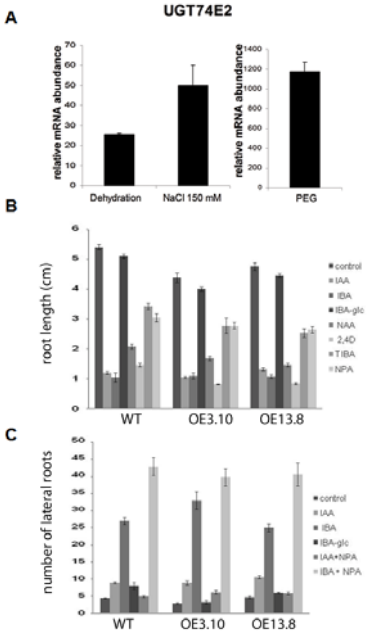
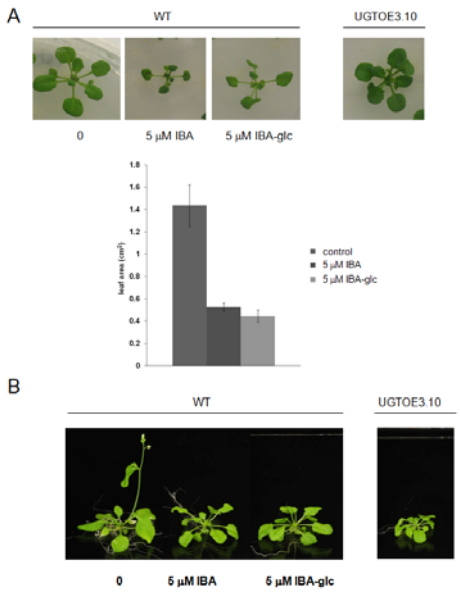


Supplemental Figure 1. UGT74E2 stress induction and auxin effects on root development.

(A) Real time RT-PCR transcript analysis of *UGT74E2* in seedlings exposed to 150 mM NaCl (3 h), 50 mM PEG (5 h), and dehydration stress (10 h). Error bars are SE (n=3).

(B) Comparative graph of root length of 4-day-old wild-type and transgenic lines grown on MS with 0.5 % sucrose agar plates and transferred to the same media containing 0.5 µM IAA, 5 µM IBA, 5 µM IBA-Glc, 100 nM NAA, 50 nM 2,4-D, 5 µM triiodobenzoic acid, or 5 µM NPA for 8 days.

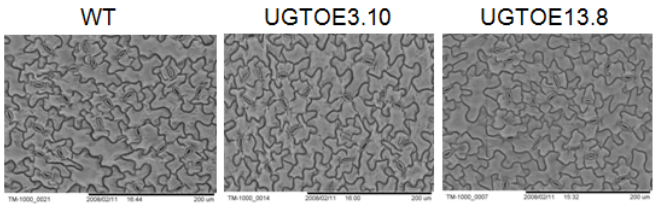
(**C**) Lateral roots counted 8 days after transfer of 4-day-old seedlings to medium supplemented with either auxins (0.5 µM IAA, 5 µM IBA, 5µM IBA-Glc) or the same auxins in combination with 5 µM NPA. Error bars are SE of four independent experiments (n=25).



Supplemental Figure 2. Auxin effects on plant morphology.

(**A**) One-month-old wild-type seedlings grown on MS 0.5% sucrose plates supplemented with the indicated concentration of IAA, IBA, or IBA-Glc. Leaf area was calculated with the ImageJ program (http://rsb.info.nih.gov/ij/) and expressed as cm^2. Error bars are SE of three independent experiments (n=10).

