

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-twohybrid 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.

| LOG2 (1 LUL1 (1 |) MGNISSSGGDØRRRRRRNHTAAPPPPPPPPPSSSLPPPPLPTEIQANPIVFAAVIPYPNENPNPVYQVPASWYHHPPPGAM |
|--|--|
| LUL3 (1 | MENNISGSNPL |
| LUL4 (1 | MeISFSNNNRRRDNNNRRHLHHYPPPPPYYYLDPPPPEPPFPPHYDYNYSNYHLSPPLPP |
| RNMGRNI (1 HsMGRN1 (1 |) MESILSRRIAGVEDIDIOANSAYRYPPKSAGNYFASHFFMGGEKFDTEPEGYLFGENMDLNFLGSRP MESILSRRIAGVEDIDIOANSAYRYPPKSGNYFASHFFMGGEKFDTEPEGYLFGENMDLNFLGSRP |
| | |
| LOG2 (81 | 91 PLPPYDHHLOHHPPHPYHNHSWAPVAMARYPYAGHMMAOPTPYVEHOKAVUIRNDWNLKKESLRUEPDPDNE |
| LUL1 (68 | MLPYNFNHLHHYPPNSYQLPHPLFHGGRYPILPPFTYVHQKAVTIRNDVNLKKKTITIIPDPENH |
| LUL2 (43) | YGYPYGYGEMASPVQYVEHQEAVTIRNDIN LKKETLR EPDEQNH |
| LUL4 (61 | QPQINSCSYGHYHYHPQPPQYFTTAQPNWWGPMMRPAYYCP-PQPQTQPPKPYLEQQNAKKVRNDVNVHRDTVRLEVDDLV |
| RnMGRN1 (69 | |
| IISHGKWI (00 | A TEL A TELE ANT DESCRIPTION AND A TRADUCTION AND A TRADUCT |
| 1002 (152 | |
| LUL1 (133 | ORLUSETEDATUSCRISVIEFARUSEDKLIAIKEDILPETILDEKGEGKERUSSGGIDESVEDVDERAAF NRLUSETEDASMPCRITVVFFATEDAEONLRATKEDTLPPITFDEGEGLOKBIQSSGGIDESVEDVDERAAF |
| LUL2 (84 | GKFLLSFIFDASVPGSITVMFFAKEGKDCNLIATKEDLFPSTQVSFAKGLECREKQACGTGIFFSDMSEADEVE-AN |
| LUL3 (158 LUL4 (142 |) GHYLVSBVFDALFDGSFTIIFFGEBESKCTIVPHLPEAFPFIKVPFOKGAGOKELOAPGTGIDLGFFSLDDESK-PS GHHLVSBVFDALFDGSFTITFFAKBEPNCTIIPOFPEVYSPTRFHFOKGPCCKELOPSGTGTDLSFFVLDDSK-PI |
| RnMGRN1 (106 | DSPTEDGEKPRVLYSLE <mark>STEDA</mark> DARVAITIYCQAV <mark>E</mark> EFVNGMTVYSCKNPSLQSETVHYKRSVSQQESLPS-FKIDFSEWKDDEINF-DI |
| HSMGRNI (105 | DSPTEDGDKPRVLYSLEENEDADARVAITTYCQASDEFLNGRAVYSPKSPSLQSETVHYKKGVSQQQSLPS-FKIDTSEWKDDFDNF-DI |
| | 271 360 |
| LOG2 (230 LUL1 (209 | DTEIYPLAVKA BAAPSGGENEEEERSGSKNAQITQAVYEKD-KGEIKIRVVKQILWVNGTRYELOBIYGIGNIVEGDDDSADDANDPO DTDYFPLAVKA BATPAEEGKSGSTNVOITOVVYTKE-KGEIKIEVVKOILWVNKRRWSTIBIYGIENTVDGSDE |
| LUL2 (160 | ETDVYHVAVKEBVVSEDDHPESGTPNRQITHVVLEKDHKCEYKARVVKQILWVNCNRYVDQEIYGIGNTVDDNGEDANERC |
| LUL3 (234) | PEEVYPLVISETVISPSSVSEEPLVHKQITQAVLEKTNDGSFKVKVMKQILWIEGERYEHQELYGIDNSITQGTAASGLEDTGC EEDVYPLVISETTISPNSISEOSSVEKOVTOAVIEKONDGSFKVKVVKOTLWIEGVEVEVELEELYGSTOGAASGLESGS- |
| RnMGRN1 (194 | DRGVFPVVIQEVVDEGDVVEVTGHAHVLLAAFEKHVDCSFSVKPLKQKQIVDRVSYLDQEIYGIENKNNQETKPSDDENSDN-S |
