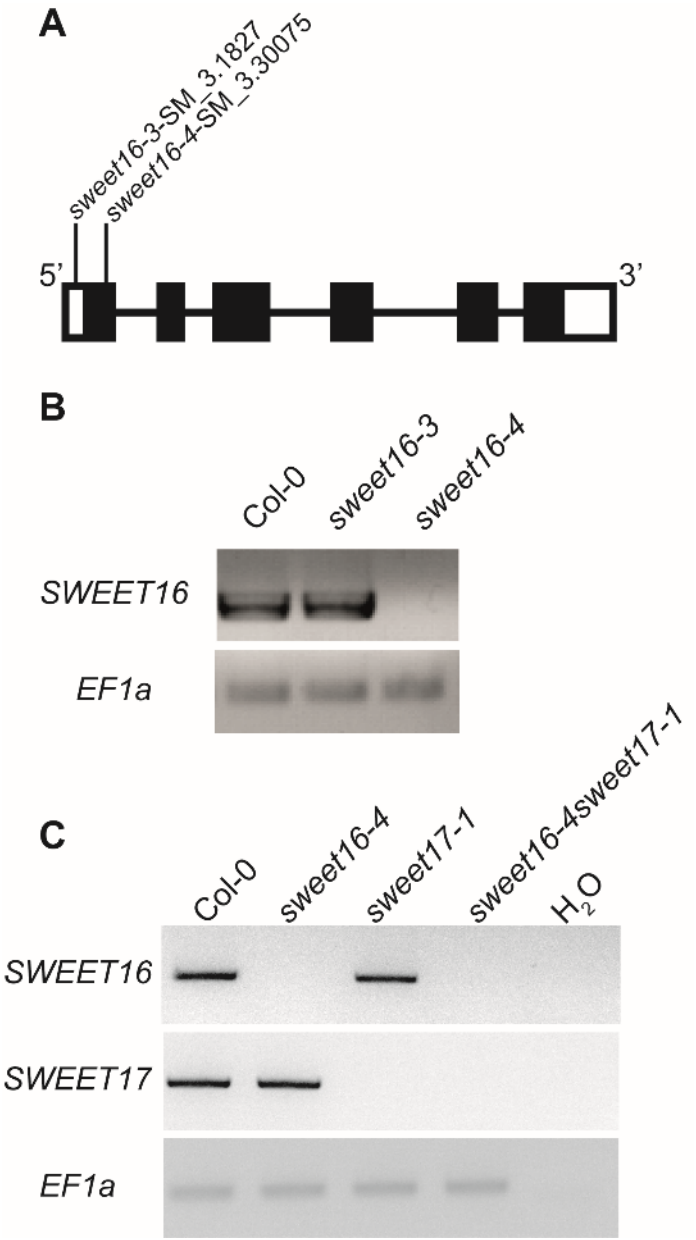


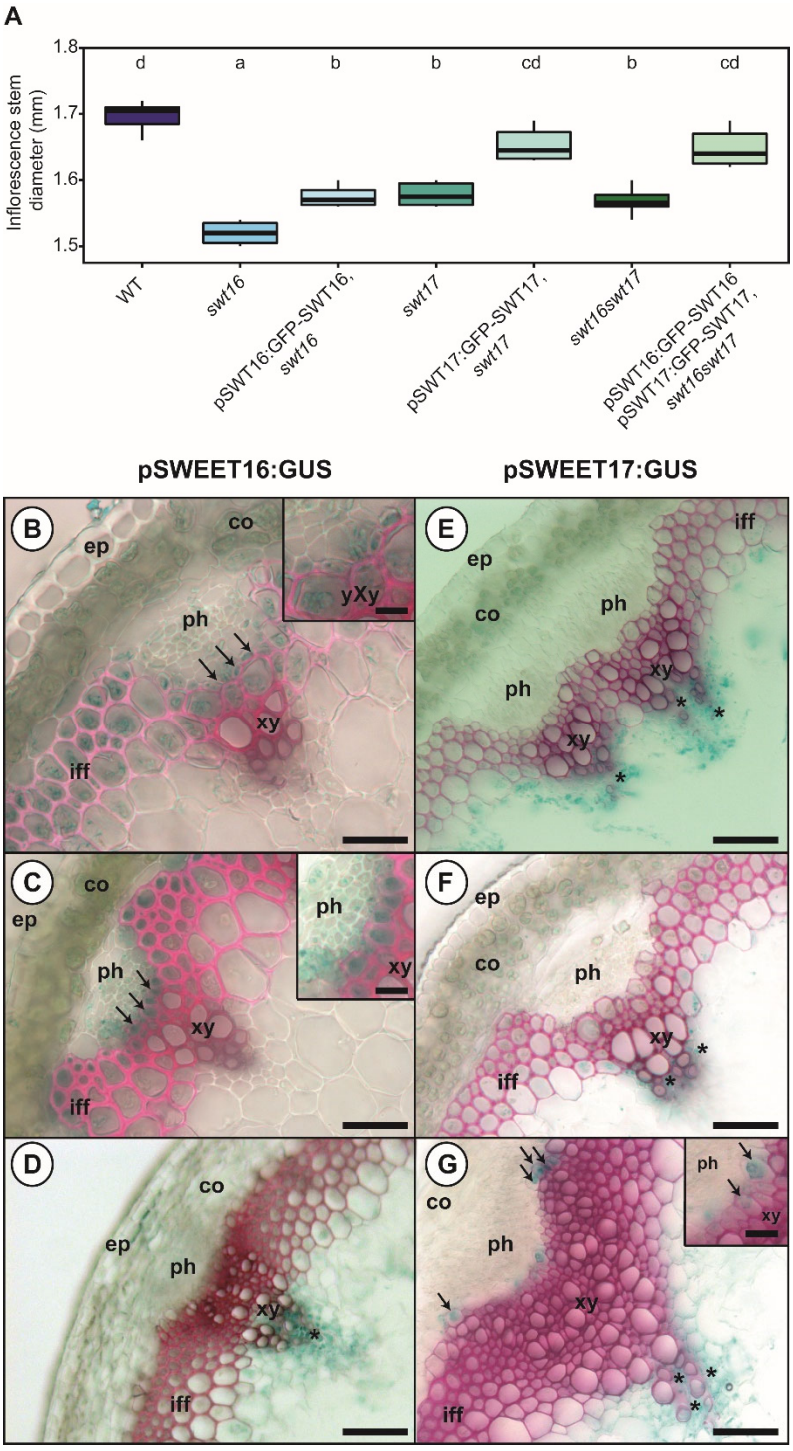
Supplemental Figure S1. Identification of *SWEET16* insertion lines and characterization of the *sweet16-4sweet17-1* mutant line.

