 and can be myristoylated in rabbit reticulocyte lysates, while the corresponding G2A mutant cannot be myristoylated.



Supplemental Figure S6. Suppression of wild type *LOG2* transcript accumulation in *log2-2*.

Semi-quantitative PCR was performed with intron-spanning primers from reverse-transcribed RNA extracted from 6-day old liquid-grown WT or *log2-2* seedlings. *UBQ10* transcript served as control.

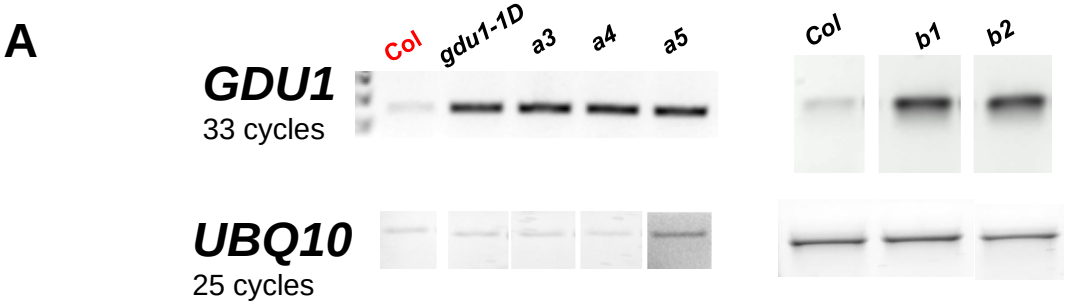


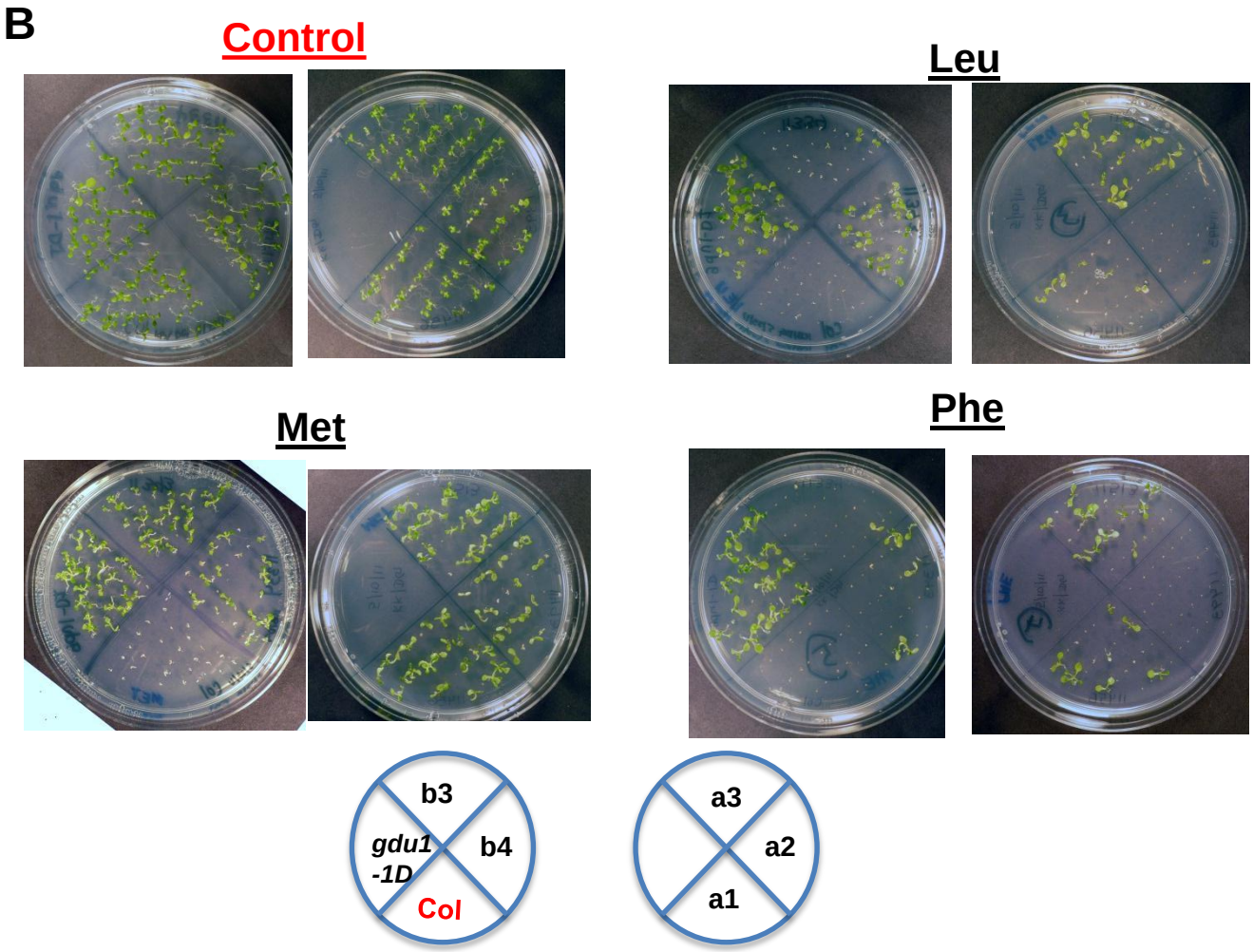
Supplemental Figure S7. *GDU1* transcript accumulation in F2 plants descended from the *gdu1-1D* x *log2-2* cross.