| HsMGRN1 (193 | DRGWFFYWICH VVDEGDVVEVIGHAHVLLAAFEKHMDCSFSVKPLKOKQIVDRVSKLDOEIVGETKPSDDENSDN-S |
| | |
| | 361 RING 448 |
| LOG2 (317 LUL1 (283) | 351 KING 448 K ECVIELSEPRDITVLPCHMCMCSGOAKVURECTNRCFICROEV ERULEIKVHGNNGSGNNTGQGETVEQE |
| LOG2 (317 LUL1 (283 LUL2 (241 | 351 KING 446 K ECVICLSEPRDTVLPCRHMCXCSGCAKVLRGTNRCFICROEV ERLLEIKVHGNNGSGNNTGQGETVEQE |
| LOG2 (317 LUL1 (283 LUL2 (241 LUL3 (319 LUL4 (300 | 351 KING 446 K ECVICLSEPRDTTVLPCRHMCVCSGCAKVLRFOTNRCFICROFV ERILEIKVHGNNGSGNNTGQGETVEQE |
| LOG2 (317 LUL1 (283 LUL2 (241 LUL3 (319 LUL4 (300 RnMGRN1 (277 | 351 KING 446 K ECVICLSEPRDTTVLPCRHMOVCSGCAKVLREGTNRGELCREV ERLEIKVHGNNGSGNNTGQGETVEQE K ECVICLSEPRDTVLPCRHMOVCSGCAKLERGTNLGEVCRGEV EMLLEINKNG |
| LOG2 (317 LUL1 (283 LUL2 (241 LUL3 (319 LUL4 (300 RnMGRN1 (277 HsMGRN1 (276 | 351 KING 446 440 440 440 K BCVV LSEPRDTTVLPCRHMOVCSGAKALRSOTNRCH CREV ERFLEIKWHGNNGSGNNTGQGETVEQE |
| LOG2 (317 LUL1 (283 LUL2 (241 LUL3 (319) LUL4 (300 RnMGRN1 (277 HsMGRN1 (276 | 351 KING 446 446 446 K 2000 LSEPRDTVLPCRHWGYCG CARVIEG TNRCH CREV EM LEIKVHGNNGSGNNTGQGETVEQE |
| LOG2 (317 LUL1 (283 LUL2 (241 LUL3 (319) LUL4 (300 RnMGRN1 (277 HsMGRN1 (276 LOG2 (389) LUL1 (338 | 351 KING 446 446 446 K ZCVI LSEPRDITVLPCRHMOVCSGAALARSOTNSCH CREV EM LEIKVHGNNGSGNNTGQGETVEQE |
| LOG2 (317 LUL1 (283 LUL2 (241 LUL3 (319) LUL4 (300 RnMGRN1 (277 HsMGRN1 (276 LOG2 (389) LUL1 (338 LUL2 (300 | 351 KING 446 446 446 K BCVI LSEPRDITVLPCRHMCKCSGCAKALRSCTNLCFVCROFV EMPLEINKNG |
| LOG2 (317 LUL1 (283 LUL2 (241 LUL3 (319 LUL4 (300 RnMGRN1 (277 HsMGRN1 (277 HsMGRN1 (276 LOG2 (389 LUL1 (338 LUL2 (300 LUL3 (379) LUL4 (360 | 351 KING 446 446 446 K BCVI LSEPRDTVLPCRHMCKGGGAKALREGTNEGI ERGEV ER LEIKVHGNNGSGNNTGQGETVEQE |
| LOG2 (317 LUL1 (283 LUL2 (241 LUL3 (319 LUL4 (300 RnMGRN1 (277 HsMGRN1 (277 HsMGRN1 (276 LOG2 (389 LUL1 (338 LUL2 (300 LUL3 (379) LUL4 (360 RnMGRN1 (367 | 351 KING 446 446 446 K BCVU LSEPRDTVLPCRHMCKGGGAKALREGTNEFU EN LEI KVHGNNGSGNNTGQGETVEQE |
| LOG2 (317 LUL1 (283 LUL2 (241 LUL3 (319 LUL4 (300 RnMGRN1 (277 HsMGRN1 (276 LOG2 (389 LUL1 (338 LUL2 (300 LUL3 (379 LUL4 (360 RnMGRN1 (367 HsMGRN1 (366 | 351 KING 446 446 446 K BCVU LSEPRDTVLPCRHMCKGGGAKALKRGTNLCFVCRCHV EN LEI KVHGNNGSGNNTGQGETVEQE |