(A) The position of the T-DNA insertions in *SWEET16*. White boxes represent the UTR sequences, the black boxes are the exon sequences and the black lines between the black boxes are the intron sequences.

(B) RT-PCR analysis of *SWEET16* expression in the single mutant lines *sweet16-3* and *sweet16-4*. Total RNA was isolated from 10-day-old *in vitro* seedlings and the resulting cDNA were used for amplification with primers designed between the start and stop codon of the

SWEET16 sequence (for primers sequence see Supplemental Table S4). Expression of EF1α was used as a loading control.

(C) RT-PCR analysis of *SWEET16* and *SWEET17* expression in the floral stem of the *sweet16-4sweet17-1* mutant line. Total RNA was isolated from 7-week-old floral stem of plants grown in long-day conditions. After reverse transcription, the cDNAs were used for amplification with primers designed between the start and stop codon of the *SWEET16* and/or *SWEET17* sequences (for primers sequences see Supplemental Table 4). Expression of EF1α was used as a loading control.

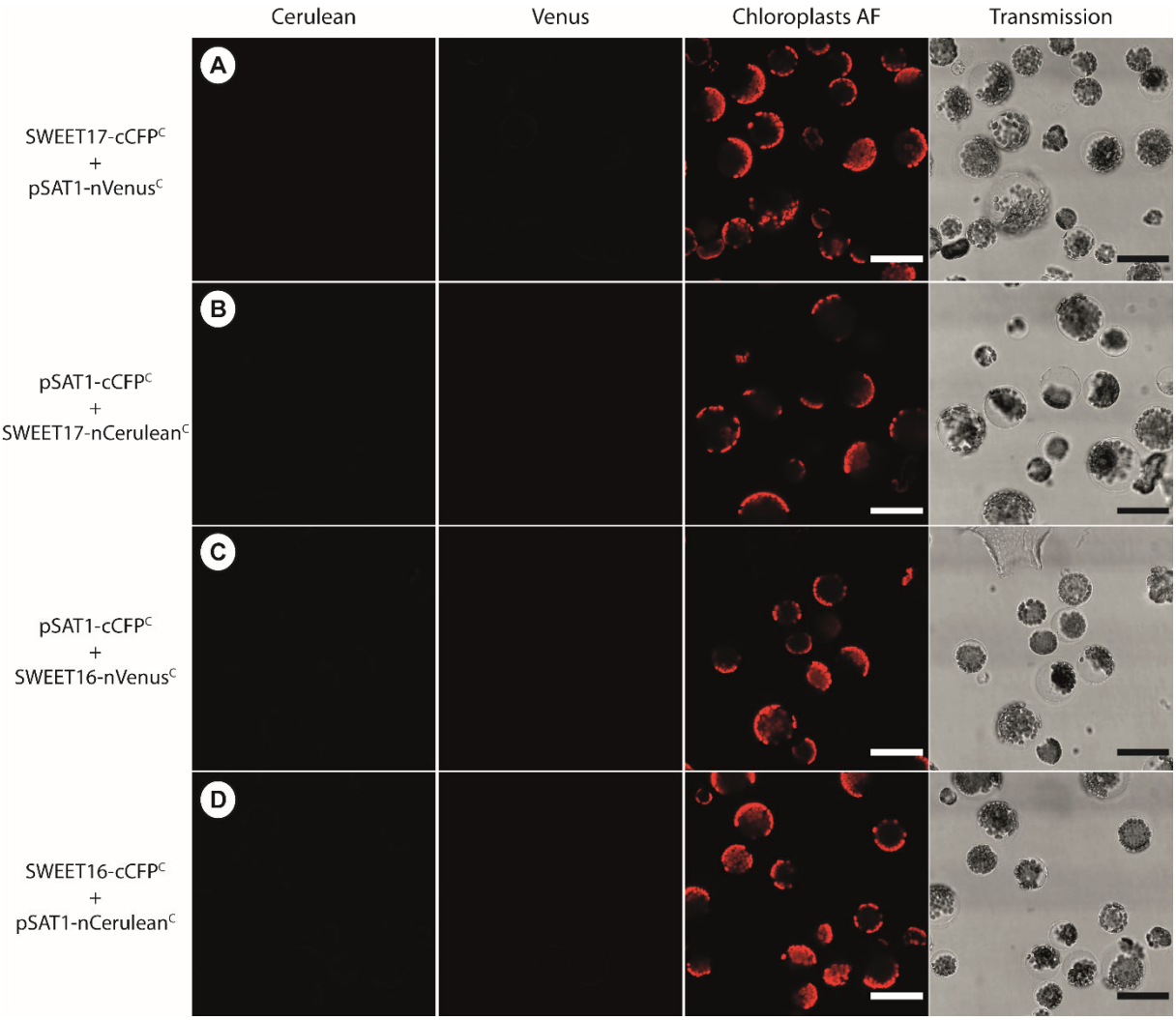


Supplemental Figure S2. Phenotypic complementation of the *swt* mutant lines.

(A) The diameter has been measured by a digital caliper at the bottom of the main inflorescence stem on plants grown for 7 weeks in long-day conditions. The lines represent median values, the tops and bottoms of the boxes represent the first