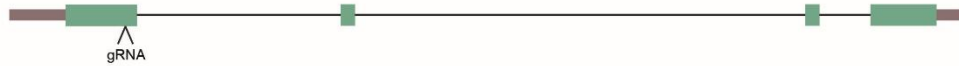


Figure S3. (A) Scheme depicting the structure of *FT2* gene and the localization of the gRNA used for CRISPR/Cas9 edition. The 5'UTR and 3'UTR are shown in grey, exons in green, and introns in black. (A-B) *FT2* and *FT1* DNA sequence (first 93 and 102 nucleotides, respectively) and the predicted protein obtained from, WT, *ft2-8*, and *ft2-10 tremula* and *alba* alleles. Alignments were performed using ClustalW Multiple alignment with a number of 1000 bootstraps. Matching nucleotides among gRNA and *FT2* or *FT1* are indicated in red ink. Insertion or deletion are indicated in blue ink.

A

FT2



DNA sequence

gRNA	-----GCCAGGGTTGATATCGGTG-----	20
WT allele <i>P. alba</i>	GGTTGTGAGCTCAAACCTCTCAAGTTGTCAACCA GCCAGGGTTGATATCGGTG GGGAAGATCTAAGACCTTCTACACTCTGGTAACATAC-----	93
WT allele <i>P. tremula</i>	GGTTGTGAGTTCAAACCTCTCAAGTTGTCAACCA GCCAGAGTTGATATCGGTG GGGAAGATCTAAGACCTTCTACACTCTGGTAACATAC-----	93
#8 allele <i>P. alba</i>	GGTTGTGAGCTCAAACCTCTCAAGTTGTCAACCA GCCAGGGTTGAT -----ATCTAAGGACCTTCTACACTCTGGTAACATAC	80
#8 allele <i>P. tremula</i>	GGTTGTGAGTTCAAACCTCTCAAGTTGTCAACCA GCCAGAGTTGATATCGCGTG GGGAAGATCTAAGACCTTCTACACTCTGGTAACATAC	94
#10 allele <i>P. alba</i>	GGTTGTGAGTTCAAACCTCTCAAGTTGTCAACCA GCCAGAGTTGATATCGGTG GGGAAGATCTAAGACCTTCTACACTCTGGTAA	89
#10 allele <i>P. tremula</i>	GGTTGTGAGCTCAAACCTCTCAAGTTGTCAACCA GCCAGGGTT ----- GTG GGGAAGATCTAAGACCTTCTACACTCTGGTAA	81

Protein

WT allele <i>P. alba</i>	MPDRDPLSVGRVIGEVLDPFTRISLRVTYNSREVNNGCELPKPSQVNVQPRVDIG---GEDLRFTYTLVMVDPDAPSPSNPNLREYLHWLVTIDIPATTGASFGQEVVC	106
WT allele <i>P. tremula</i>	MPDRDPLSVGRVIGEVLDPFTRISLRVSYNSREVNNGCEFPKPSHVNVQPRVDIG---GEDLRFTYTLVMVDPDAPSPSNPNLREYLHWLVTIDIPATTGASFGQEVVC	106
#8 allele <i>P. alba</i>	MPDRDPLSVGRVIGEVLDPFTRISLRVTYNSREVNNGCELPKPSQVNVQPRVDI-----	55
#8 allele <i>P. tremula</i>	MPDRDPLSVGRVIGEVLDPFTRISLRVSYNSREVNNGCEFPKPSHVNVQPRVDIA-----	56
#10 allele <i>P. alba</i>	MPDRDPLSVGRVIGEVLDPFTRISLRVTYNSREVNNGCELPKPSQVNVQPR-----VVGKI-----	57
#10 allele <i>P. tremula</i>	MPDRDPLSVGRVIGEVLDPFTRISLRVSYNSREVNNGCEFPKPSHVNVQPRVDIG-----	56
WT allele <i>P. alba</i>	YESPRPTAGIHRFVFLFRQLGRQTVYAPGWRQNFNTRDFAEYVNLGSPVAAVYFNCQRESGSGGRRS	174
WT allele <i>P. tremula</i>	YESPRPTAGIHRFVFLFRQLGRQTVYAPGWRQNFNTRDFAEYVNLGSPVAAVYFNCQRESGSGGRRS	174
#8 allele <i>P. alba</i>	-----WGR---SKDLLH-----SGYGGP--	55
#8 allele <i>P. tremula</i>	-----WGR---SKDLLH-----SGYGGP--	71
#10 allele <i>P. alba</i>	-----WGR---SKDLLH-----SGYGGP--	57
#10 allele <i>P. tremula</i>	-----WGR---SKDLLH-----SGYGGP--	71