| LOG2 (317 LUL1 (283 LUL2 (241 LUL3 (319 LUL4 (300 RnMGRN1 (277 HsMGRN1 (277 HsMGRN1 (276 LOG2 (389 LUL1 (338 LUL2 (300 LUL3 (379 LUL4 (360 RnMGRN1 (367 HsMGRN1 (366 | 351 KING 446 K BCVVI LSEPRDTIVL PCRHWCKG GCAKVUR CTNEGT LEFT LEFT KUHGNNGSGNNTGQGETVEQE |
| LOG2 (317 LUL1 (283 LUL2 (241 LUL3 (319 LUL4 (300 RnMGRN1 (277 HsMGRN1 (277 HsMGRN1 (276 LOG2 (389 LUL1 (338 LUL2 (300 LUL3 (379 LUL4 (360 RnMGRN1 (367 HsMGRN1 (366 LOG2 (389 LUL1 (338 | 351 KING 446 446 446 K 20VI LSEPRDTVLPCRHMCKGGCAKVIRGOTNEGT NEGT EREF ER LEI KVHGNNGSGNNTGQGETVEQE |
| LOG2 (317 LUL1 (283 LUL2 (241 LUL3 (319 LUL4 (300 RnMGRN1 (277 HsMGRN1 (276 LOG2 (389 LUL1 (308 LUL2 (300 LUL3 (379 LUL4 (360 RnMGRN1 (367 HsMGRN1 (366 LOG2 (389 LUL4 (388 LUL2 (300 LUL1 (338 LUL2 (300 | 351 KING 446 446 446 K 2CVI LSEPRDTIVL PORHMONOG GANALKINGTNLOFVCROFV EM LEI KVHGNNGSGNNTGQGETVEQE |
| LOG2 (317 LUL1 (283 LUL2 (241 LUL3 (319 LUL4 (300 RnMGRN1 (277 HsMGRN1 (276 LOG2 (389 LUL1 (308 LUL2 (300) LUL3 (379 LUL4 (360 RnMGRN1 (367 HsMGRN1 (366 LOG2 (389 LUL1 (338 LUL2 (300) LUL1 (338 LUL2 (300) LUL3 (379) LUL4 (360) | 351 KING 446 K 20VI LSEPRDTVL PORHMONG GANALKROTNLOFV CROPV ENDLELKVHGNNGSGNNTGQGETVEQE |
| LOG2 (317 LUL1 (283 LUL2 (241 LUL3 (319 LUL4 (300 RnMGRN1 (277 HsMGRN1 (276 LOG2 (389 LUL1 (300 LUL2 (300 LUL3 (379 LUL4 (360 RnMGRN1 (367 HsMGRN1 (366 LOG2 (389 LUL1 (338 LUL2 (300 LUL1 (338 LUL2 (300 LUL3 (379 LUL4 (360 RnMGRN1 (457) | 351 KING 446 K DECVI SUSPERDITVL PORHMONG GANALER OT NEGEL REFUELE KVHGNNGSGNNTGQGETVEQE |
| LOG2 (317 LUL1 (283 LUL2 (241 LUL3 (319 LUL4 (300 RnMGRN1 (277 HsMGRN1 (276 LOG2 (389 LUL1 (338 LUL2 (300 LUL3 (379 LUL4 (360 RnMGRN1 (367 HsMGRN1 (366 LOG2 (389 LUL1 (338 LUL2 (300 LUL3 (379 LUL4 (360 RnMGRN1 (457) HsMGRN1 (456) | 351 KING 446 K DECVI SUSPERDITIVL PORHMONG GOAKALER OT NEGEL REFUELE KVHGNNGSGNNTGQGETVEQE |
| LOG2 (317 LUL1 (283 LUL2 (241 LUL3 (319 LUL4 (300 RnMGRN1 (277 HsMGRN1 (276 LOG2 (389 LUL1 (338 LUL2 (300 LUL3 (379 LUL4 (360 RnMGRN1 (367 HsMGRN1 (366 LOG2 (389 LUL1 (338 LUL2 (300 LUL3 (379) LUL4 (360 RnMGRN1 (457 HsMGRN1 (456 | 351 RING 446 K BCVVI LSEPRDTTVL PCRHWGYG GCAKVIRE OTNEGT REGEV EM LEI KVHGNNGSGNTGQGETVEQE |