A. Deduced genotypes of F2 plants from the *gdu1-1D log2-2* cross. The indicated gDNA regions were PCR-amplified with primers specific to each locus. proGDU1: GDU1 native promoter. *gdu1-1D* T-DNA: T-DNA in the GDU1 promoter harboring 4 copies of the 35S enhancer that gives rise to the Gdu1D phenotype.

B. *GDU1* transcript levels are not affected by the *log2-2* mutation. *GDU1* transcript was PCR amplified from first-strand cDNA synthesized from total RNA extracted from 6-day old liquid-grown plants. *UBQ10* transcript served as a control.

C. Relative quantitation of *GDU1* transcript abundance by the efficiency-calibrated qPCR model. Each bar represents the abundance of *GDU1* transcript (relative to *UBQ10* transcript) derived from three cDNA samples. Error bars correspond to standard error of three biological replicates.

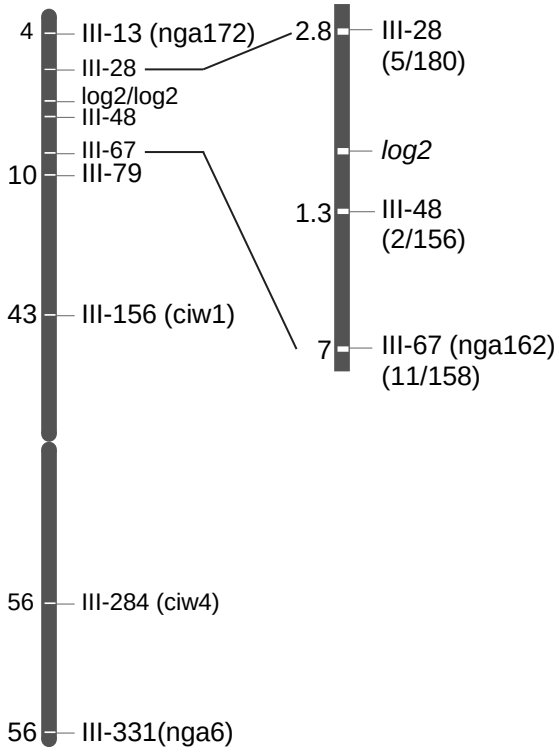




Supplemental Figure S8. *GDU1* transcript accumulation and amino acid sensitivity phenotypes of *gdu1-1D* plants over-expressing the *LOG2-amiRNA*.

A.*GDU1* transcript levels are not affected by the over-expression of *LOG2-amiRNA*a and b. *GDU1* transcript was PCR amplified from first-strand cDNA synthesized from total RNA extracted from 6-day old liquid-grown plants. a3-5, b1-2: plants expressing amiRNA "a" or "b" in the *gdu1-1D* background. *UBQ10* transcript served as a control.

B. *LOG2*-directed artificial microRNAs "a" and "b" partially suppressed the amino acid resistance phenotype conferred by *GDU1* over-expression. Experiments were repeated three or more times with 25 seeds from each line. Each plate is oriented with quadrants as shown in the model.



Supplemental Figure S9: Positional cloning of *log2-1*.

The position of the single sequence length polymorphism markers used for the localization of *log2-1* are indicated on the physical map of the Arabidopsis chromosome 3. The numbers on the left indicate the percentage of recombination between *log2-1* and the corresponding markers. The numbers of observed recombination events are indicated in parentheses for markers III-28, III-48 and III-67.