and third quartiles, respectively, and the ends of the whiskers represent maximum and minimum data points. Values represent means from six biological replicates. A one-way analysis of variance combined with the Tukey's

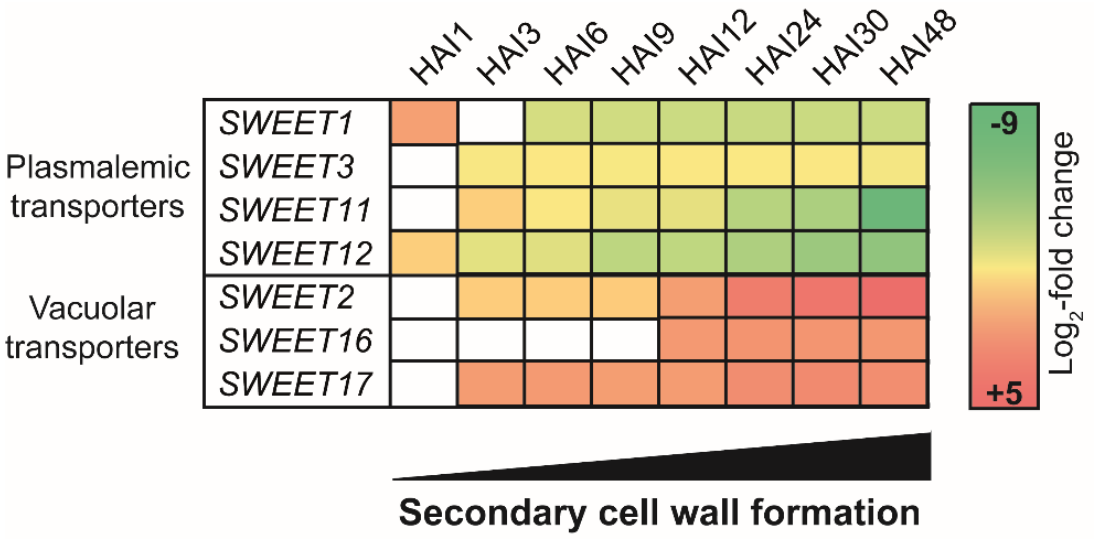
comparison post-test have been performed. The values marked with the same letter were not significantly different from each other, whereas different letters indicate significant differences ($P < 0.05$).

(B to D) *pSWEET16:GUS* expression pattern in sections taken at different positions in the inflorescence stem of 8-week-old plants. (E to G) *pSWEET17:GUS* expression pattern in sections taken at different positions in the inflorescence stem section of 8-week-old plants. Sections were taken in a stem region where growth was still rapid (B, E and inset), in a stem region where elongation growth had finished but where thickening of the secondary cell wall was still ongoing (C, F and inset), and at the bottom of the stem, a region that corresponds to a mature stem (D, G and inset). Arrows point to cells showing blue GUS staining and asterisks indicate xylary parenchyma cells. Lignin is colored pink after phloroglucinol staining. The intensity of the pink color indicates the level of lignification of the xylary vessels. ep: epidermis; co: cortex; iff: interfascicular fibers; ph: phloem; xy: xylem. Scale bar = 50 µm (B-G) or 25 µm (insets in B, C and G).



