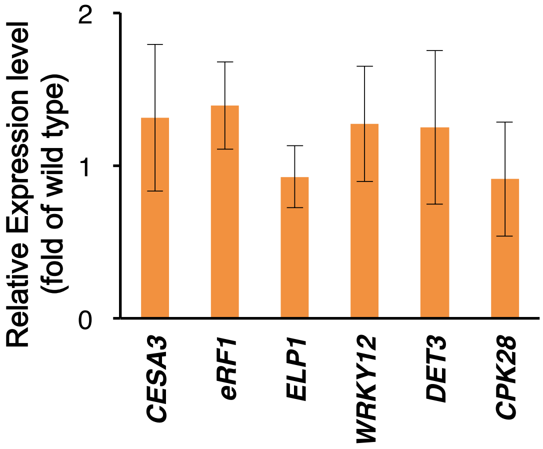
Supplemental Figure 1

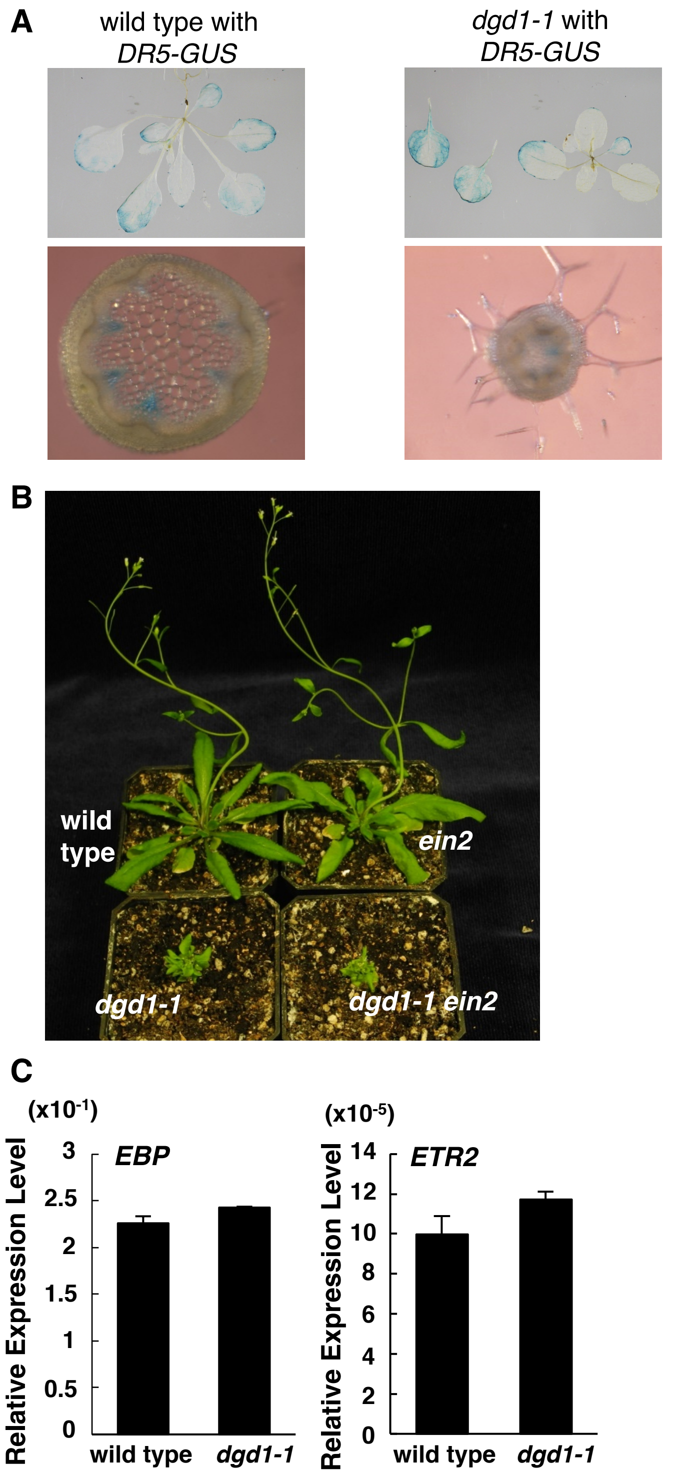
Supplemental Figure 1. Visible phenotypes of the two *dgd1* mutant alleles. Plants were grown for 35 days on a 16 h light/8 h dark cycle. The inserts show close-up views of the two *dgd1* mutants.

Supplemental Figure 2



Supplemental Figure 2. Level of expression of genes, mutations of which result in ectopic lignification. Wild-type and *dgd1-1* mutant plants were grown for 10 days on MS plates, then were harvested for total RNA isolation. Gene expression levels were analyzed by quantitative RT-PCR and normalized to *UBQ10* gene expression in the same sample, then expression in the *dgd1-1* mutant was expressed as a fold value compared to the wild type. Values are means ± SD of four independent plant batches.