Supplemental Table S1: Free amino acid content of plants over-expressing *LOG2-amiRNA*.
Free amino acid content in rosette leaves of 4-week old wild type, 35S-GDU1-Myc and two lines over-expressing *LOG2-amiRNAb* in the 35S-GDU1-Myc background showing wild type phenotype. Means ± SD of three biological replicates are shown. Significant differences from the wild type (*t* test) are as follows: * $P < 0.05$, ** $P < 0.005$.

	Ala	Arg	Asn	Asp	Gln	Glu	His	Ile	Leu	Phe	Pro	Ser	Thr	Trp	Tyr	Val	sum
Wild type	6.9 ± 0.4	1.2 ± 0.3	4.1 ± 0.4	9.8 ± 1.4	28.5 ± 6	29.1 ± 7.9	0.4 ± 0	0.5 ± 0.1	0.6 ± 0.1	1.9 ± 0.6	1.8 ± 0.4	15.1 ± 2.7	5.1 ± 0.9	0 ± 0	0.1 ± 0	0.3 ± 0	105.3 ± 2.8
35S-GDU1-Myc	2.7 ± 0.3 **	17.5 ± 2.8 **	25.4 ± 0.9 **	8.7 ± 0.8	497.6 ± 36.8 **	113.5 ± 3.8 **	4.6 ± 0.3 **	2.4 ± 0.5 **	2.3 ± 0.4 **	3 ± 0.2	128 ± 44.8	13.4 ± 1.3	8.8 ± 2.9	0.6 ± 0.1 **	0.8 ± 0 **	0.9 ± 0.1 **	830.2 ± 80.1 **
249A	2.4 ± 0.3 **	2.8 ± 0.3	22.8 ± 4.2 **	16 ± 2.3	248.7 ± 21.5	110.7 ± 40.3	1.2 ± 0.1 **	1.8 ± 0.6 **	1.2 ± 0.1	1.8 ± 0.5	6.8 ± 2.4	17.6 ± 4.2	10.2 ± 1.8	0.2 ± 0	0.5 ± 0.2 **	0.3 ± 0.1	445 ± 69.5
249B	2.1 ± 0.3 **	1.8 ± 0.7	10.5 ± 1 **	9.4 ± 1.1	76.6 ± 10	83.9 ± 11.8	0.8 ± 0.1 **	0.5 ± 0.1 **	0.8 ± 0.1	0.9 ± 0.1	4.3 ± 1.8	14.1 ± 1.7	6.2 ± 0.1 **	0.1 ± 0	0.1 ± 0 **	0.3 ± 0	212.4 ± 18.3

[a]nmol mg^{-1} DW.

Supplemental Table S2. Sequence of the oligonucleotides used for this study.