| LOG2 (317 LUL1 (283 LUL2 (241 LUL3 (319) LUL4 (300 RnMGRN1 (277 HsMGRN1 (276 LOG2 (389 LUL1 (338 LUL2 (300) LUL3 (379) LUL4 (360 RnMGRN1 (366 LOG2 (389 LUL1 (338 LUL2 (300) LUL3 (379) LUL4 (360 RnMGRN1 (457 HsMGRN1 (456 LOG2 (389) LUL4 (328) | 351 KING 444 K DCVVI SEPERDITVL PCRHWGYG GOAKALER OT NEGE CROEV EM LE KVHGNNGSGNNTGQGETVEQE |
| LOG2 (317 LUL1 (283 LUL2 (241 LUL3 (319) LUL4 (300 RnMGRN1 (277 HsMGRN1 (277 HsMGRN1 (276 LOG2 (389 LUL1 (338 LUL2 (300 LUL3 (379 LUL4 (360 RnMGRN1 (366 LOG2 (389 LUL1 (338 LUL2 (300 LUL3 (379) LUL4 (360 RnMGRN1 (457 HsMGRN1 (456 LOG2 (389 LUL1 (338 LUL2 (300) LUL4 (308) LUL4 (308 | 351 444 X DCVVC LSEPRDT TVL PCRHWC VCS GCAKVERECTNRCPI CROPV ERVLEH KVHGNNGSGNNTGQGETVEQE |
| LOG2 (317 LUL1 (283 LUL2 (241 LUL3 (319) LUL4 (300 RnMGRN1 (277 HsMGRN1 (277 HsMGRN1 (276 LOG2 (389 LUL1 (338 LUL2 (300 LUL3 (379) LUL4 (360 RnMGRN1 (366 LOG2 (389 LUL1 (338 LUL2 (300 LUL3 (379) LUL4 (360 RnMGRN1 (457 HsMGRN1 (456 LOG2 (389 LUL1 (338 LUL2 (300 LUL4 (360 RnMGRN1 (457 HsMGRN1 (456) LOG2 (389 LUL4 (360 RnMGRN1 (456) LOG2 (389 LUL4 (360 RnMGRN1 (456) LOG2 (389 LUL4 (360 RnMGRN1 (456) LOG2 (389 LUL4 (360 RnMGRN1 (456) LOG2 (389 LUL4 (360) RnMGRN1 (456) LOG2 (379 LUL4 (360) RnMGRN1 (456) LOG2 (379 LUL4 (360) RnMGRN1 (456) LOG2 (389) LUL4 (360) RnMGRN1 (456) LOG2 (389) LUL4 (360) RnMGRN1 (456) LOG2 (379) LUL4 (360) RnMGRN1 (456) LOG2 (389) LUL4 (360) RnMGRN1 (456) LOG2 (389) LUL4 (360) RnMGRN1 (456) LOG2 (389) LUL4 (360) RnMGRN1 (456) LOG2 (389) LUL4 (360) LUL4 (360) RnMGRN1 (456) LOG2 (389) LUL4 (360) LUL4 (360) LU | 301 RINC 446 X DOWN SLEEPRDITUL PORH MONGG GANVLERCONNER EROPY END LE KVHGNNGSGNNTGQGETVEQE |
| LOG2 (317 LUL1 (283 LUL2 (241 LUL3 (319) LUL4 (300 RnMGRN1 (277 HsMGRN1 (277 HsMGRN1 (276 LOG2 (389 LUL1 (338 LUL2 (300 LUL3 (379) LUL4 (360 RnMGRN1 (366 LOG2 (389 LUL1 (338 LUL2 (300 LUL3 (379) LUL4 (360 RnMGRN1 (457 HsMGRN1 (456 LOG2 (389 LUL1 (338 LUL2 (300 LUL3 (379) LUL4 (360 RnMGRN1 (456 LOG2 (389) LUL4 (360 RnMGRN1 (456 LOG2 (389) LUL4 (360 RnMGRN1 (534 | 351 RINC 446 KI BCW SLEEPRDTTUL PCRHWCCG GCARVERFONDE FOR VERTER KUHGNNGSGNNTGQGETVEQE 446 K BCW SLEEPRDTTUL PCRHWCCG GCARVERFONDE FOR VERTER KUHGNNGSGNNTGQGETVEQE 5000000000000000000000000000000000000 |