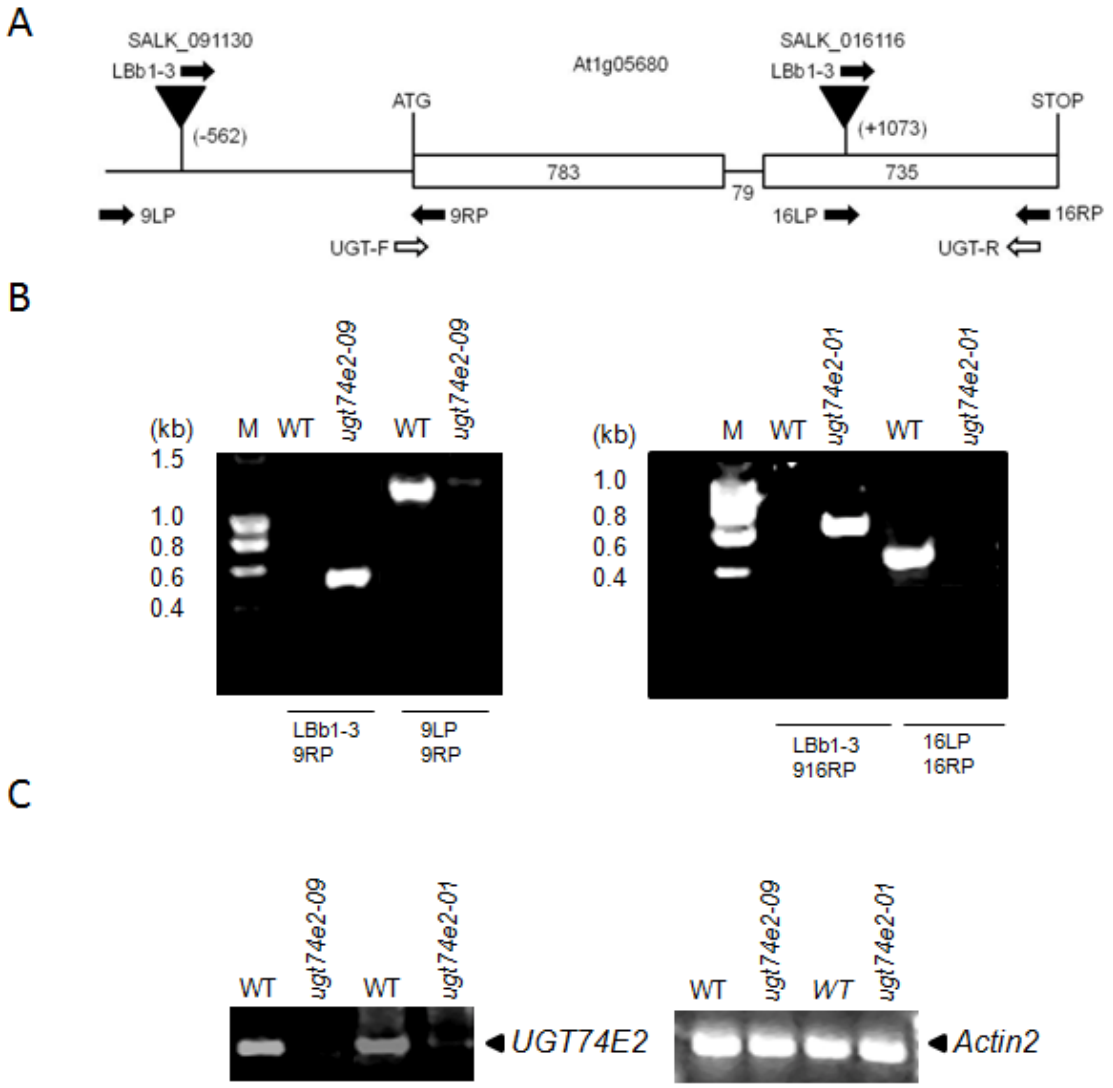
(**B**) Effect of auxin on flowering time in 48-day-old plants grown on MS 0.5% sucroseon magenta boxes supplemented with auxin. Late-flowering transition phenotype of the UGT74E2OE plants compared to wild-type plants.



	cell density (cells/mm²)	stomatal density (stomata/mm²)	stomate diametre (µm)
WT	670.3 ± 6.8	321.66 ± 33.6	21.3 ± 0.8
UGT3.10	676.2 ± 10.2	240.68 ± 14.7	20.7 ± 0.6
UGT13.8	722.3 ± 3.4	309.68 ± 31.1	21.0 ± 0.9

Supplemental Figure 3. Analysis of epidermal cells in UGT74EOE plants.