Name	Sequence(5'-3')	Purpose	Direction
	GGGGACAAGTTTGTACAAAAAAGCAGGCTCGGAAGGAGATATACATATGGGAAACATTAGCAGCAGC	Addition of Kozak sequence to LOG2 for myristoylation assay	FWD
	GGGGACAAGTTTGTACAAAAAAGCAGGCTGAAGGAGATATACATACATGGGAAACATTAGCAGCAGC	Addition of Shine-Delgarno sequence to LOG2	FWD
	GGGGACAAGTTTGTACAAAAAAGCAGGCTGAAGGAGATATACATACATGGGGAATCTGATCAGTTTG	Addition of Shine-Delgarno sequence to LUL1	FWD
LOG2 -150 f	CTAAACTCTCTCTGCTTTTGCTT	Amplification of LOG2 CDS from log2-1	FWD
LOG2 BamXho r	AAGGATCCCTCGAGTCCGTTCTTGTTAATCTCCA	Amplification of LOG2 CDS from log2-1	REV
	TAGCATCTGAATTTCATAACCAATCTC	Amplification of log2-2 SAIL_729 T-DNA junction	REV
	CCACCCACGAGGAGCATC	Anneals to 35S promoter	FWD
	GCTGCACTGAGCAGCGTAATC	Anneals to 3xHA tag in pGWB14	REV
	TTGGCCCCAGCGGCCGCAGCAGCACCAGCAGGATCCTTGTACAGCTCGTCCA	Anneals to YFP tag in pEG101	REV
GDU1 180 BE f	TTTGGATCCAAGAATTCATGCGCCTGTCTTCCTCCG	Cloning cGDU1 in pGBT9 and pGBKT7	FWD
GDU1 XbB r	TTTGGATCCTTCTAGAGTGACTTGTAGTAGTTGTC	Cloning cGDU1 in pGBT9 and pGBKT7	REV
LOG2p Bam r 2	AAAGGATCCTGGCGTTAAACCCAGATCAAAAAGAC	Cloning of LOG2 promoter	FWD
LOG2p Pst f 2	TTTCTGCAGGGAACTTGCGAATTGGTTGGAA	Cloning of LOG2 promoter	REV
	GGGGACCACTTTGTACAAGAAAGCTGGGTCCTATTTACCAGGATCATTAGCATC	Deletion of RING finger domain of LOG2	FWD
GDU1 Eco f	TTGAATTCATGAAAAAGTGTACGTGTGGTGG	Deletion of the VIMAG domain	FWD
GDU1 Eco r	TTGAATTCCTCGTAAGCTCCGTTCG	Deletion of the VIMAG domain	REV
pRS300 attB1	GACAAGTTTGTACAAAAAAGCAGGCTTACCCCAAACACACGCTCGG	Gateway cloning of amiRNA	FWD
pRS300 attB2	GACCACTTTGTACAAGAAAGCTGGGTACCCCATGGCGATGCCTTA	Gateway cloning of amiRNA	REV
LOG2 miRa f	GATTAAGGAATTACGAAAAGCAGTCTCTCTTTTGTATTCC	Gateway cloning of amiRNAa	FWD
LOG2 miRa r	GACTGCTTTTCGTAATTCCTTAATCAAAGAGAATCAATGA	Gateway cloning of amiRNAa	REV
LOG2 miRa* f	GACTACTTTTCGTAAATCCTTATTCACAGGTCGTGATATG	Gateway cloning of amiRNAa	FWD
LOG2 miRa* r	GAATAAGGATTTACGAAAAGTAGTCTACATATATATTCCT	Gateway cloning of amiRNAa	REV
LOG2 miRb f	GATATTAGGATAGGGAGTACCGGTCTCTCTTTTGTATTCC	Gateway cloning of amiRNAb	FWD
LOG2 miRb r	GACCGGTACTCCCTATCCTAATATCAAAGAGAATCAATGA	Gateway cloning of amiRNAb	REV
LOG2 miRb* f	GACCAGTACTCCCTAACCTAATTTCACAGGTCGTGATATG	Gateway cloning of amiRNAb	FWD
LOG2 miRb* r	GAAATTAGGTTAGGGAGTACTGGTCTACATATATATTCCT	Gateway cloning of amiRNAb	REV
LOG2 miRc f	GATGTTACGAATCGTTACGCCTTTCTCTCTTTTGTATTCC	Gateway cloning of amiRNAc	FWD
LOG2 miRc r	GAAAGGCGTAACGATTCGTAACATCAAAGAGAATCAATGA	Gateway cloning of amiRNAc	REV
LOG2 miRc* f	GAAAAGCGTAACGATACGTAACTTCACAGGTCGTGATATG	Gateway cloning of amiRNAc	FWD
LOG2 miRc* r	GAAGTTACGTATCGTTACGCTTTTCTACATATATATTCCT	Gateway cloning of amiRNAc	REV
LOG2 miRd f	GATTTAACCCATAGTGTCCGCTTTCTCTCTTTTGTATTCC	Gateway cloning of amiRNAd	FWD
LOG2 miRd r	GAAAGCGGACACTATGGGTTAAATCAAAGAGAATCAATGA	Gateway cloning of amiRNAd	REV