Supplemental Figure 3



Supplemental Figure 3. The *dgd1* phenotypes are not caused by activation of auxin or ethylene signaling. **(A)** GUS staining of wild-type and *dgd1-1* plants containing the auxin-responsive *DR5-GUS* reporter transgene. The whole seedlings (top panels) and cross-sections of inflorescence stems (bottom panels) were from 17- or 35-day-old plants, respectively. **(B)** Visible phenotypes of 39-day-old wild-type, *ein2* single mutant, *dgd1-1* single mutant and *dgd1-1 ein2* double mutant plants. **(C)** Expression of ethylene-responsive genes. Plants were grown for 10 days on MS plates, then expression of the ethylene-responsive genes *EBP* and *ETR2* was analyzed by quantitative RT-PCR and expressed relative to *UBQ10* gene expression. Values are means ± SD of three technical replicates.

Supplemental Table 1. Lipid composition of the wild-type and various mutant plants. Plants were grown on a 16 h light/8 h dark cycle for 10 days on MS plates, then were moved to soil for another 10 days. The means ± SEM for at least three independent plant batches are shown. Values are relative peak area (%). MGDG, monogalactosyldiacylglycerol; DGDG, digalactosyldiacylglycerol; PG, phosphatidylglycerol; PC, phosphatidylcholine; PE, phosphatidylethanolamine; PS, phosphatidylserine; PI, phosphatidylinositol; SQDG, sulphoquinovosyldiacylglycerol; L-MGDG, Lyso-MGDG; L-DGDG, Lyso-DGDG; L-PG, Lyso-PG; L-PC, Lyso-PC; L-PE, Lyso-PE; L-PI, Lyso-PI; DAG, diacylglycerol; TAG, triacylglycerol.

	wild type	*dgd1-1*	*dgd1-2*	*coi1-30*	*coi1-30 dgd1-1*	*aos*	*aos dgd1-1*	*aos dgd1-2*
MGDG	33.5±8.3	28.4±3.8	24.0±3.4	30.6±5.6	31.0±5.4	30.5±8.9	29.1±3.5	31.9±4.3
DGDG	6.2±1.4	0.5±0.2	0.4±0.04	6.1±1.0	0.6±0.1	5.8±1.2	0.5±0.1	0.5±0.2
PG	27.2±4.7	33.5±2.3	36.6±2.4	28.5±3.2	31.6±1.2	28.7±4.0	30.5±0.5	31.8±2.3
PC	11.2±3.8	9.0±6.3	13.9±1.3	12.8±3.8	13.3±4.2	12.8±4.4	14.8±3.0	12.2±4.3
PE	16.6±1.8	22.2±3.8	19.2±5.4	16.6±1.1	18.6±1.5	17.2±1.3	19.5±0.6	18.2±1.0
PS	0.11±0.01	0.12±0.03	0.10±0.03	0.10±0.03	0.10±0.02	0.13±0.05	0.12±0.03	0.12±0.04
PI	0.33±0.02	0.39±0.05	0.29±0.10	0.26±0.10	0.29±0.05	0.24±0.11	0.22±0.09	0.29±0.03
SQDG	2.4±0.6	3.0±0.6	3.1±0.4	2.6±0.8	2.2±1.2	2.5±0.7	3.2±0.5	2.8±1.0
L-MGDG	0.14±0.11	0.07±0.01	0.04±0.02	0.10±0.07	0.11±0.08	0.06±0.07	0.07±0.05	0.10±0.09
L-DGDG	0.67±0.10	0.99±0.17	0.81±0.14	0.72±0.10	0.83±0.12	0.69±0.09	0.82±0.11	0.72±0.11
L-PG	0.05±0.03	0.14±0.13	0.07±0.05	0.02±0.02	0.07±0.08	0.03±0.01	0.04±0.02	0.07±0.09
L-PC	0.09±0.03	0.11±0.01	0.09±0.02	0.06±0.02	0.09±0.02	0.07±0.01	0.08±0.01	0.08±0.02
L-PE	0.08±0.03	0.09±0.00	0.07±0.01	0.05±0.02	0.07±0.02	0.06±0.01	0.06±0.01	0.06±0.02
L-PI	0.005±0.001	0.006±0.003	0.005±0.001	0.003±0.001	0.005±0.001	0.005±0.001	0.004±0.000	0.004±0.002
DAG	0.49±0.15	0.62±0.14	0.58±0.19	0.55±0.18	0.77±0.07	0.46±0.24	0.48±0.23	0.60±0.28
TAG	0.87±0.21	0.60±0.12	0.56±0.19	0.93±0.37	0.42±0.06	0.73±0.28	0.42±0.07	0.60±0.20

Supplemental Table 2. Primers used for quantitative RT-PCR and genotyping.

