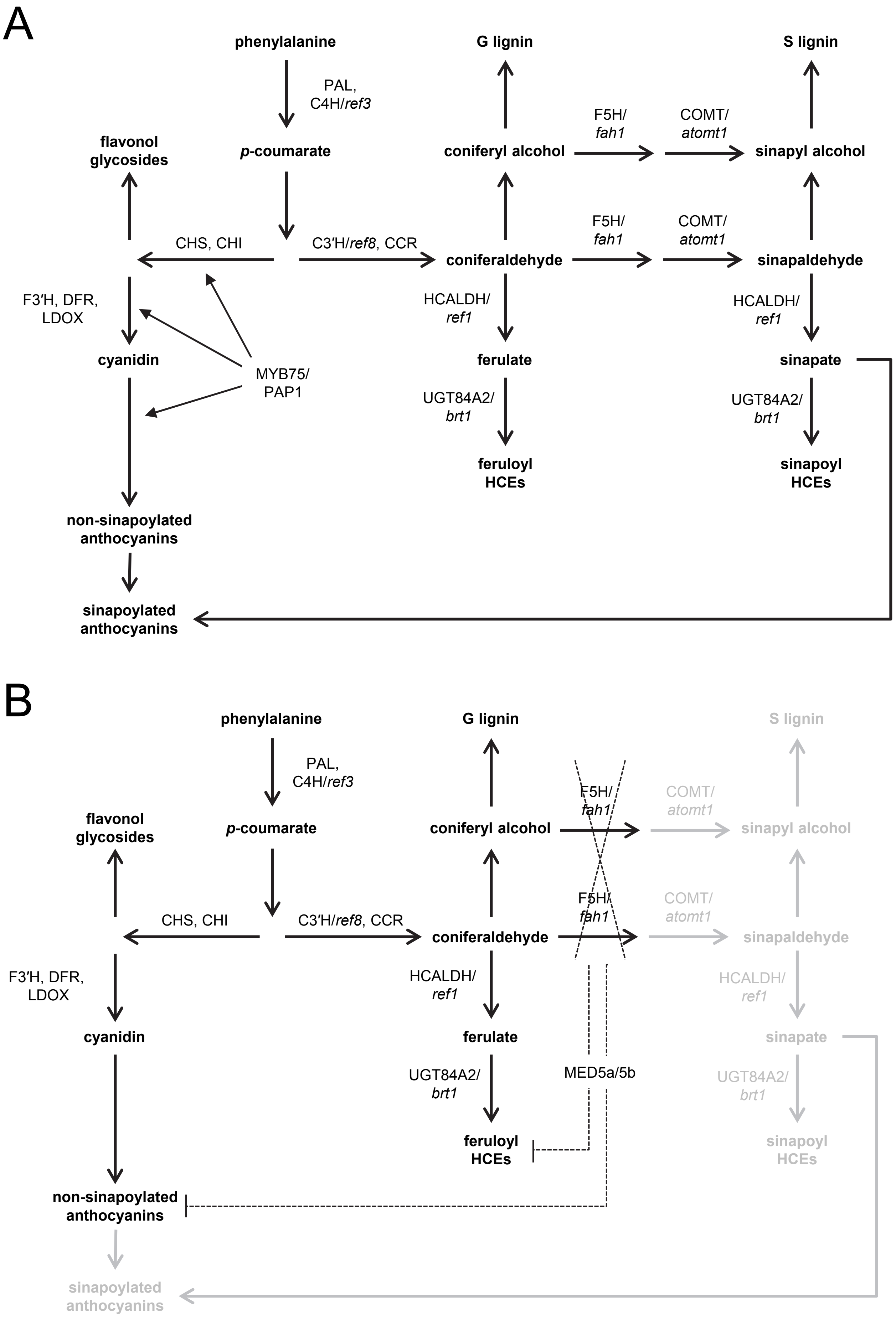
A
phenylalanine
PAL, C4H/*ref3*
*p*-coumarate
flavonol glycosides
CHS, CHI
C3′H/*ref8*, CCR
F3′H, DFR, LDOX
cyanidin
MYB75/PAP1
non-sinapoylated anthocyanins
sinapoylated anthocyanins
G lignin
coniferyl alcohol
coniferaldehyde
HCALDH/*ref1*
ferulate
UGT84A2/*brt1*
feruloyl HCEs
F5H/*fah1*
COMT/*atomt1*
S lignin
sinapyl alcohol
sinapaldehyde
HCALDH/*ref1*
sinapate
UGT84A2/*brt1*
sinapoyl HCEs
B
phenylalanine
PAL, C4H/*ref3*
*p*-coumarate
flavonol glycosides
CHS, CHI
C3′H/*ref8*, CCR
F3′H, DFR, LDOX
cyanidin
non-sinapoylated anthocyanins
sinapoylated anthocyanins
G lignin
coniferyl alcohol
coniferaldehyde
HCALDH/*ref1*
ferulate
UGT84A2/*brt1*
feruloyl HCEs
F5H/*fah1*
COMT/*atomt1*
MED5a/5b
S lignin
sinapyl alcohol
sinapaldehyde
HCALDH/*ref1*
sinapate
UGT84A2/*brt1*
sinapoyl HCEs