LOG2 miRd* f	GAAAACGGACACTATCGGTTAATTCACAGGTCGTGATATG	Gateway cloning of amiRNAd	FWD
LOG2 miRd* r	GAATTAACCGATAGTGTCCGTTTTCTACATATATATTCCT	Gateway cloning of amiRNAd	REV
GDU1 180 attB1	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGCGCCTGTCTTCCTCCG	Gateway cloning of cGDU1	FWD
GDU1 stop attB2	GGGGACCACTTTGTACAAGAAAGCTGGGTATTAGTGACTTGTAGTAGTTGTCT	Gateway cloning of cGDU1 / GDU1 with stop	REV
GDU1 no stop attB2	GGGGACCACTTTGTACAAGAAAGCTGGGTAGTGACTTGTAGTAGTTGTCT	Gateway cloning of cGDU1 / GDU1 without stop	REV
GDU2 170 attB1	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGAGACTCTCCGGCTCCGCT	Gateway cloning of cGDU2	FWD
GDU2 stop attB2	GGGGACCACTTTGTACAAGAAAGCTGGGTACTACCCTCTTCTTCCTTC	Gateway cloning of cGDU2	REV
GDU3 170 attB1	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGCGTCTCTCCGGTTATCTA	Gateway cloning of cGDU3	FWD
GDU3 stop attB2	GGGGACCACTTTGTACAAGAAAGCTGGGTATCAATGTGTCTCACCGTT	Gateway cloning of cGDU3	REV
GDU4 190 attB1	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGCGCTTGTCAACCTCC	Gateway cloning of cGDU4	FWD
GDU4 stop attB2	GGGGACCACTTTGTACAAGAAAGCTGGGTATCACTGACTCGTTGTTTC	Gateway cloning of cGDU4	REV
GDU5 170 attB1	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGAGGCTCTCGCGGCAGACA	Gateway cloning of cGDU5	FWD
GDU5 stop attB2	GGGGACCACTTTGTACAAGAAAGCTGGGTATCAGTGGTTTTCTTCTGTTACTTT	Gateway cloning of cGDU5	REV
GDU6 120 attB1	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGAAACCTTCTTCCTCTAGC	Gateway cloning of cGDU6	FWD
GDU6 stop attB2	GGGGACCACTTTGTACAAGAAAGCTGGGTATTAGGTTGAGATGACAGT	Gateway cloning of cGDU6	REV
GDU7 150 attB1	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGCATAAGCAAACTTCGAATTCATG	Gateway cloning of cGDU7	FWD
GDU7 stop attB2	GGGGACCACTTTGTACAAGAAAGCTGGGTATCATGCATTGATCTGGGT	Gateway cloning of cGDU7	REV
GDU1 ATG attB1	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGAGACCATTGAGCGTA	Gateway cloning of GDU1	FWD
MGRN1 ATG attB1	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGGCTCCATTCTCAGC	Gateway cloning of HsMGRN1	FWD
MGRN1 stop attB2	GGGGACCACTTTGTACAAGAAAGCTGGGTATCAGAGTGGGGTCAGCTC	Gateway cloning of HsMGRN1	REV
LOG2 ATG attB1	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGGAAACATTAGCAGCAGCGG	Gateway cloning of LOG2	FWD
LOG2 stop attB2	GGGGACCACTTTGTACAAGAAAGCTGGGTACTACTCTTGTTCAACTGTTT	Gateway cloning of LOG2 with stop	REV
LOG2 no stop attB2	GGGGACCACTTTGTACAAGAAAGCTGGGTACTCTTGTTCAACTGTTTC	Gateway cloning of LOG2 without stop	REV
LUL1 ATG attB1	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGGGAATCTGATCAGT	Gateway cloning of LUL1	FWD
LUL1 stop attB2	GGGGACCACTTTGTACAAGAAAGCTGGGTATCATCCGTTCTTGTTAATCTCCAA	Gateway cloning of LUL1	REV