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).



BRI1-GFP

Merge

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 μ m.



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.



В

| | gdu1-1D | wт | log2-2 gdu1-1D | log2-2 |
|---------------------------|---------|----|-------------------|--------|
| GDU1 28 cycles | - | | - | |
| UBQ10 31 cycles | | | | - |

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 efficiencycalibrated 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.

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

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*

| Supplemental Table S2. Seq | uence of the oligonucleotides used for this study. | | |
|----------------------------|--|---|--------------|
| Name | Sequence(5'-3') | Purpose | Direction |
| | GGGGACAAGTTTGTACAAAAAAGCAGGCTCGGAAGGAGATATACATATGGGAAACATTAGCAGCAGC | Addition of Kozak sequence to LOG2 for myristoylation assay | FWD |
| | GGGGACAAGTTIGTACAAAAAAGCAGGCTGAAGGAGATATACATACATGGGAAAACATTAGCAGCAGC | Addition of Shine-Delgarno sequence to LOG2 | EW/D |
| | | Addition of Shine Delgamo sequence to LUL1 | EWD. |
| 1000 150 (| GGGGGACAAGTTTGTACAAAAAAGCAGGCTGAAGGAGATATACATAC | Addition of Shine-Deigano Sequence to LOLI | FWD |
| 1002-1501 | | Amplification of LOG2 CDS from log2-1 | FWD |
| LOG2 BamXno 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 |
| | TTGGCCCCAGCGCCGCAGCAGCACCAGCAGGATCCTTGTACAGCTCGTCCA | Anneals to YFP tag in pEG101 | REV |
| GDU11 180 BE f | TTEGATCCAAGAATCATGCGCCTGICTTCCTCCG | Cloning cGDU1 in pGBT9 and pGBKT7 | EW/D |
| CDUI1 YbB r | | Cloning cGDU1 in pGPT9 and pGPKT7 | PEV |
| GDUIXDBI | | | REV ELLIP |
| 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 |
| nRS300 attB1 | 201120142440120242440121202424401202444404404404404040 | Gateway cloning of amiRNA | FWD |
| pR5300 attB2 | | Cateway cloning of amiDNA | DE1/ |
| pRS300 attB2 | GALLALITIGTALAAGAAAGETGGGTALCCCATGGCGATGCCTTA | Gateway cloning of amikinA | 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 | GATATTAGGATAGGGAGTACCGGTCTCTCTTTGTATTCC | Gateway cloning of amiRNAb | FWD |
| LOG2 miRb r | GACCGGTACTCCCTATCCTAATATCAAAGAGAATCAATGA | Gateway cloning of amiRNAb | REV |
| | | Cateway cloning of annihilad | ILV END |
| LOG2 IIIKD I | GACCAGIACTECETAACTAATTEACAGICGTGATATG | Galeway cioning of aniikinab | FWD |
| LOG2 miRb* r | GAAATTAGGTTAGGGAGTACTGGTCTACATATATTCCT | 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 miBc* r | GAAGTTACGTATCGTTTTCTACATATATATTCCT | Gateway cloning of amiRNAc | REV |
| LOG2 miRd f | | Gateway cloning of amiPNAd | EW/D |