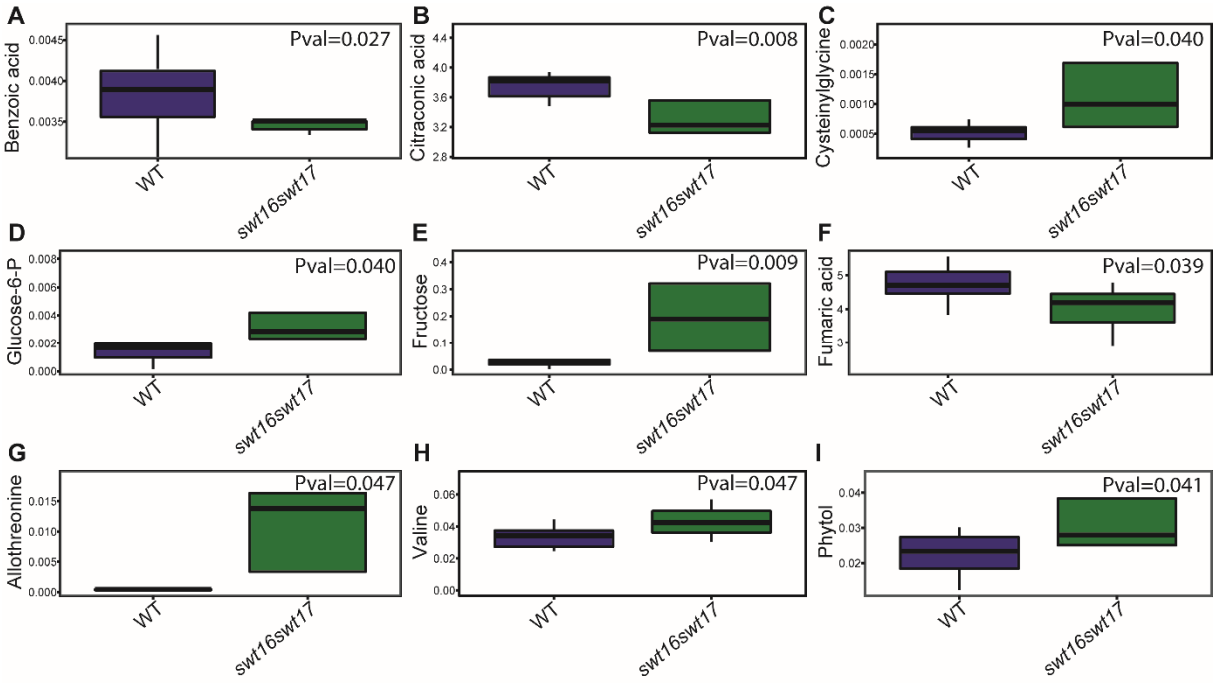
Supplemental Figure S3. Negative controls for BIFC experiment.

Arabidopsis mesophyll protoplasts expressing SWEET17-cCFP^C and pSAT1-nVenus^C (A), pSAT1-cCFP^C and SWEET17-nCerulean^C (B), pSAT1-cCFP^C and SWEET16-nVenus^C (C) and SWEET16-cCFP^C and pSAT1-nCerulean^C (D). No yellow (A and C) or cyan (B and D) fluorescence is reconstituted in the absence of one of the proteins. Chloroplasts autofluorescence is in false color red. The last picture of each row represents the bright field image. Scale bar = 50 µm.



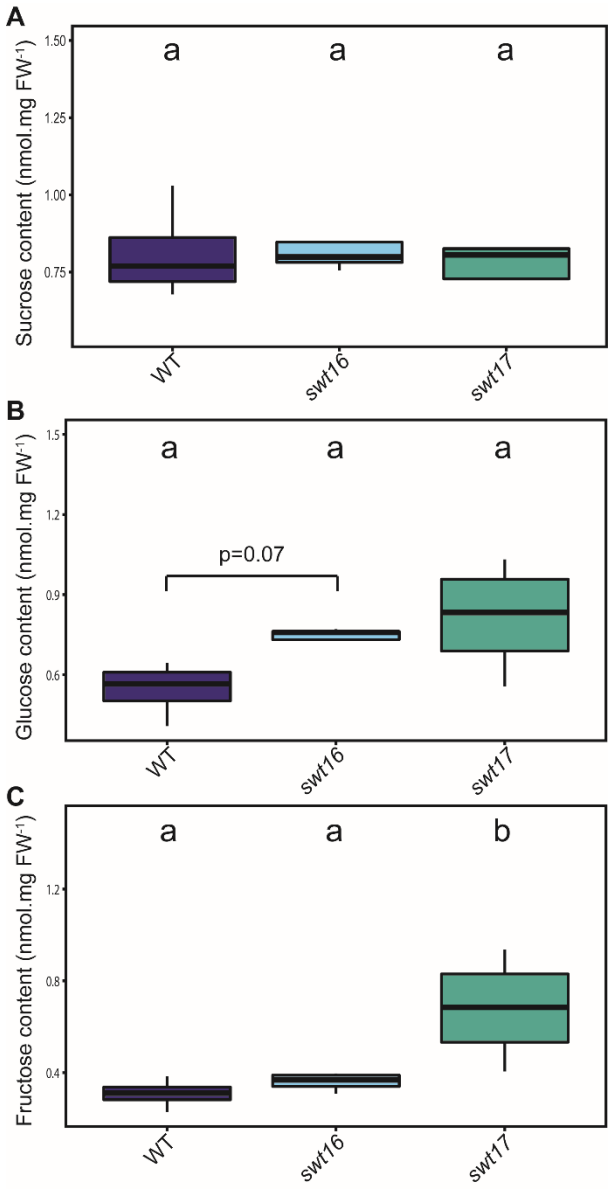
Supplemental Figure S4. Differential expression of *SWEET* genes during the secondary cell wall formation of the xylem vessels.

Changes in transcript levels are extracted from RNA-seq analysis performed in Li et al. (2016) and presented as log_2-fold changes in comparison with the control (DMSO-treated of the DEX-inducible VND7 line) in colored boxes. HAI1-48 refer to the number of Hours After DEX Induction. White squares indicate that the gene was not differentially expressed at this time point.



Supplemental Figure S5. Nine out of 158 metabolites identified by GC-MS differ significantly between the wild type and the *swt16swt17* double mutant.