**Figure S1** Schematic representation of the phenylpropanoid pathway in wild-type Arabidopsis and in the F5H-deficient *fah1* mutant. A) The relative positions in the phenylpropanoid pathway of the enzymes examined in this paper (a non-comprehensive list), as well as their respective mutant designations (in lower case italics): phenylalanine ammonia lyase (PAL); cinnamate 4-hydroxylase (C4H, *ref3*); *p*-coumaroylshikimate 3′-hydroxylase (C3′H, *ref8*); cinnamoyl-CoA reductase (CCR); ferulic acid 5-hydroxylase (F5H, *fah1*); caffeic acid/5-hydroxyferulic acid *O*-methyltransferase (COMT, *atomt1*); hydroxycinnamaldehyde dehydrogenase (HCALDH, *ref1*); sinapic acid:UDP-glucose glucosyltransferase (UGT84A2, *brt1*); chalcone synthase (CHS); chalcone isomerase (CHI); flavonoid 3′-hydroxylase (F3′H); dihydroflavonol reductase (DFR); leucoanthocyanidin dioxygenase (LDOX). MYB75 (PAP1) is a transcription factor that activates anthocyanin synthesis. MED5a/5b are subunits of the Mediator complex that have been previously implicated in the regulation of phenylpropanoid metabolism. B) The impact on phenylpropanoid accumulation of the metabolic block at F5H in the Arabidopsis *fah1* mutant. Metabolites downstream of F5H, the loss of which is anticipated in *fah1* mutants, are shown in gray. Those that are repressed in *fah1* mutants via the Mediator-dependent mechanism described here are connected to the metabolic block at F5H by dashed lines running through MED5a/5b.

.