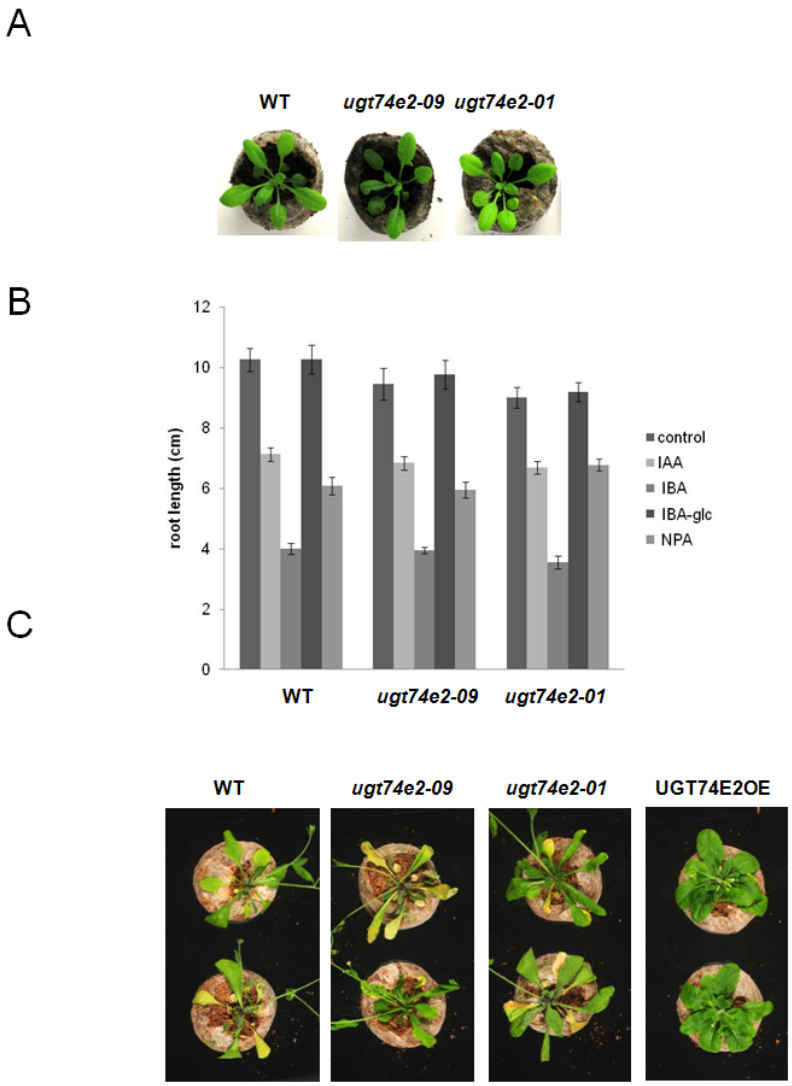
Epidermal cells of the 3rd leaf of 21-day-old plants grown under short-day conditions determined by scanning electron microscopy (Hitachi tabletop microscope IM-1000). Bars = 200 µm. Data are means ± SE (n =6).



Supplemental Figure 4. Identification of homozygous insertion mutants at the *UGT74E2* locus.

(**A**) Schematic diagram of the *UGT74E2* gene (At1g05680) from *Arabidopsis* and localization of the T-DNA insertions in *ugt74e2-09* (SALK_091130) and *ugt74e2-01* (SALK_016116) alleles. Numbering begins at the ATG translation start codon (+1). Exons are represented by white boxes and introns by lines. Exon and intron lengths are indicated in base pairs inside the box or below each line, respectively. The position of the T-DNA insertion is indicated in a bracket with respect to the ATG start codon. Black arrows show the positions and orientations of the primers used for genotyping and white arrows for primers used for PCR expression analysis.