B

FT1

DNA sequence

gRNA	-----GCCAGGGTTGATATCGGTG-----	20
WT allele <i>P. alba</i>	GGTTGCGAGCTCAAACCTCTCAGGTTGCCAACC GCCTAGGGTTGATATTCGCG GGGAAGATCTAAGACCTTCTACACTCTGGTACGTCTCTGCAGCCTCCTC	105
WT allele <i>P. tremula</i>	GGTTGCGAGCTCAAACCTCTCAGGTTGCCAACC GCCAGGGTTGATATTCGCG GGGAAGATCTAAGACCTTCTACACTCTGGTACGTCTCTGCAG---CCTC	102
#8 allele <i>P. alba</i>	GGTTGCGAGCTCAAACCTCTCAGGTTGCCAACC GCCTAGGGTTGATATTCGCG GGGAAGATCTAAGACCTTCTACACTCTGGTACGTCTCTGCAGCCTCCTC	105
#8 allele <i>P. tremula</i>	GGTTGCGAGCTCAAACCTCTCAGGTTGCCAACC GCCAGGGTTGATATTCGCG GGGAAGATCTAAGACCTTCTACACTCTGGTACGTCTCTGCAG---CCTC	102
#20 allele <i>P. alba</i>	GGTTGCGAGCTCAAACCTCTCAGGTTGCCAACC GCCTAGGGTTGATATTCGCG GGGAAGATCTAAGACCTTCTACACTCTGGTACGTCTCTGCAGCCTCCTC	105
#20 allele <i>P. tremula</i>	GGTTGCGAGCTCAAACCTCTCAGGTTGCCAACC GCCAGGGTTGATATTCGCG GGGAAGATCTAAGACCTTCTACACTCTGGTACGTCTCTGCAG---CCTC	102

Protein

WT allele <i>P. alba</i>	MSRDRDPLSVGRVIGEVLDPFETKSIPLRVYNSREVNNGCELPKPSQVANQPRVDIGGEDLRFTYTLVMVDPDAPSPSPDPSLREYLHWLVTIDIPATTGASFGHETVCYESP	110
WT allele <i>P. tremula</i>	MSRDRDPLSVGRVIGEVLDPFETKSIPLRVYNSREVNNGCELPKPSQVANQPRVDIGGEDLRFTYTLVMVDPDAPSPSPDPSLREYLHWLVTIDIPATTGASFGHETVCYESP	110
#8 allele <i>P. alba</i>	MSRDRDPLSVGRVIGEVLDPFETKSIPLRVYNSREVNNGCELPKPSQVANQPRVDIGGEDLRFTYTLVMVDPDAPSPSPDPSLREYLHWLVTIDIPATTGASFGHETVCYESP	110
#8 allele <i>P. tremula</i>	MSRDRDPLSVGRVIGEVLDPFETKSIPLRVYNSREVNNGCELPKPSQVANQPRVDIGGEDLRFTYTLVMVDPDAPSPSPDPSLREYLHWLVTIDIPATTGASFGHETVCYESP	110
#20 allele <i>P. alba</i>	MSRDRDPLSVGRVIGEVLDPFETKSIPLRVYNSREVNNGCELPKPSQVANQPRVDIGGEDLRFTYTLVMVDPDAPSPSPDPSLREYLHWLVTIDIPATTGASFGHETVCYESP	110
#20 allele <i>P. tremula</i>	MSRDRDPLSVGRVIGEVLDPFETKSIPLRVYNSREVNNGCELPKPSQVANQPRVDIGGEDLRFTYTLVMVDPDAPSPSPDPSLREYLHWLVTIDIPATTGASFGHETVCYESP	110
WT allele <i>P. alba</i>	RPTMGIHRFVFLFRQLGRQTVYAPGWRQNFNTRDFAEYVNLGSPVAAVYFNCQRESGSGGRRR	174
WT allele <i>P. tremula</i>	RPTMGIHRFVFLFRQLGRQTVYAPGWRQNFNTRDFAEYVNLGSPVAAVYFNCQRESGSGGRRR	174
#8 allele <i>P. alba</i>	RPTMGIHRFVFLFRQLGRQTVYAPGWRQNFNTRDFAEYVNLGSPVAAVYFNCQRESGSGGRRR	174
#8 allele <i>P. tremula</i>	RPTMGIHRFVFLFRQLGRQTVYAPGWRQNFNTRDFAEYVNLGSPVAAVYFNCQRESGSGGRRR	174
#20 allele <i>P. alba</i>	RPTMGIHRFVFLFRQLGRQTVYAPGWRQNFNTRDFAEYVNLGSPVAAVYFNCQRESGSGGRRR	174
#20 allele <i>P. tremula</i>	RPTMGIHRFVFLFRQLGRQTVYAPGWRQNFNTRDFAEYVNLGSPVAAVYFNCQRESGSGGRRR	174