| | GATTIAACCATAGTGCCGCTTTCCCTTTTGTATCC | Gateway cioning of aniikinad | FWD |
| LUG2 MIRd F | GAAAGUGGALACTATIGGGTTAAATUAAAGAGAATUAATGA | Gateway cloning of amikiNAd | 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 |
| GDI11 stop attB2 | GGGGACCACTITIGTACAAGAAAGCTGGGTATTAGTGACTIGTAGTAGTAGTAGTGTCT | Gateway cloning of cGDU1 / GDU1 with ston | REV |
| GDUI1 no stop attB2 | | Cateway cloning of cCDU1 / CDU1 without stop | PEV |
| GDU1 no stop attB2 | GGGGACCACTITIGTACAAGAAAGCTGGGTAGTGGCTGGACTGTAGTAGTGTCT | 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 | GGGGACCACTITIGIAGAAAAGCIGGGTATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG | Gateway cloning of cGDU3 | REV |
| GD05 3(0) 4(102 | | Cateway cloning of cCDU4 | EW/D |
| GD04 190 attB1 | GGGACAAGTTGTACAAAAAAGCAGGCTTAATGCGCTTGTCAACCTCC | Galeway cioning of CODO4 | 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 | | Gateway cloning of cGDU6 | FWD |
| CDUE stop attp2 | | Cateway cloning of cODUC | DE1/ |
| GDU6 stop attB2 | GGGGACCACTITIGTACAAGAAAGCTGGGTATTAGGTTGAGATGACAGT | 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 | 200111TE0112000104TE01120001044040404040404040404040400000 | Gateway cloning of HsMGRN1 | FWD |
| MGRN1 stop attB2 | GGGACCACTUCTACAAGAAGCTGGGTATAGAGTGGGGTCAGGTC | Gateway cloning of HeMGPN1 | PEV |
| MGRN1 Stop attB2 | GGGGGCCCCTTTGTACAAGAAAAGCTGGGTATCAGAGTGGGGTAGCTC | | REV FILID |
| 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 |
| LUL 2 ATG att P1 | GGGGACAAGTTGTACAAAAAAGCAGGCTTAATGGGCAATGTCATAAGC | Gateway cloning of LUL2 | EW/D |
| LULZ AIG allBI | GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGGCAATGTCATAAGC | | 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 |
| IIII 4 stop attB2 | GGGGACCACTITIGTACAAGAAAGCTGGGTACTAGTGTTGTTCATCACT | Gateway cloping of LULA | REV |
| LOL4 Stop attb2 | | CDU4 and time DCD (A) | |
| | 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 | Genotyning log2-2 | REV |
| MCRN1 R | CCCCACCACCACCACCACCACCACCACCACCACCACCAC | Isolation of MGRN1 from Patis DNA | DEV/ |
| MGRNIK | GGGGACCACTITGTACAAGAAAGCTGGGTCTTACTCCTCTATACCAACAGAGCACG | Isolation of MIGRN1 from Rat CDNA | KEV |
| 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 O f | GGTAACATTGTGCTCAGTGGTGG | aPCB Actin2 | FW/D |
| Act2 Q 1 | | | 1000 |
| Act2 Q F | AACGACCITAATCITCATGCIGC | qPCR Actin2 | KEV |
| GDU1 Qf | ATGGCCGGAGAAGATTTGC | qPCR GDU1 | FWD |
| GDU1 Qr | CGCCTTCTCATCTTCTCTCC | qPCR GDU1 | REV |
| LOG2 +800 f | TTCGAGAAAGGACTTGGTCAGA | qPCR LOG2 | FWD |
| LOG2 +900 r | CTGCCTTAACCGCTAATGGATA | aPCR LOG2 | RFV |