LUL2 ATG attB1	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGGCAATGTCATAAGC	Gateway cloning of LUL2	FWD
LUL2 stop attB2	GGGGACCACTTTGTACAAGAAAGCTGGGTACTAGTTCCTGTCGTTGTT	Gateway cloning of LUL2	REV
LUL3 ATG attB1	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGGGATCTCCTTAAGC	Gateway cloning of LUL3	FWD
LUL3 stop attB2	GGGGACCACTTTGTACAAGAAAGCTGGGTATCAGTGTTGTTCATCACT	Gateway cloning of LUL3	REV
LUL4 ATG attB1	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGGAATCTCCTTTAGC	Gateway cloning of LUL4	FWD
LUL4 stop attB2	GGGGACCACTTTGTACAAGAAAGCTGGGTACTAGTGTTGTTCATCACT	Gateway cloning of LUL4	REV
	ACCGCCGAAGAGGTAAGGAA	GDU1 real-time PCR (A)	REV
	CCGTTAATCACCACGGAGTGA	GDU1 real-time PCR (S)	FWD
	CTTCCTTCATTATTTACCTCCAGC	Genotyping gdu1-1D	FWD
	AAGAGGCGACCAATCACCAACG	Genotyping gdu1-1D	REV
	TCCCTGTCCGGTGTTATTCCCGC	Genotyping log2-2	FWD
	TGCAACCGTCTCCGGAAGGTAGAT	Genotyping log2-2	REV
MGRN1 R	GGGGACCACTTTGTACAAGAAAGCTGGGTCTTACTCCTCTATACCAACAGAGCACG	Isolation of MGRN1 from Rat cDNA	REV
MGRN1 F	GGGGACAAGTTTGTACAAAAAAGCAGGCTCGATGGGCTCCATCCTGAGTCGC	Isolation of MGRN1 from Rat cDNA	FWD
	AAGGAGTCTCTTAGGCTTGAACC	LOG2 semi-quantitative RT-PCR	FWD
	ACCAGGATCATTAGCATCATCAG	LOG2 semi-quantitative RT-PCR	REV
Act2 Q f	GGTAACATTGTGCTCAGTGGTGG	qPCR Actin2	FWD
Act2 Q r	AACGACCTTAATCTTCATGCTGC	qPCR Actin2	REV
GDU1 Qf	ATGGCCGGAGAAGATTTGC	qPCR GDU1	FWD
GDU1 Qr	CGCCTTCTCTCATCTTCTCTTCC	qPCR GDU1	REV
LOG2 +800 f	TTCGAGAAAGGACTTGGTCAGA	qPCR LOG2	FWD
LOG2 +900 r	CTGCCTTAACCGCTAATGGATA	qPCR LOG2	REV
	GGGGACCACTTTGTACAAGAAAGCTGCGTCCTCTTGTTCAACTGTTTCTCCC	Remove STOP codon from LOG2	
UBQ10sqPCR F	TCAATTCTCTCTACCGTGATCAAG	Semi-quantitative PCR amplification of UBQ10	FWD
UBQ10sqPCR R	TTACATGAAACGAAACATTGAACTTC	Semi-quantitative PCR amplification of UBQ10	REV
ADH 3' r	ATACCTGAGAAAGCAACCTGACCTA	Sequencing cGDU1 in Y2H vector	REV
GAL4 DB f	ATAGAATAAGTGCGACATCATCATC	Sequencing cGDU1 in Y2H vector	FWD
	CTTTTCCTCCATATTGACCATCATAC	Sequencing gdu1-1D SKI105 T-DNA junction	FWD
GAL4 Act f	AATACCACTACAATGGATGATG	Sequencing inserts in pACT / pACT2	FWD
GAL4 r	ATGAAAGAAATTGAGATGGTG	Sequencing inserts in pACT / pACT2	REV
pDONR f	GTTGTAAAACGACGGCCAGT	Sequencing inserts in pDONR 221 / Zeo	FWD
pDONR r	GCTGCCAGGAAACAGCTATGA	Sequencing inserts in pDONR 221 / Zeo	REV
LOG2 -1650 f	CACTACCTTCGTATGGGAAT	Sequencing LOG2 promoter	FWD
LOG2 -2350 f	ATTCCTCATTACGAACCACA	Sequencing LOG2 promoter	REV
	TCGCGTTAACGCTAGCATGGATCTC	Sequencing pDONR 201 insert	FWD
	ACGGGCCAGAGCTGCAGCTG	Sequencing pDONR 201 insert	REV
	CGTATTAAATGTATAATTGCGGGAC	Sequencing pGWB construct	REV
pJH f	CCCAGGCTTTACACTTTATGCTTCC	Sequencing RIG2 promoter in pUTkan	FWD
Rbcs +60 r	TGCCATAATACTCAAACTCAG	Sequencing RIG2 promoter in pUTkan	REV
	CAGACAAATCGAGCACCCATTGCAAGGCAACCTGTTGAAAGGC	Site-Directed Mutagenesis of LOG2 CC354/357AA	FWD