Primers for quantitative RT-PCR

Gene name	ATG number	Primer sequence		Reference
UBQ10	At4g05320	**Fw**	TCC GGA TCA GCA GAG GCT TA	
		Rv	TCA GAA CTC TCC ACC TCA AG	
VSP1	At5g24780	**Fw**	GGG CGT ACT GGT CGT GGT TA	
		Rv	TCC CGA GTT CCA AGA GGT TTT	
PDF1.2	At5g44420	**Fw**	TGT TCT CTT TGC TGC TTT CGA CGC	
		Rv	TGT GTG CTG GGA AGA CAT AGT TGC	
LOX2	At3g45140	**Fw**	GCC ATT GAG TTG ACT TGT CC	Grebner et al., 2013
		Rv	CAC TTA GTT GTC TAT TTG CCG C	
EBP	At3g16770	**Fw**	CTG GGG TTT CTA TTC CAC CTC	
		Rv	CCT TCT TCA CTG CCT CCT CTT	
ETR2	At3g23150	**Fw**	TGA TCC AAA CTC ATC TCT TTC AGA	
		Rv	TTT ATA GCT AAA ACC GGA GAA ACA A	
CesA3	At5g05170	**Fw**	CCA GAT TGA GAG AGA TTC AGA GAG T	
		Rv	AAA CGT CGG AAT AGT TCA AAT CA	
eRF1-1	At5g47880	**Fw**	ACT GCC TTT GAT TCC GAG GA	
		Rv	GCG ATG GTG AGG ATT TGA TTG	
ELP1	At1g05850	**Fw**	TGC CTT ACC CAT TTA CTG GAA	
		Rv	GGG TGG TTC AAG AGA TCA GC	
WRKY12	At2g44745	**Fw**	GGT GGT TAA TGA TGA TCA GGA GA	
		Rv	TTC CAC TAT TTG ATC TCC ACC A	
DET3	At1g12840	**Fw**	CGT GTC GCA GAT AAT TTC AGG	
		Rv	CAC TTT GTT CAA AAT CAC GGA CT	
CPK28	At5g66210	**Fw**	TTG AGG ATG ACG ATT ACG TCT ATA TT	
		Rv	GGA GTA CCG ATT ACC TTT CTT GG	
LOX3	At1g17420	**Fw**	TCC CTG CCG ATC TAA	Grebner et al., 2013
		Rv	GTT TGG GAC GTA GCC A	
LOX4	At1g72520	**Fw**	GCT TGC TTA GAT ACG ACA CT	Grebner et al., 2013
		Rv	ATG TGG TCT TCC GTG AGA GC	
LOX6	AT1g67560	**Fw**	CGA AGA TTC CAC TGA CAC CA	
		Rv	TCG GAA GGT AGG CAT GGT T	
AOC1	AT3g25760	**Fw**	AACTCCGGTACCACCGTCTA	
		Rv	GGCTTAAGCGCCTTAGCTTC	
AOC2	AT3g25770	**Fw**	AATTAGATCGACACAGCCCCAAG	Stenzel et al., 2012
		Rv	CCGAGACCGAACATTAAGCTGA	
AOC3	AT3g25770	**Fw**	CGAAGGAGATAGAAACAGTCCAGC	Stenzel et al., 2012
		Rv	GGAGTTCACGCGCTTAAATCC	

Gene name	ATG number	Primer sequence		Reference
AOC4	AT1g13280	**Fw**	GCCGTTCTCGTAAGCGTAATGT	Stenzel et al., 2012
		Rv	GGAGTTCACGCGCTTAAATCC	
AOS	AT5g42650	**Fw**	CACCGGCGTTAGTCAAATCT	
		Rv	CCGGCGGATTCTAAGAAAA	
PLA-Iα2	At2g31690	**Fw**	TGAGGACAGTGACAATGTTGCATTA	
		Rv	CACGGCATTGGACCAATACATC	
PLA-Iβ2	At4g16820	**Fw**	GTAATAACGGGAGAAGTCC	Seo et al., 2009
		Rv	CCGTCGACTAAGTGCAAG	
PLA-Iγ1	At1g06800	**Fw**	GCGAGTTGGGAACATTCG	
		Rv	CTCAACACCTTCACTCCCAAT	
PLA-Iγ2	At2g30550	**Fw**	CGAGAGTTGGGAACGTTAGG	Seo et al., 2009
		Rv	CTCTCATCACTTTCACTCCCAAT	
PLA-Iγ3	At1g51440	**Fw**	GTTTCAGTTTCAGAAGTATGTG	Seo et al., 2009
		Rv	CTCTTCTCTGCTTCTTCGTC	
DGL	AT1g05800	**Fw**	GGCGGTTAATGAAGACAATTTTGGCGGC	
		Rv	ATGCCGCATTGGTCGCTGCGTTTGTAAA	
DAD1	AT2g44810	**Fw**	GATAACGTTAAGATGACAGCG	Seo et al., 2009
		Rv	GTGGCCACATTGATGCTG	

Primers for genotyping

Mutant name	Mutant line number	Primer sequence	
coi1-30	SALK_035548	**LP**	TGG ACC ATA TAA ATT CAT GCA GTC
		RP	CTG CAG TGT GTA ACG ATG CTC
dgd1-2	SAIL_851_G12	**LP**	CAT TAT GAT GGT GGG TTT TGG
		RP	TCG CTT TTG TGT TTA GCC ATC

Supplemental References

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