Figure S4. Bar plot showing the quantification branch number of WT, *ft2-8*, and *ft2-10* soil grown plants under LD conditions. The y-axis indicates the number of branches once WT plants reached full growth and the x-axis the genotype analysed.

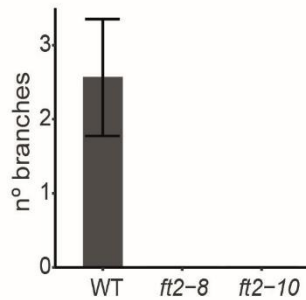


Figure S5. Bar plot showing the relative mRNA level of GA sensing genes *GID1A1* and *GID1A2* in *ft2-8* and WT shoot apex. Plotted values and error bars are fold-change means $\pm$ s.d. of two biological replicates. Asterisks (*) represent statistical differences assessed by one-way ANOVA ($p < 0.05$). *Ubiquitin7* is used as the housekeeping gene.

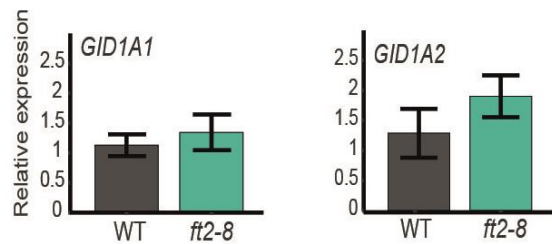


Figure S6. (A-B) Images showing WT shoot apex after 0 μ M (A) or 100 μ M (B) of PAC treatment for 15 days. Scale bar = 1 cm.

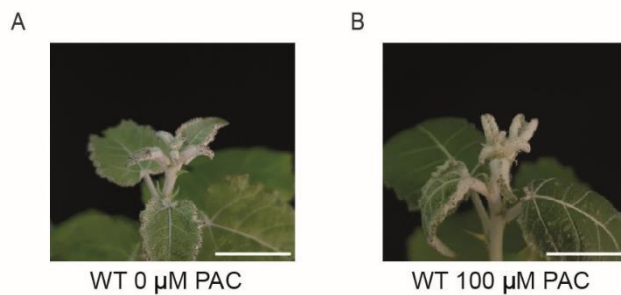


Figure S7. Bar plot showing the relative mRNA level of GA sensing genes *GID1A1* and *GID1A2* in *ft2-8* and WT leaf. Plotted values and error bars are fold-change means $\pm$ s.d. of two biological replicates. Asterisks (*) represent statistical differences assessed by one-way ANOVA ($p < 0.05$). *Ubiquitin7* is used as the housekeeping gene.

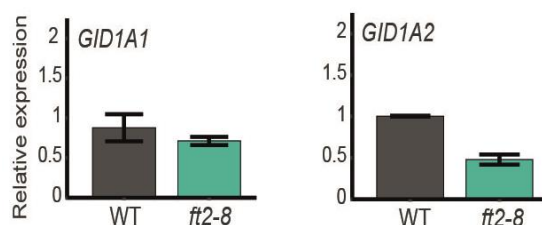


Figure S8. Bar plot showing the relative mRNA level of *GA2ox* genes in WT leaf. Plotted values and error bars are fold-change means $\pm$ s.d. of two biological replicates. *Ubiquitin7* is used as the housekeeping gene.