Boxplots showing the relative quantity of benzoic acid (A), citraconic acid (B), cyteinylglycine (C), glucose-6-phosphate (D), fructose (E), fumaric acid (F), allothreonine (G), valine (H) and phytol (I) in the inflorescence stem of the wild type and the *swt16swt17* mutant grown in long-day conditions for seven weeks. The box-and-whisker plots represents values from 8 individual plants for each genotype. The lines represent median values, the tops and bottoms of the boxes represent the first and third quartiles, respectively, and the ends of the whiskers represent maximum and minimum data points. *P* values of the Student's *t*-test are presented directly on the graphs as well as in Supplemental Table S3.



Supplemental Figure S6. Fructose accumulation in the inflorescence stem of the *swt17* mutant.

(A-C) Boxplots showing the sucrose (A), glucose (B) and fructose (C) contents in the inflorescence stems of the wild type, the *swt16* and the *swt17* mutants grown under long-day conditions for seven weeks. The box-and-whisker plots represents values from 4 biological replicates for each genotype. The lines represent median values, the tops and bottoms of the boxes represent the first and third quartiles, respectively, and the ends of the whiskers represent maximum and minimum data points. A one-way analysis of variance combined with the Tukey's comparison post-test have been performed. The values marked with the same letter were not significantly different from each other, whereas different letters indicate significant differences ($P < 0.05$).

Supplemental Table S1. *p* values from pairwise comparisons (Tukey post-hoc test) between genotypes of anatomical parameters measured in the inflorescence stem xylem tissue.

WT: wild type, *s16*: *swt16*, *s17*: *swt17* and *s16s17*: *swt16swt17*. Values in grey boxes were significantly different at the 95% confidence level.

Compared genotypes	Stem height	Stem diameter	Total xylem area	Fiber area	Vessel area	Total xylem number	Fibers number	Vessels number	Ratio Vessels/fibers
WT - *s16*	1	0.04	0.05	0.864	0.994	<0.001	<0.001	0.350	1
WT - *s17*	0.930	0.055	0.999	0.538	0.875	0.909	0.786	0.999	0.998
WT - *s16s17*	0.999	0.002	0.036	1	0.999	0.031	0.074	0.026	0.904
s16 - s17	0.953	0.980	0.035	0.998	0.998	<0.001	<0.001	0.680	0.999
s16s17 - s16	0.999	0.999	0.999	0.899	0.999	0.976	0.852	0.970	0.941
s16s17 - s17	0.899	0.951	0.025	0.614	0.990	0.002	0.002	0.143	0.999

Supplemental Table S2. Genes co-regulated during the secondary cell wall formation.

Genes related to secondary cell wall formation and sugar transport were selected from differentially expressed genes associated with Cluster 21, as identified in Supplemental Table S7 in Li et al. (2016).

AGI	Name	Biological process
AT1G43790	TED6	Cellulose biosynthesis/assembly
AT3G16920	CTL2	Cellulose biosynthesis/assembly
AT4G18780	CesA8	Cellulose biosynthesis/assembly
AT5G03170	AtFLA11	Cellulose biosynthesis/assembly
AT5G17420	CesA7	Cellulose biosynthesis/assembly
AT5G44030	CesA4	Cellulose biosynthesis/assembly
AT1G28470	SND3	Transcriptional regulation
AT1G62990	IRX11	Transcriptional regulation
AT1G63910	MYB103	Transcriptional regulation
AT1G66230	MYB20	Transcriptional regulation
AT2G45420	LBD18	Transcriptional regulation
AT4G00220	LBD30	Transcriptional regulation
AT4G12350	MYB42	Transcriptional regulation
AT4G22680	MYB85	Transcriptional regulation
AT4G28500	SND2	Transcriptional regulation
AT5G12870	MYB46	Transcriptional regulation
AT1G19300	PARVUS	Xylan biosynthesis
AT1G27440	IRX10/GUT2	Xylan biosynthesis
AT2G28110	FRA8	Xylan biosynthesis
AT2G37090	IRX9	Xylan biosynthesis
AT3G18660	GUX1	Xylan biosynthesis
AT3G50220	IRX15	Xylan biosynthesis
AT4G33330	GUX2	Xylan biosynthesis
AT5G46340	RWA1	Xylan biosynthesis
AT5G54690	IRX8	Xylan biosynthesis
AT5G67210	IRX15L	Xylan biosynthesis
AT4G15920	SWEET17	Fructose transport
AT3G14770	SWEET2	Glucose transport
AT1G08920	ESL1	Hexoses transport
AT1G11260	STP1	Hexoses/H+ co-transport
AT5G26340	STP13	Hexoses/H+ co-transport
AT2G20780	PMT4	Polyol/monosaccharides transport

Supplemental Table S3. *p* values from *t*-test of metabolites identified from the GC-MS analysis. Values in red boxes were significantly different at the 95% confidence level. Metabolites are organized in classes according to the Golm metabolome database (http://gmd.mpimp-golm.mpg.de/Metabolites/List.aspx).