	GCCTTTCAACAGGTTGCCTTGCAATGGGTGCTCGATTTGTCTG	Site-Directed Mutagenesis of LOG2 CC354/357AA	REV
	GGGGACAAGTTTGTACAAAAAAGCAGGCTCGGAAGGAGATATACATATGGCGAACA TTAGCAGCAG C	Site-Directed Mutagenesis of LOG2 G2A	FWD
LOG2	GACAAGTTTGTACAAAAAAGCAGGCTTAATGGCAAACATTAGCAGCAGCGG	Site-Directed Mutagenesis of LOG2 G2A, gateway cloning	FWD
LOG2	GCGGTGGTGAAGGTAAACGCCGTCGACGGCGAAAC	Site-Directed Mutagenesis of LOG2 R12K	FWD
	CAGACAAATCTGGCACCAGTTGCAAGACAACCTGTTGAGATGC	Site-Directed Mutagenesis of LUL1 CC320/323AA	FWD
	GCATCTCAACAGGTTGTCTTGCAACTGGTGCCAGATTTGTCTG	Site-Directed Mutagenesis of LUL1 CC320/323AA	REV
I-040.s f	GGCTTTCTCGAAATCTGTCC	SSLP genetic marker chr I	FWD
I-040.s r	TTACTTTTTGCCTCTTGTCATTG	SSLP genetic marker chr I	REV
I-123.s f	AGGTTTTATTGCTTTTCACA	SSLP genetic marker chr I	FWD
I-123.s r	CTTTCAAAAGCACATCACA	SSLP genetic marker chr I	REV
I-234.s f	ACATTTTCTCAATCCTTACTC	SSLP genetic marker chr I	FWD
I-234.s r	GAGAGCTTCTTTATTTGTGAT	SSLP genetic marker chr I	REV
I-267.s f	CTGATCTCACGGACAATAGTGC	SSLP genetic marker chr I	FWD
I-267.s r	GGCTCCATAAAAAGTGCACC	SSLP genetic marker chr I	REV
I-353.s f	CTCCAGTTGGAAGCTAAAGGG	SSLP genetic marker chr I	FWD
I-353.s r	TGTTTTTTAGGACAAATGGCG	SSLP genetic marker chr I	REV
II-016.s f	CCCAAAAGTTAATTATACTGT	SSLP genetic marker chr II	FWD
II-016.s r	CCGGGTTAATAATAAATGT	SSLP genetic marker chr II	REV
II-088.s f	GAAACTCAATGAAATCCACTT	SSLP genetic marker chr II	FWD
II-088.s r	TGAACTTGTTGTGAGCTTTGA	SSLP genetic marker chr II	REV
II-157.s f	CGCTACGCTTTTCGGTAAAG	SSLP genetic marker chr II	FWD
II-157.s r	GCACAGTCCAAGTCACAACC	SSLP genetic marker chr II	REV
II-212.s f	TCGTCTACTGCACTGCCG	SSLP genetic marker chr II	FWD
II-212.s r	GAGGACATGTATAGGAGCCTCG	SSLP genetic marker chr II	REV
III-013.s f	AGCTGCTTCCTTATAGCGTCC	SSLP genetic marker chr III	FWD
III-013.s r	CATCCGAATGCCATTGTTC	SSLP genetic marker chr III	REV
III-028.s f	CCTCGTTCTTGTAAGTTGTATCCA	SSLP genetic marker chr III	FWD
III-028.s r	CAAAAGTTATGAGTTTCTGAGGGAT	SSLP genetic marker chr III	REV
III-044.s f	GAAAAAACGCTACTTTCGTGG	SSLP genetic marker chr III	FWD
III-044.s r	CAAGAGCAATATCAAGAGCAGC	SSLP genetic marker chr III	REV
III-048.s f	TGCTCGTATCAACACACAGGTA	SSLP genetic marker chr III	FWD
III-048.s r	ATGGGGATTTCTGGATAAGTTG	SSLP genetic marker chr III	REV
III-067.s f	CATGCAATTTGCATCTGAGG	SSLP genetic marker chr III	FWD
III-067.s r	CTCTGTCACTCTTTTCCTCTGG	SSLP genetic marker chr III	REV
III-079.s f	TAACCACACACATCGTGTTTTTGTCC	SSLP genetic marker chr III	FWD
III-079.s r	GGGTCTGCTCATTCTTCAGTTCTTGT	SSLP genetic marker chr III	REV
III-098.s f	AAGAGAAATATGTGCGTCCAAA	SSLP genetic marker chr III	FWD
III-098.s r	AGAATAACGTAGTCTCCTACCAA	SSLP genetic marker chr III	REV
III-156.s f	CCCCGAGTTGAGGTATT	SSLP genetic marker chr III	FWD
III-156.s r	GAAGAAATTCCTAAAGCATTC	SSLP genetic marker chr III	REV
III-284.s f	GTTCATTAAACTTGCGTGTGT	SSLP genetic marker chr III	FWD
III-284.s r	TACGGTCAGATTGAGTGATTC	SSLP genetic marker chr III	REV
III-331.s f	TGGATTTCTTCCTCTCTTCAC	SSLP genetic marker chr III	FWD
III-331.s r	ATGGAGAAGCTTACACTGATC	SSLP genetic marker chr III	REV
IV-013.s f	GGTTAAAAATTAGGGTTACGA	SSLP genetic marker chr IV	FWD
IV-013.s r	AGATTTACGTGGAAGCAAT	SSLP genetic marker chr IV	REV
IV-105.s f	CTCGTAGTGCACTTTCATCA	SSLP genetic marker chr IV	FWD
IV-105.s r	CACATGGTTAGGGAAACAATA	SSLP genetic marker chr IV	REV
IV-126.s f	AATTTGGAGATTAGCTGGAAT	SSLP genetic marker chr IV	FWD
IV-126.s r	CCATGTTGATGATAAGCACAA	SSLP genetic marker chr IV	REV
IV-207.s f	GCGAAAAAACAAAAAAATCCA	SSLP genetic marker chr IV	FWD
IV-207.s r	CGACGAATCGACAGAATTAGG	SSLP genetic marker chr IV	REV
V-012.s f	CCACTTGTTTCTCTCTCTAG	SSLP genetic marker chr V	FWD
V-012.s r	TATCAACAGAAACGCACCGAG	SSLP genetic marker chr V	REV
V-066.s f	GTTTTGGGAAGTTTTGCTGG	SSLP genetic marker chr V	FWD
V-066.s r	CAGTCTAAAAGCGAGAGTATGATG	SSLP genetic marker chr V	REV
V-105.s f	TAGTGAAACCTTTCTCAGAT	SSLP genetic marker chr V	FWD
V-105.s r	TTATGTTTTCTTCAATCAGTT	SSLP genetic marker chr V	REV
V-120.s f	TTAGTTGAAGGTTTTATTTGGGAA	SSLP genetic marker chr V	FWD
V-120.s r	AGCAAATGAAAAGTCAAGATGAA	SSLP genetic marker chr V	REV
V-138.s f	AATTGTGGGAAGGACAACAACCAAA	SSLP genetic marker chr V	FWD
V-138.s r	GAGAGAGGACGTGAGATGTCACAGA	SSLP genetic marker chr V	REV
V-156.s f	GAATCTCTAACCTGTAAAATAAAGTGT	SSLP genetic marker chr V	FWD
V-156.s r	CTTCATCACTCAGTTCTTGTCCA	SSLP genetic marker chr V	REV
V-182.s f	CTCTATCCTTACTTATGTATTTTGT	SSLP genetic marker chr V	FWD
V-182.s r	AAATCATTGTCGTATATGTTCCA	SSLP genetic marker chr V	REV
V-195.s f	CTCAGAGAATTCCCAGAAAAATCT	SSLP genetic marker chr V	FWD
V-195.s r	AAACTCGAGAGTTTTGTCTAGATC	SSLP genetic marker chr V	REV
V-249.s f	CAGACGTATCAAATGACAAATG	SSLP genetic marker chr V	FWD
V-249.s r	GACTACTGCTCAAACTATTCGG	SSLP genetic marker chr V	REV
V-359.s f	CCGACTACCGCAAATAGAATACGAAA	SSLP genetic marker chr V	FWD
V-359.s r	GTCAACCACATACACGCACCATACATAA	SSLP genetic marker chr V	REV
V-378.s f	CCACATTTTCCTTCTTTCATA	SSLP genetic marker chr V	FWD
V-378.s r	CAACATTTAGCAAATCAACTT	SSLP genetic marker chr V	REV