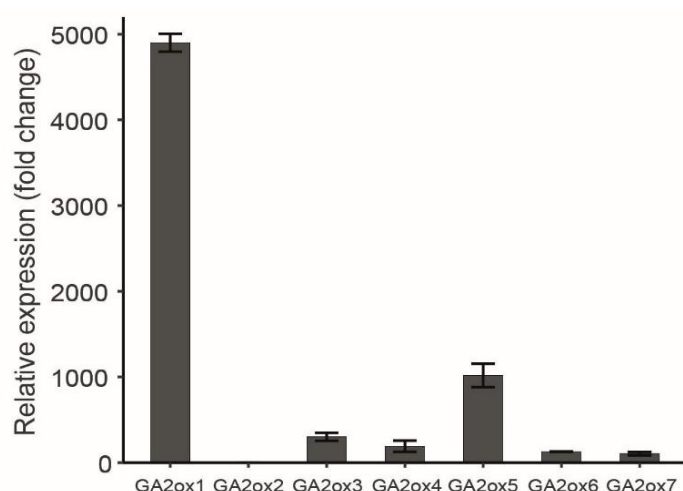


Table S1. List of primers used.

Gene	Gene ID	Primer name	Sequence
U6 promoter	Jacobs et al., 2015	Swal_MtU6F	GATATTAATCTCTTCGATGAAATTTATGCCTATCTT ATATGATCAATGAGG
U6 promoter	Jacobs et al., 2015	MtU6R	AAGCCTACTGGTTCGCTTGAAG
Scaffold	Jacobs et al., 2015	ScaffoldF	GTTTTAGAGCTAGAAATAGCAAGTT

Scaffold	Jacobs et al., 2015	SpeI_ScaffoldR	GTCATGAATTGTAATACGACTCAAAAAAAGCACC GACTCGGTG
p201	Jacobs et al., 2015	Sequence_p201_Ubi3	ACATGCACCTAATTTCACTAGATGT
FT2	Potri.010G179700	Grna_FT2	TCAAGCGAACCAGTAGGCTT— GCCCAGGGTTGATATCGGTG— GTTTTAGAGCTAGAAATAGC
FT2	Potri.010G179700	Genotype_FT2_fwd	ACCCTCTTAGTGTTGGCCGTGT
FT2	Potri.010G179700	Genotype_FT2_rev	TCACCGCTCATCAGGTTTCAAG
FT1	Potri.008G077700	Genotype_FT1_rev	AAACATGCACGTTTGGCTGC
GA2ox1	Potri.001G378400	GA2ox1_qPCR_fwd	TTCTTCTCATTACCGCTCTCTG
GA2ox1	Potri.001G378400	GA2ox1_qPCR_rev	TCTACCCAGCCCACATCAC
GA2ox2	Potri.002G191900	GA2ox2_qPCR_fwd	GGATGCCTTCCAGGTTTTAACGA
GA2ox2	Potri.002G191900	GA2ox2_qPCR_rev	GCGGAGAGATCCATGCGTTG
GA2ox3	Potri.004G065000	GA2ox3_qPCR_fwd	GGACCTCCTAACCTTTTGG
GA2ox3	Potri.004G065000	GA2ox3_qPCR_rev	CAGCAGAGCGGAAAATCTGTGG
GA2ox4	Potri.008G101600	GA2ox4_qPCR_fwd	AGGTAGGGTTTGGAGAGCAT
GA2ox4	Potri.008G101600	GA2ox4_qPCR_rev	GGTAGCGGGATCAGGTGTTA
GA2ox5	Potri.010G149700	GA2ox5_qPCR_fwd	GCACCCCCACTTAATGCAAG
GA2ox5	Potri.010G149700	GA2ox5_qPCR_rev	TATCTCCAAGTCGAGAGCA
GA2ox6	Potri.011G095600	GA2ox6_qPCR_fwd	CAAGCCAGCACTTCAACAGT
GA2ox6	Potri.011G095600	GA2ox6_qPCR_rev	ATTCTCACATGCCTTAACC
GA2ox7	Potri.014G117300	GA2ox7_qPCR_fwd	TTGCTTGACGATGGTTTGT
GA2ox7	Potri.014G117300	GA2ox7_qPCR_rev	GCCTCACGCTTTTAAATCTCCC
GA3ox1	Potri.001G176600	GA3ox1_qPCR_fwd	TGGCTCTCCTCTTGAGCATT
GA3ox1	Potri.001G176600	GA3ox1_qPCR_rev	AACCATGTCAACCTCCTTG
GA3ox2	Potri.003G057400	GA3ox2_qPCR_fwd	AACTCCCTATCTCGCTCAATCT
GA3ox2	Potri.003G057400	GA3ox2_qPCR_rev	AGTCAAGGTGCTTTTGGTGTAG
GA20ox2_1	Potri.002G151300	GA20ox2-1_qPCR_fwd	CGAAAAACCATGCCTTGAATC