(**B**) and (**C**) Validation of the mutant lines by PCR analysis (**B**) or by qRT-PCR analysis (**C**) of UGT74E2 transcripts on genomic DNA. The *Actin2* gene (At3g18780) served as a control. M corresponds to molecular mass markers. PCR primers are indicated above each lane.



Supplemental Figure 5. Phenotype and auxin response of UGT74E2 knockout mutants.

(**A**) Rosette shapes of 1-month-old wild-type, UGT74E2OE, and *ugt74e2* knockout mutant plants grown under long-day regime.

(**B**) Comparative graph of root length of 4-day-old wild-type and knockout mutants transferred to media containing 0.5 µM IAA, 5 µM IBA, 5 µM IBA-Glc, or 5 µM NPA for 10 days. Error bars are SE of two independent experiments (n=25).

(**C**) Plants of wild-type, *ugt74e2* mutants, and UGTOE13.8 lines grown under a controlled watering regime for 3.5 weeks and deprived from further watering for 17 days.

Supplemental Table 1. Phenotypic comparison of wild-type and UGT74E2OE plants. Wild-type plants and transformants grown in soil for 51 days in the growth chamber under short-day conditions. Gas exchange in 1-month-old leaves at 500 μmol m^{-2} s^{-1} and chlorophyll *a* fluorescence were measured as described (Methods). Data are means ±SE (n =3). Statistically significant differences are indicated in bold ($P < 0.005$).

	Wild type	UGTOE3.10	UGTOE13.8
Chlorophyll *a*+*b* (μg cm^{-1})	**12.5 ± 0.2**	**17.6 ± 0.3**	**15 ± 0.2**
Height (cm)	**18.1 ± 0.6**	**9.2 ± 0.0.5**	**9.0 ± 0.6**
Net CO_2 assimilation (μmol CO_2 m^{-2} s^{-1})	12.8 ±0.6	12.3 ± 0.8	13.5 ± 00.4
Stomatal conductance (mol H_2O m^{-2} s^{-1})	0.23 ± 0.01	0.22 ± 0.02	0.26 ± 0.02
Rosette fresh weight (g)	14.9 ± 0.8	13.8 ± 1.5	13.4 ± 0.7
Root length on MS without sucrose after 10 days (n=5)	**3.45± 0.1**	**2.2 ± 0.2**	**1.6 ± 0.1**

Supplemental Table 2. Differential genes in UGT74E2OE plants as determined by full-genome microarray analysis**.** Probe sets with a *P* value <0.05 and 1.5-fold change were retained.