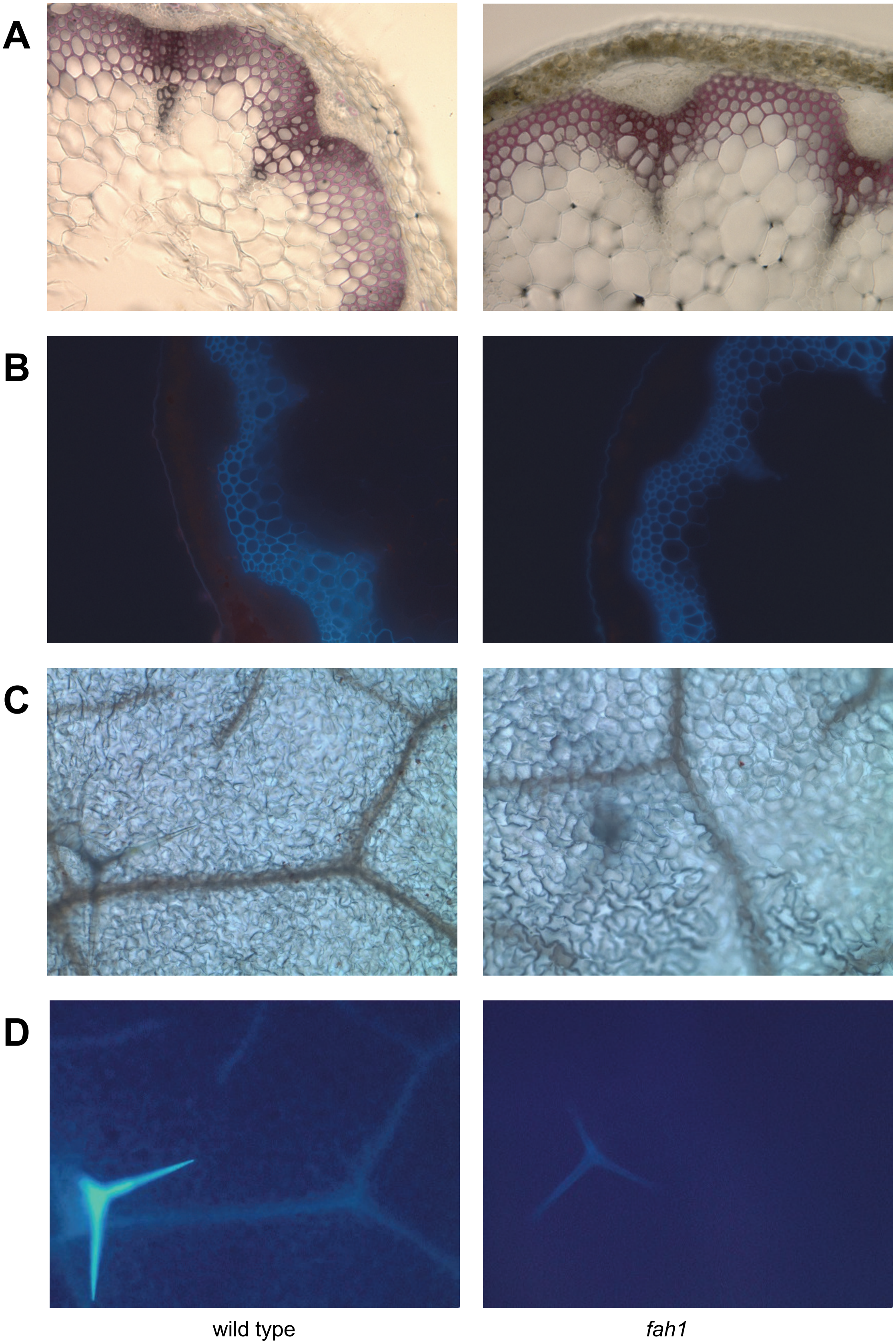

**Figure S2** *fah1* mutants do not show ectopic lignification. A) Phloroglucinol staining of inflorescence stem cross sections. B) Autofluorescence of inflorescence stem cross sections. C) Phloroglucinol staining of cleared wild-type and *fah1* leaves. D) Autofluorescence of leaves.