<i>GA20ox2_1</i>	Potri.002G1 51300	GA20ox2- 1_qPCR_rev	GCCAAAGGATCTCCAGTGAG
<i>GA20ox3</i>	Potri.005G1 84400	GA20ox3_qPCR _fwd	CTTCGGATCTCGTTGTGCTAG
<i>GA20ox3</i>	Potri.005G1 84400	GA20ox3_qPCR _rev	CCAATATGGCAAAGGATAAATC
<i>GA20ox5</i>	Potri.007G1 03800	GA20ox5_qPCR _fwd	GAGCAGTTGCAACCTCATCA
<i>GA20ox5</i>	Potri.007G1 03800	GA20ox5_qPCR _rev	ACTTGCCCACAGAGTTCATG
<i>GA20ox6</i>	Potri.012G1 32400	GA20ox6_qPCR _fwd	CCAATTTGACGCTTTTGTGCG
<i>GA20ox6</i>	Potri.012G1 32400	GA20ox6_qPCR _rev	AAGCAAGAGATTTTCTTGGCG
<i>GA20ox8</i>	Potri.015G1 34600	GA20ox8_qPCR _fwd	TGGTGTCGAAGAACTTGTGC
<i>GA20ox8</i>	Potri.015G1 34600	GA20ox8_qPCR _rev	CATCAAAACCATGCCATCC
<i>LAP1</i>	Potri.008G0 98500	LAP1_qPCR_fw d	ATGCCGAGGTTGCCTTGATC
<i>LAP1</i>	Potri.008G0 98500	LAP1_qPCR_re v	GAATACCTCTCATGGCGTTCGAG
<i>AIL1</i>	Potri.002G1 14800	AIL1_qPCR_fw d	CTGGAATCAGTTATGGAGTCGGAG
<i>AIL1</i>	Potri.002G1 14800	AIL1_qPCR_rev	GGTTGTGATCTAGTGAGAGCTTCC
<i>GID1A1</i>	Potri.005G0 40600	GID1A1_qPCR_ fwd	ACCGTGGGACTAGCCTTCTT
<i>GID1A1</i>	Potri.005G0 40600	GID1A1_qPCR_ rev	ACAACGTCCGAGTTGACAGGC
<i>GID1A2</i>	Potri.013G0 28700	GID1A2_qPCR_ fwd	GGACCGAGATTGGTACTGGA
<i>GID1A2</i>	Potri.013G0 28700	GID1A2_qPCR_ rev	TAAACCAGCCACCACAACAA
<i>GID1B1</i>	Potri.014G1 35900	GID1B1_qPCR_ fwd	GATCATGTTGATCGCACCAC
<i>GID1B1</i>	Potri.014G1 35900	GID1B1_qPCR_ rev	GTGCTCAAGGGCTTTTCAAGC
<i>GID1B2</i>	Potri.002G2 13100	GID1B2_qPCR_ fwd	GAGAGGGCCAGTTCCGG
<i>GID1B2</i>	Potri.002G2 13100	GID1B2_qPCR_ rev	ACCTCCCCTAGCACTGTGG
35S promot er		35Sfwd	CTATCCTTCGCAAGACCCTTC
Cas9		Cas9rev	TTCCTCAGATGATATATGGTTGGG

Table S2. Values of GA₁₉, GA₂₀, GA₁, and GA₄ quantification in leaf and shoot apex of *ft-8* and WT obtained for three biological replicates.

Tissue	Genotype	GA ₁₉ (ng/g)	GA ₂₀ (ng/g)	GA ₁ (ng/g)	GA ₄ (ng/g)
Shoot apex	WT	12,76	0,46	9,98	0,23
Shoot apex	WT	13,64	0,49	8,88	0,14
Shoot apex	WT	15,55	0,60	8,52	0,15
Shoot apex	<i>ft2-8</i>	7,57	0,19	5,46	0,23
Shoot apex	<i>ft2-8</i>	6,31	0,11	8,29	0,15
Shoot apex	<i>ft2-8</i>	5,19	0,14	3,47	0,16
Leaves	WT	1,38	0,51	2,65	0,10
Leaves	WT	1,68	0,35	1,72	0,11
Leaves	WT	2,72	0,41	1,46	0,11
Leaves	<i>ft2-8</i>	0,67	0,30	4,26	0,07
Leaves	<i>ft2-8</i>	0,39	0,30	5,62	0,10
Leaves	<i>ft2-8</i>	1,05	0,34	5,52	0,07