Supplemental Text S1: EMS mutagenesis and positional cloning

About 22,000 seeds from recapitulation line *gdu1-5D* (Pilot et al., 2004, construct E2), containing two T-DNAs inserted in tandem in the 3' region of gene AT5G09340, were mutagenized and screened as previously described (Pratelli and Pilot, 2006). The *log2-1* mutation was positioned in the genome from analysis of 97 Gdu1D progenies from a cross between the *log2-1 gdu1-5D* double mutant (in the Col-7 background) and *Ler*, using single sequence length polymorphism markers obtained from the Monsanto polymorphism release (Jander et al., 2002), Bell and Ecker (1994), Kwon et al. (2005), Lukowitz et al. (2000) and Jander (2006).

Supplemental Text S2: LC-MS analysis details

For LC-MS/MS, an Agilent 1200 series HPLC system, employing an Agilent Xorbax Eclipse XDB-C18 4.6x50mM 1.8 micron column was used. Ion pairing chromatography was performed using solvent A consisting of 0.1% formic acid and 0.05% heptafluorobutyric acid in water and solvent B consisting of 0.1% formic acid and 0.05% heptafluorobutyric acid in acetonitrile. The step gradient was:

Step	Total time (min)	Flow rate (µl/min)	A (%)	B (%)
0	0.10	1000	98.0	2.0
1	2.30	1000	80.0	20.0
2	4.00	1000	60.0	40.0
3	4.10	1000	98.0	2.0
4	6.00	1000	98.0	2.0

Column effluent was then analyzed by admission into an AB Sciex 3200 QTrap tandem mass spectrometer fitted with a Turbo V ion source operated with the following conditions:

Curtain Gas Pressure:	35 psi
Ion Spray Voltage:	5500 V
Turbo Gas Temperature:	600°C
Gas 1 Pressure:	60 psi
Gas 2 Pressure:	60 psi
Entrance Potential:	10 V

Declustering Potentials, Collision Entrance Potentials, and Collision Energies were individually optimized for the various analytes, based in parameters published by Gu et al. (2007).

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