| | GGGGACCACTTTGTACAAGAAAGCTGCGTCCTCTTGTTCAACTGTTTCTCCC | Remove STOR codon from LOG2 | |
| 10010000 5 | | Remove STOP COUCH HOLE COZ | |
| URGIORALCK E | ICAATICICICICGIGAICAAG | 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 |
| | | Sequencing adult 1D SKI10E T DNA innetion | EW/D |
| | | Sequencing guut-1D SKITOS 1-DINA 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 |
| DONR r | GCTGCCAGGAAACAGCTATGA | Sequencing inserts in nDONR 221 / Zoo | REV |
| | | Sequencing inserts in poorin 221 / 200 | |
| LUG2 -1650 f | CACTACCTTCGTATGGGAAT | Sequencing LUG2 promoter | FWD |
| LOG2 -2350 f | ATTCCTCATTACGAACCACA | Sequencing LOG2 promoter | REV |
| | TCGCGTTAACGCTAGCATGGATCTC | Sequencing pDONR 201 insert | FWD |
| | ACGGGCCAGAGCTGCAGCTG | Sequencing nDONR 201 insert | REV |
| | CGTATTAAATCTATAATTGCGGGGAC | Sequencing poort 201 insert | DEV |
| | | Sequencing powe 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 | ACATTITICICAATCCITACTC | 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 | TGTTTTTAGGACAAATGGCG | SSLP genetic marker chr I | REV |
| II-016.5 f | | SSLP genetic marker chr II | FWD |
| II-016.5 r | | SSLP genetic marker chr II | REV |
| II-088.5 T | | SSLP genetic marker chr II | FWD |
| II-088.5 F | | SSLP genetic marker chr II | REV |
| II-157.51 | COCIACOCITICOGIAAAO | SSLP genetic marker chr II | P VV D |
| 11-137.51 | | SSLP genetic marker chr II | EWD |
| II-212.31 | | SSLP genetic marker chr II | P WD |
| II-212.51 | | SSLP genetic marker chr III | EW/D |
| III-013 s r | | SSLP genetic marker chr III | REV |
| III-013.51 III-028 c f | | SSLP genetic marker chr III | FW/D |
| III 028.51 | | SSLP genetic marker chr III | PEV |
| 111-020.31 | | SSLP genetic marker chr III | EW/D |
| 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 | CATGCAATTIGCATCIGAGG | 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 | TGGATTTCTTCCTCTTCAC | 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 | GCGAAAAAAAAAAAAAACCA | 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 | AAACILGAGAGIITTGTCTAGATC | SSLP genetic marker chr V | REV |
| V-249.s f | CAGACGTATCAAATGACAAATG | SSLP genetic marker chr V | FWD |
| V-249.s r | GALIALIGUILAAACTATTCGG | SSLP genetic marker chr V | REV |
| V-359.51 | | SSLP genetic marker chr V | FWD |
| V-359.5 ľ | GILAALLALAIALGLALLAIALAIAA | SSLP genetic marker chr V | REV |
| V-5/8.ST | | SSLP genetic marker chr V | FWD |
| v-5/8.5 F | CAACATTTAGCAAATCAACTT | SSLP genetic marker onr v | KEV |

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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