Metabolites	*p* value	Class
aspartic acid 1	0,410	Acid (Amino)
aspartic acid 2	0,101	Acid (Amino)
Beta- alanine 1	0,678	Acid (Amino)
DL-3-aminoisobutyric acid 2	0,893	Acid (Amino)
DL-isoleucine 1	0,580	Acid (Amino)
DL-isoleucine 2	0,345	Acid (Amino)
gamma-aminobutyric acid (GABA)	0,344	Acid (Amino)
glycine	0,550	Acid (Amino)
L-alanine 2	0,553	Acid (Amino)
L-allothreonine 2	0,047	Acid (Amino)
L-asparagine 2	0,115	Acid (Amino)
L-glutamic acid 2	0,066	Acid (Amino)
L-glutamic acid 3 (dehydrated)	0,602	Acid (Amino)
L-glutamine 1	0,941	Acid (Amino)
L-glutamine 2	0,224	Acid (Amino)
L-glutamine 3	0,106	Acid (Amino)
L-leucine 2	0,547	Acid (Amino)
L-lysine 2	0,372	Acid (Amino)
L-ornithine 2	0,178	Acid (Amino)
L-proline 2	0,283	Acid (Amino)
L-serine 1	0,096	Acid (Amino)
L-serine 2	0,066	Acid (Amino)
L-threonine 1	0,415	Acid (Amino)
L-threonine 2	0,232	Acid (Amino)
L-tryptophan 2	0,497	Acid (Amino)
L-valine 2	0,047	Acid (Amino)
norvaline 1 (pmm)	0,973	Acid (Amino)
Phenylalanine 1	0,162	Acid (Amino)
Phenylalanine 1	0,124	Acid (Amino)
tyrosine 2	0,319	Acid (Amino)
citrulline 2	0,200	Acid (Amino), non proteinogen
acetyl-L-serine 1	0,153	Acid (Amino, N-acyl-)

Metabolites	*p* value	Class
4-hydroxybenzoic acid	0,634	Acid (Aromatic)
benzoic acid (pmm)	0,027	Acid (Aromatic)
mandelic acid	0,552	Acid (Aromatic)
salicylic acid	0,955	Acid (Aromatic)
glycolic acid (sl)	0,931	Acid (carboxy)
glyoxylic acid	0,736	Acid (carboxy)
adipic acid	0,222	Acid (Dicarboxylic)
azelaic acid	0,352	Acid (Dicarboxylic)
citraconic acid 1	0,008	Acid (Dicarboxylic)
citraconic acid 3	0,857	Acid (Dicarboxylic)
citraconic acid 5	0,763	Acid (Dicarboxylic)
fumaric acid	0,039	Acid (Dicarboxylic)
glutaconic acid 1	0,158	Acid (dicarboxylic)
glutaric acid (pmm)	0,662	Acid (Dicarboxylic)
itaconic acid	0,114	Acid (Dicarboxylic)
maleic acid	0,556	Acid (Dicarboxylic)
malonic acid 1	0,143	Acid (Dicarboxylic)
oxalic acid	0,668	Acid (Dicarboxylic)
succinic acid	0,548	Acid (Dicarboxylic)
arachidic acid	0,779	Acid (Fatty acid trimethylsilyl ester)
capric acid	0,698	Acid (Fatty acid trimethylsilyl ester)
elaidic acid	0,787	Acid (Fatty acid trimethylsilyl ester)
lauric acid	0,505	Acid (Fatty acid trimethylsilyl ester)

Metabolites	*p* value	Class
linoleic acid	0,711	Acid (Fatty acid trimethylsilyl ester)
myristic acid	0,253	Acid (Fatty acid trimethylsilyl ester)
Myristic Acid d27	0,387	Acid (Fatty acid trimethylsilyl ester)
oleic acid	0,956	Acid (Fatty acid trimethylsilyl ester)
palmitic acid	0,609	Acid (Fatty acid trimethylsilyl ester)
palmitoleic acid	0,544	Acid (Fatty acid trimethylsilyl ester)
stearic acid	0,569	Acid (Fatty acid trimethylsilyl ester)
hexanoic acid (sl)	0,277	Acid (Fatty acid)
D-saccharic acid	0,625	Acid (Hexaric)
galactonic acid 2	0,717	Acid (Hexonic)
gluconic acid 2	0,669	Acid (Hexonic)
gluconic acid lactone 1	0,249	Acid (Hexonic, lactone)
galacturonic acid 1	0,302	Acid (Hexuronic)
citramalic acid	0,460	Acid (hydroxy ducarboxy)
dehydroascorbic acid 1	0,525	Acid (Hydroxy)
dehydroascorbic acid 4	0,728	Acid (Hydroxy)
D-malic acid	0,795	Acid (Hydroxy)
glyceric acid	0,731	Acid (Hydroxy)
L-(+) lactic acid (sl)	0,562	Acid (Hydroxy)
L-ascorbic acid	0,162	Acid (Hydroxy)
pantothenic acid 2	0,784	Acid (Hydroxy)
quinic acid	0,195	Acid (Hydroxy)
shikimic acid	0,744	Acid (Hydroxy)
tagatose 1	0,051	Acid (Hydroxy)
threonic acid	0,535	Acid (Hydroxy)
erythrono-1,4-lactone	0,915	Acid (Hydroxy, lactone)
alpha ketoglutaric acid	0,114	acid (Keto)
nicotinic acid	0,308	Acid (N-heterocycle)
B28pyruvic acid (sl)	0,940	Acid (Oxo)
3,5-dimethoxy-4-hydroxycinnamique	0,322	Acid (Phenylpropanoic)