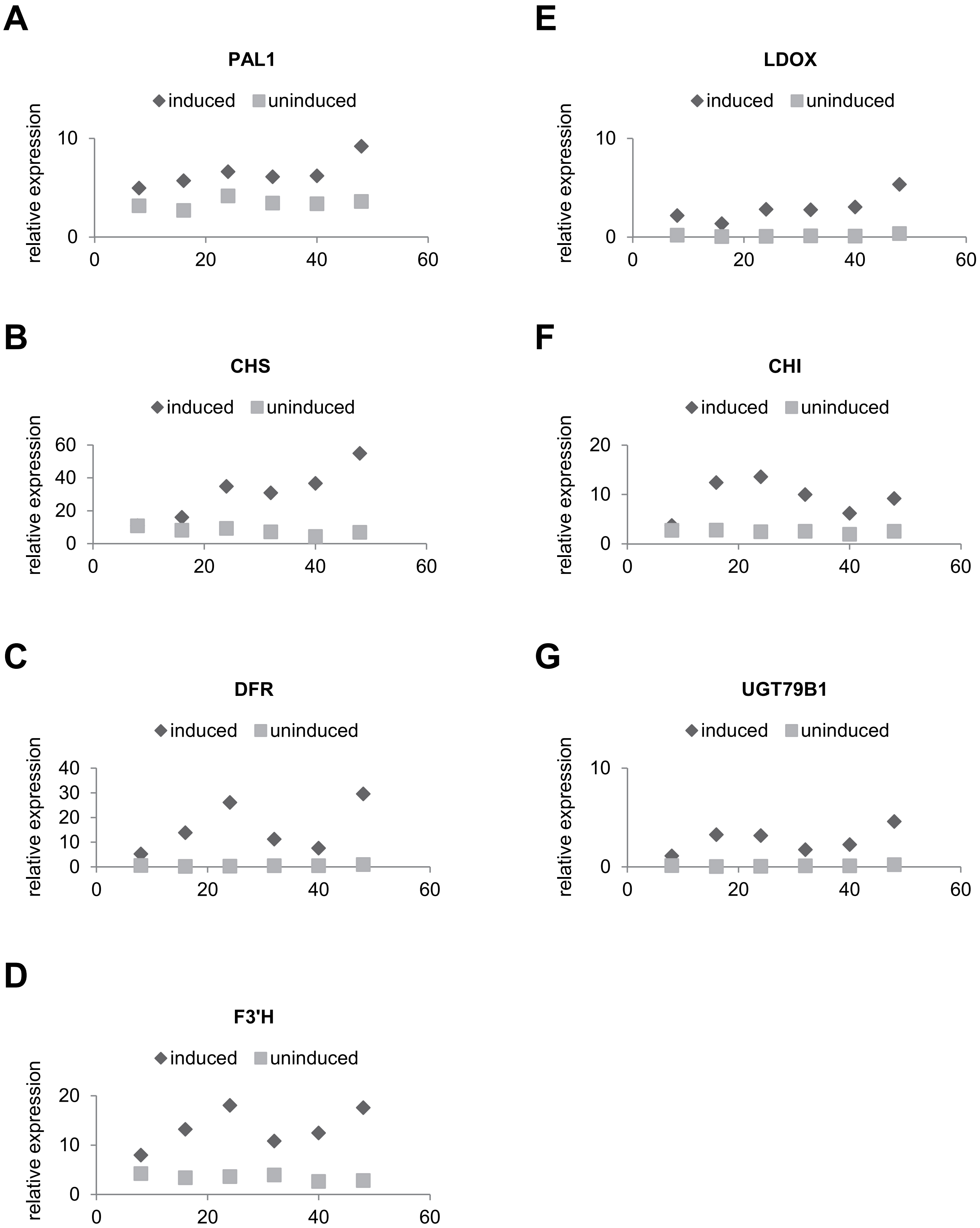

**Figure S3** Time course of transcript abundance of anthocyanin biosynthetic genes with or without induction with sucrose stress.

**Table S1** Hydroxycinnamoyl ester and flavonol glycoside metabolic profile of *fah1* plants and other plants with disrupted lignin biosynthesis

| genotype | HCE | | flavonol glycoside | |
|---|---|---|---|---|
| | | nmol mg$^{-1}$ fresh tissue | | nmol mg$^{-1}$ fresh tissue |
| wild type | 5-hydroxy feruloylmalate | 44.0 ± 3.74 | F1 | 33.9 ± 21.9 |
| | sinapoylglucose | 115 ± 57.1 | F2 | 18.8 ± 11.1 |
| | sinapoylmalate | 1.76x10$^3$ ± 502 | F3 | 42.2 ± 17.3 |
| *ref3* | cinnamoylglucose | 7.31 ± 2.21 | F1 | 18.1 ± 6.00 |
| | cinnamoylmalate | 19.2 ± 6.06 | F2 | 5.37 ± 1.82 |
| | sinapoylglucose | 47.1 ± 7.83 | F3 | 23.7 ± 6.35 |
| | sinapoylmalate | 576 ± 154 | | |
| *ref8* | *p*-coumaroylglucose | 350 ± 38.6 | F1 | 469 ± 9.19 |
| | *p*-coumaroylmalate | 269 ± 47.7 | F2 | 180 ± 20.6 |
| | *p*-coumaroyl shikimate | 991 ± 261 | F3 | 470 ± 36.4 |
| | sinapoylglucose | 51.0 ± 1.78 | | |
| | sinapoylmalate | 524 ± 86.7 | | |
| *ccr1* | feruloylglucose | 13.6 ± 12.6 | F1 | 69.7 ± 9.30 |
| | feruloylmalate | 606 ± 62.4 | F2 | 17.8 ± 2.52 |
| | sinapoylglucose | 99.4 ± 15.8 | F3 | 62.5 ± 7.42 |
| | sinapoylmalate | 901 ± 54.2 | | |
| *fah1* | feruloylglucose | 13.6 ± 1.44 | F1 | 18.4 ± 6.39 |
| | feruloylmalate | 32.1 ± 9.87 | F2 | 8.51 ± 2.59 |
| | | | F3 | 28.4 ± 8.42 |
| *atomt1* | 5-hydroxy feruloylglucose | 70.5 ± 13.7 | F1 | 23.4 ± 1.84 |
| | 5-hydroxy feruloylmalate | 386 ± 77.3 | F2 | 8.13 ± 1.75 |
| | sinapoylglucose | 20.4 ± 1.52 | F3 | 24.2 ± 18.9 |
| | sinapoylmalate | 514 ± 72.7 | | |

F1, kaempferol 3-*O*-β-[β-D-glucopyranosyl (1-6)-D-glucopyranoside]-7-*O*-α-L-rhamnopyranoside;
F2, kaempferol 3-*O*-β-D-glucopyranoside-7-*O*-α-L-rhamnopyranoside;
F3, kaempferol 3-*O*-α-L-rhamnopyranoside-7-*O*-α-L-rhamnopyranoside.