Probe set	**AGI code**	**Description**	**Fold change**	***P*-value**
263231_at	AT1G05680	UGT74E2 IBA-glycosyltransferase	178.31	9.64E-12
256940_at	AT3G30720	Expressed protein	5.98	6.70E-06
251428_at	AT3G60140	Dark-inducible DIN2 glycosyl hydrolase	2.08	7.47E-03
245306_at	AT4G14690	ELIP2 early light-induced protein (chlorophyll binding)	1.99	6.13E-03
252629_at	AT3G44970	Cytochrome P450 CYP708A4	1.97	3.36E-04
254828_at	AT4G12550	AIR1 auxin-induced in root cultures	1.84	4.71E-02
250142_at	AT5G14650	Polygalacturonase/pectinase	1.75	8.95E-03
261768_at	AT1G15550	Gibberellin 3-β-dioxygenase GA4	1.72	2.00E-02
263689_at	AT1G26820	Ribonuclease RNS3	1.71	4.71E-02
251743_at	AT3G55890	Yippee family protein, zinc-binding protein	1.65	3.63E-02
263549_at	AT2G21650	Myb family transcription factor	1.64	5.10E-03
255517_at	AT4G02290	Glycosyl hydrolase	1.55	1.92E-02
253024_at	AT4G38080	Hydroxyproline-rich glycoprotein	1.54	3.43E-02
245982_at	AT5G13170	Nodulin MtN3 family protein	0.66	3.43E-02
259640_at	AT1G52400	Glycosyl hydrolase BGL1	0.65	1.92E-02
265053_at	AT1G52000	Jacalin lectin myrosinase binding	0.64	1.38E-02
250828_at	AT5G05250	Mitochondrial expressed protein	0.64	1.92E-02
259080_at	AT3G04910	WNK1 protein kinase	0.62	4.57E-03
262661_s_at	AT1G14230	Nucleoside phosphatase	0.62	1.92E-02
255795_at	AT2G33380	RD20 EF-hand protein induced by ABA, salt and drought	0.62	1.80E-02
250012_x_at	AT5G18060	Auxin-inducible SAUR (Small Auxin Up RNAs)	0.61	5.46E-03
259417_at	AT1G02340	HFR1 bHLH protein involved in phytochrome signaling	0.57	1.68E-03
245422_at	AT4G17470	Palmitoyl protein thioesterase	0.54	1.85E-03
248270_at	AT5G53450	ORG1 OBP3-responsive SA-induced protein kinase	0.53	4.60E-03
266141_at	AT2G02120	Plant defensin-fusion protein, putative PDF2.1	0.51	3.43E-02
250942_at	AT5G03350	Legume lectin family protein	0.49	2.34E-02
261684_at	AT1G47400	Expressed protein	0.48	1.92E-02
251677_at	AT3G56980	ORG3 OBP3-responsive SA-induced bHLH protein	0.46	6.13E-03
245692_at	AT5G04150	Mitochondrion/nucleus bHLH protein	0.43	1.28E-03
256766_at	AT3G22231	PCC1 pathogen and circadian controlled	0.24	1.11E-03
251772_at	AT3G55920	Peptidyl-prolyl cis-trans isomerase cyclophilin	0.09	9.62E-09

Supplemental Table 3. Auxin effect on photosynthesis. Wild-type and transgenic plants grown on MS 0.5% sucrose agar plates were transferred to new plates supplemented with polyethylene glycol (PEG), mannitol (M), or both PEG and auxin: M+IBA, M+IBA-Glc, and PEG+IAA. Seedlings were also germinated on plates supplemented with IBA, IBA-Glc, or IAA and, after 2 weeks, transferred to new PEG or M plates supplemented with IBA (M+IBA-IBA treated), IBA-Glc (M+IBA-Glc-IBA-Glc treated) or IAA (PEG+IAA-IAA treated). Chlorophyll *a* fluorescence was measured after 8 days of stress as described (Methods). Data are means ± SE of two independent experiments (n=25). Statistically significant differences (α=0.05) were obtained by weighted ANOVA (see Methods).

Lines and treatments	ETRmax
Wild type control	35.0 ± 1.1
UGTOE13.8 control	33.2 ± 1.2
UGTOE3.10 control	36.1 ± 0.5
Wild-type M	24.4 ± 0.7[*1*2]
UGTOE13.8 M	30.0 ± 1.0[*1]
UGTOE3.10 M	32.6 ± 1.0[*1]
Wild type M+IBA	12.2 ± 0.5[*3*4]
Wild type M+IBA-IBA treated	15.9 ± 0.2[*3*4]
Wild type M+IBA-Glc	20.8 ± 1.1[*3]
Wild type M+IBA-Glc-IBA-Glc treated	18.5 ± 0.7[*3*4]
Wild type PEG	26.3 ± 1.3[*1*2]
UGTOE13.8 PEG	34.5 ± 0.8[*1]
UGTOE3.10 PEG	32.7 ± 0.4[*1]
Wild type PEG+IAA	22.1 ± 1.0[*3]
Wild type PEG+IAA-IAA treated	32.7 ± 1.1

[*1]*P* <0.01 between UGTOE and wild type; [*2]*P* <0.01 between PEG or M and control growth conditions; [*3]*P* <0.01 between auxin treatment and UGTOE lines under PEG or M treatment; [*4]*P* <0.01 between auxin treatment and wild-type plants under PEG or M treatments. ETRmax: maximal electron transfer rate.