Metabolites	*p* value	Class
cinnamic acid	0,847	Acid (Phenylpropanoic)
ferulic acid	0,943	Acid (Phenylpropanoic)
phosphoric acid	0,059	Acid (Phosphate)
citric acid	0,421	Acid (Tricarboxylic)
isocitric acid	0,343	Acid (Tricarboxylic)
trans-aconitic acid	0,282	Acid (Tricarboxylic)
1-decanol (decyl alcohol)	0,114	alcohol
1-nonanol	0,490	alcohol
ethanolamine	0,741	Alcohol (Amino)
triethanolamine	0,560	Alcohol (Amino)
phytol 2	0,041	Alcohol (Isoprenoid)
beta-glycerolphosphate	0,540	Alcohol (Phosphate)
glycerol 1-phosphate	0,305	Alcohol (Phosphate)
urea	0,093	Amide
allantoin 1	0,100	Amide (N-heterocycle)
allantoin 3	0,078	Amide (N-heterocycle)
putrescine	0,891	Amine (Poly)
galactinol 2	0,656	Conjugate (Hexosyl, Inositol)
galactitol	0,910	Conjugate (Hexosyl, Inositol)
2,3-butanediol 2	0,157	misc
2-hydroxypyridine	0,942	misc
3-(methylthio)-propylamine	0,449	misc
3-indoleacetonitrile	0,225	misc
4-hydroxypyridine	0,369	misc
acetohydroxamic acid	0,930	misc
benzothiazole	0,496	misc
cyclohexanamine	0,890	misc
cysteinylglycine 1	0,040	misc
homovanillic acid (HVA)	0,839	misc
isopropyl beta-D-1-thiogalacto	0,728	misc
loganin	0,357	misc
neohesperidin	0,222	misc
N-ethylglycine 2	0,824	misc
N-methylalanine	0,317	misc

Metabolites	*p* value	Class
O-phosphocolamine	0,158	misc
porphine 1	0,736	misc
tyramine	0,691	misc
adenosine 5'-diphosphate	0,589	Nucleoside
D-sorbitol	0,539	Polyol (Hexitol)
myo-inositol	0,171	Polyol (Inositol)
glycerol	0,444	Polyol (Triol)
adenine 1	0,357	Purine
uric acid 1	0,711	Purine
9H-purine-6-amine	0,133	purine (cytokinine)
beta-gentiobiose 2	0,481	Sugar (Disaccharide)
lactose 1	0,461	Sugar (Disaccharide)
leucrose	0,386	Sugar (Disaccharide)
maltose 2	0,716	Sugar (Disaccharide)
melibiose 1	0,846	Sugar (Disaccharide)
Sucrose	0,995	Sugar (Disaccharide)
fructose 1	0,071	Sugar (Hexose)
fructose 2	0,009	Sugar (Hexose)
D (+)altrose 1	0,336	Sugar (Hexose, aldose)
D-(+) trehalose	0,073	Sugar (Hexose, aldose)
D-glucose 1	0,200	Sugar (Hexose, aldose)
D-glucose 2	0,325	Sugar (Hexose, aldose)
D-mannose 1	0,383	Sugar (Hexose, aldose)
Glucopyranose	0,285	Sugar (Hexose, aldose)
1,5-anhydro-D-sorbitol	0,303	Sugar (Hexose, aldose, anhydride)
1,6-anhydro-glucose	0,435	Sugar (Hexose, aldose, anhydride)
rhamnose 1	0,339	Sugar (Hexose, deoxy)
rhamnose 2	0,330	Sugar (Hexose, deoxy)
arabinose	0,639	Sugar (Pentose, aldose)
ribose	0,524	Sugar (Pentose, aldose)

Metabolites	*p* value	Class
xylose 2	0,591	Sugar (Pentose, aldose)
xylulose	0,773	Sugar (Pentose, ketose)
D-glucose-6-phosphate 1	0,126	Sugar (Phosphate)
D-glucose-6-phosphate 2	0,040	Sugar (Phosphate)
fructose 6-phosphate	0,104	Sugar (Phosphate)
sedoheptulose 7-phosphate	0,221	Sugar (Phosphate)
Raffinose (pmm)	0,931	Sugar (Trisaccharide)
beta-sitosterol	0,212	Terpenoid (Sterols)
cholesterol	0,816	Terpenoid (Sterols)

Supplemental Table S4. Primers used for characterizing mutant lines.