**Table S2** Hydroxycinnamoyl ester and hydroxycinnamic acid derivative metabolic profile of the leaf tissue

| genotype | HCE | pmol mg$^{-1}$ fresh tissue |
|---|---|---|
| wild type | sinapoylglucose | 74.4 ± 16.9 |
| | sinapoylmalate | 1.19x10$^3$ ± 101 |
| *fah1* | feruloylglucose | 6.88 ± 2.78 |
| | feruloylmalate | 34.5 ± 13.1 |
| | #1 | 4.85 ± 4.50 |
| | #2 | 3.13 ± 2.21 |
| | #3 | 8.32 ± 3.78 |
| | #4 | 8.96 ± 4.82 |
| | #6 | 0.82 ± 1.43 |
| *med5a/5b* | sinapoylglucose | 641 ± 185 |
| | sinapoylmalate | 1.88x10$^3$ ± 453 |
| | feruloylglucose | 40.0 ± 5.24 |
| | feruloylmalate | 6.09 ± 3.87 |
| | #1 | 58.0 ± 0.65 |
| | #2 | 50.0 ± 2.6 |
| | #3 | 40.0 ± 8.6 |
| | #4 | 29.0 ± 3.4 |
| | #5 | 25.0 ± 0.4 |
| | #6 | 29.0 ± 11.0 |
| *med5a/5b fah1* | feruloylglucose | 36.7 ± 10.2 |
| | feruloylmalate | 57.0 ± 5.94 |
| | #1 | 140 ± 33.9 |
| | #2 | 119 ± 27.7 |
| | #3 | 157 ± 14.9 |
| | #4 | 119 ± 14.6 |
| | #5 | 60.6 ± 9.63 |
| | #6 | 119 ± 20.8 |

#1 is a feruloylglucose-coniferyl alcohol coupling product (guaiacylglycerol feruloylglucose),
#2 is a modified glycoside of a coniferyl alcohol dimer (lariciresinol or dihydrodehydrodiconiferyl alcohol),
#3 is a glycoside of a coniferyl alcohol dimer (pinoresinol or dehydrodiconiferyl alcohol),
#4 is a feruloylmalate-coniferyl alcohol coupling product (guaiacylglycerol feruloylmalate),
#5 is a feruloylglucose-coniferyl alcohol coupling product (dehydroconiferyl feruloylglucose), and
#6 is a feruloylmalate-coniferyl alcohol coupling product (dehydroconiferyl feruloylmalate).

**Table S3** list of relevant primers

*qPCR primers*

| | |
|---|---|
| qPCR reference (At1g13320) | GTTCTCCACAACCGCTTGGT<br>TAACGTGGCCAAAATGATGC |
| UGT84A1 (At4g15480) | CGACCGAGGAGAGGGTAGTG<br>ACTGTCGCTTCCAAAAGCTTC |
| UGT84A3 (At4g15490) | CCGGACATCAGCGTTGAAAT<br>GCTTGGGATCTCGTCATGCT |
| PAL1 (At2g37040) | GGAAGCTTTCAAATTAGCAGGAAT<br>GACTACCGCGAGACCTTCCTTA |
| CHS (At5g13930) | CGTGTTGAGCGAGTATGGAAAC<br>CTGACTTCCTCCTCATCTCGTCTA |
| CHI (At5g05270) | CCGGTTCATCGATCCTCTTC<br>TTTCGAAAACGCAACCGTAAG |
| DFR (At5g42800) | TGGTGGTCGGTCCATTCAT<br>GAGAGAGCGCGGTGATAAGG |
| F3′H (At5g07990) | GCAACCGCAGCCACAAC<br>ATGATGGGCCATGGGTTTG |
| LDOX (At4g22880) | CCGGGTTTGCAGCTTTTCT<br>ATCAGGAACACATTTTGCAGTGA |
| UGT79B1 (At5g54060) | TGGAGGTGGCGGTTGAA<br>CTTTGCCGCGAGAACCA |

*Cloning primers*

UGT84A1 (At4g15480)
CC2382
GGGGACAAGTTTGTACAAAAAAGCAGGCTTACATACAAATAATTCTTTACTTCACCA
CC2383
GGGGACCACTTTGTACAAGAAAGCTGGGTGAATATAGACAGTCAAAGACTTTTGC

UGT84A3 (At4g15490)
CC2384
GGGGACAAGTTTGTACAAAAAAGCAGGCTTACTAGTTCTTAAAGAAACTAGAAATCC
CC2385
GGGGACCACTTTGTACAAGAAAGCTGGGTCGGATATTTTCGAGACATCA