Accession number	Primer name	Sequence (5'→3')	Amplicon size (bp)	Purpose
At3g16690	sweet16-3_LP	TGCAACTATGGAAATGGAAGG	1655	Genotyping
	sweet16-3_RP	GATTCAGCAAGAGCACCAAAG		
	sweet16-4_LP	TGCAAATAATTTAGCAACCGC	1742	
	sweet16-4_RP	TATAAATGATCTGGGGCCATC		
	SWEET16CDS +stopF	ATGGCAGACTTGAGTTTTTATGTC	693	Full-length PCR
	SWEET16CDS +stopR	TTAAGCGAGGAGAGGTTGATTT		
	SWEET16CDS +stopF	ATGGCAGACTTGAGTTTTTATGTC	693	BIFC experiment
	SWEET16CDS +stopR	TTAAGCGAGGAGAGGTTGATTT		
	SWEET16CDS-stopR	AGCGAGGAGAGGTTGATTT	690	
	Bam-pS16-5'	CGGGATCCTGATTACAACATTACAACATTCAGTG	1295	GFP fusions cloning
	EcoI-pS16-3'	CGGAATTCCTCTGAGGATGGGTTTCTGAG		
	Not-S16-5'	ATAAGAATGCGGCCGCATGGCAGACTTGAGTTTTTATG	1863	
	Eco5-S16-3'	ATAAGAATGCGGCCGCCATGGCAGACTTGAGTTTTTATGT		
At4g15920	sweet17-1_LP	TGATGTGAGGCCTTCCTCTT	771	Genotyping
	sweet17-1_RP	CCGTTTTGGTTGTCGTTTTT		
	SWEET17CDS +stopF	ATGGCAGAGGCAAGTTTCTATATC	726	Full-length PCR
	SWEET17CDS +stopR	TTAAGAGAGGAGAGGTTCAACACG		
	SWEET17CDS +stopF	ATGGCAGAGGCAAGTTTCTATATC	726	BIFC experiment
	SWEET17CDS +stopR	TTAAGAGAGGAGAGGTTCAACACG		
	SWEET17CDS-stopR	AGAGAGGAGAGGTTCAACACG	723	
	Sal-pS17-5'	ACGCGTCGACAAAGAGATAAATTAAATGAGATTTGTATGG	2004	GFP fusions cloning
	Kpn-pS17-3'	GGGGTACCTATTGGAGAAAGAGTTTCTGAG		
	Not-S17-5'	ATAAGAATGCGGCCGCCATGGCAGAGGCAAGTTTCTATATC	2601	
	Eco5-S17-3'	CCCGGATATCTTAAGAGAGGAGAGGTTCAACACG		
eGFP	Eco1-eGFP5'	CGGAATTCATGGTGAGCAAGGGCGAGGA	714	Cloning
	Not-eGFP-3'0stop	ATAAGAATGCGGCCGCCTTGTACAGCTCGTCCATGCC		

Supplemental Table S5. Primers used for quantifying genes by RT-qPCR.

Accession number	Gene name	Forward sequence (5'→3')	Reverse sequence (5'→3')	Size (bp)	Efficiency	Reference
At5g12870	*MYB46*	GAATGTGAAGAAGGTGATTGGTACA	CGAAGGAACCTCAGTGTTCATCA	150	73.5	(Takeuchi et al., 2018)
At3g08500	*MYB83*	GTCGCCTTCGCTGGATCAAT	AAGCCGCTTCTTCAATGTCG	191	85.8	(Shafi et al., 2019)
At5g61480	*PXY*	TTCAAACCGACGAATCCATGT	TTATCCACTTGTAAAGTGTAAGCATATTCT	85	95.4	(Smetana et al., 2019)
At1g46480	*WOX4*	GACAAGAACATCATCGTCACTAGACA	TTCTCCACCATTGGTTCTCTCA	51	92.4	(Smetana et al., 2019)
At1g32770	*SND1/ NST3*	GCAGCAACTGGGCTAGTCTT	CCCATCGCTGCATCATAGTA	126	93.6	This study
At4g32880	*AtHB8*	AACACCACTTGACCCCTCAACATCAG	CACGCAACCAACAAGGCTTATCC	276	91.9	(Carlsbecker et al., 2010)
At5g44030	*CESA4*	TGCCTATGGATCGGAAAATGGA	ACGTTCTTTCCACTCCGCAT	145	95.4	(Shafi et al., 2019)
At5g17420	*CESA7*	TTGTGTACGTGTCCCGTGAG	ATTTGTGAGTACGCCTGCCA	98	101.1	(Shafi et al., 2019)
At4g18780	*CESA8*	AGGTCTCCCATCTGCAACAC	CTCATCGTAAGGATTGCCGC	168	97.9	(Shafi et al., 2019)
At1g28470	*SND3*	TTCTTCCACCGGCCATCAAA	CTGGCGACCATAGTTGGTGT	183	103.8	(Shafi et al., 2019)
At1g63910	*MYB103*	GGGAAACAGGTGGGCTCATA	TGGTAGAGGCCTCGATGGTA	197	100.3	(Shafi et al., 2019)
At1g62990	*KNAT7*	GAAGCTGTTATGGCTTGCCG	TCGGTAGCAACGGACCAAAT	190	95.3	(Shafi et al., 2019)
At1g79180	*MYB63*	GACAAACCCGATCTGCTGGA	CCCGAGTTCGCTTTCTAGGT	189	99.8	(Shafi et al., 2019)
At1g16490	*MYB58*	AAGCGGGTTCAAAAGGTTCT	GCATCATCGTCTTTGCTTGA	109	98	This study
At5g13180	*VNI2*	CTCCTTTGCCAGCTTCAATC	GGTTAGACCGGTTCCCATTT	138	97.8	This study
At5g64530	*XND1*	CCCGACCTTGATCTTTACCA	CCCAATACCCATTGCTTGTC	124	94.9	This study
At4g39620	*MYB4*	ACAGAGGGATTGATCCAACG	TCGACCTTTGGAGCAGAAGT	133	97.9	This study
At1g17950	*MYB52*	CCGGTCGAACTGATAACGCT	ACCAATCATCCCAGTCGCAG	131	103	(Shafi et al., 2019)
At1g73410	*MYB54*	AACCGAAACCCTTTCACGGA	ACGAGGCTTAGAGGTTTGGC	174	87.8	(Shafi et al., 2019)
At5g16600	*MYB43*	CCATGCGCAACTTGGCAATA	CCCTTGAGCTTGTTGTGAAGC	178	100.1	(Shafi et al., 2019)
At3g62250	*UBQ5*	CCAAGCCGAAGAAGATCAAG	ACTCCTTCCTCAAACGCTGA	105	98.6	This study

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