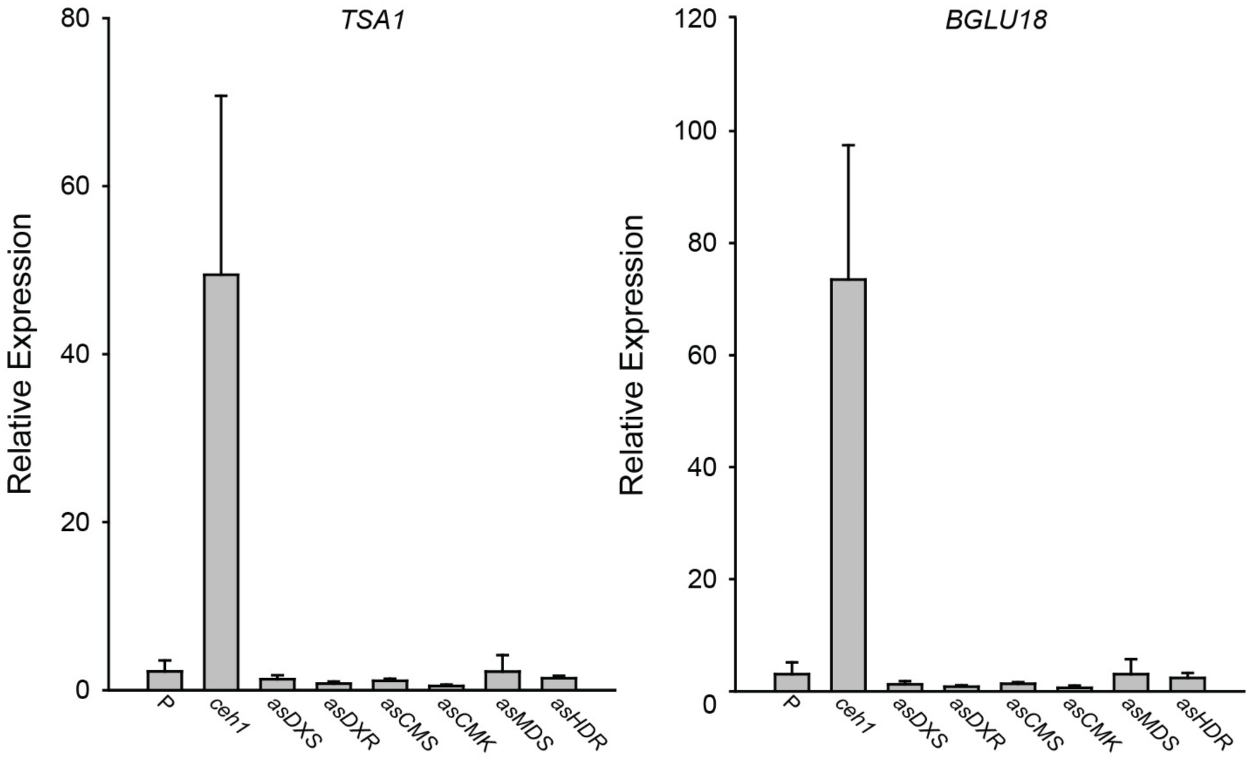
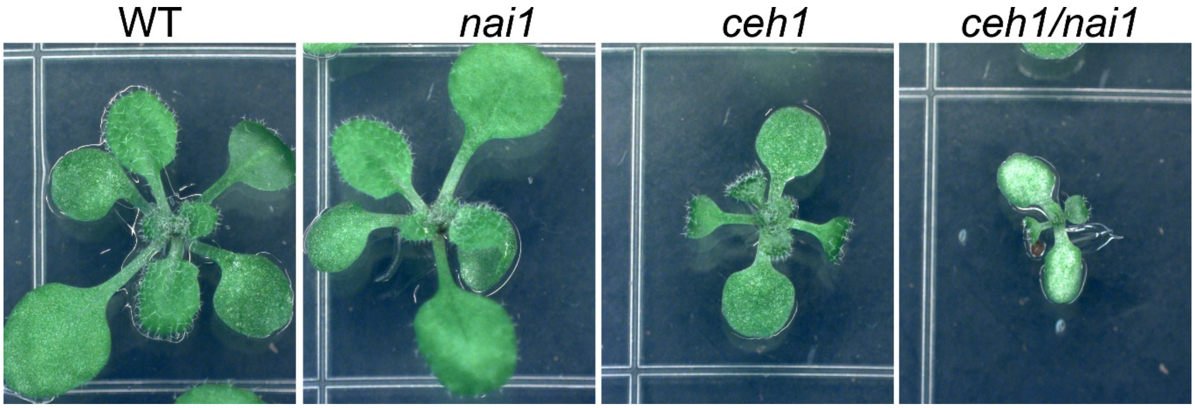
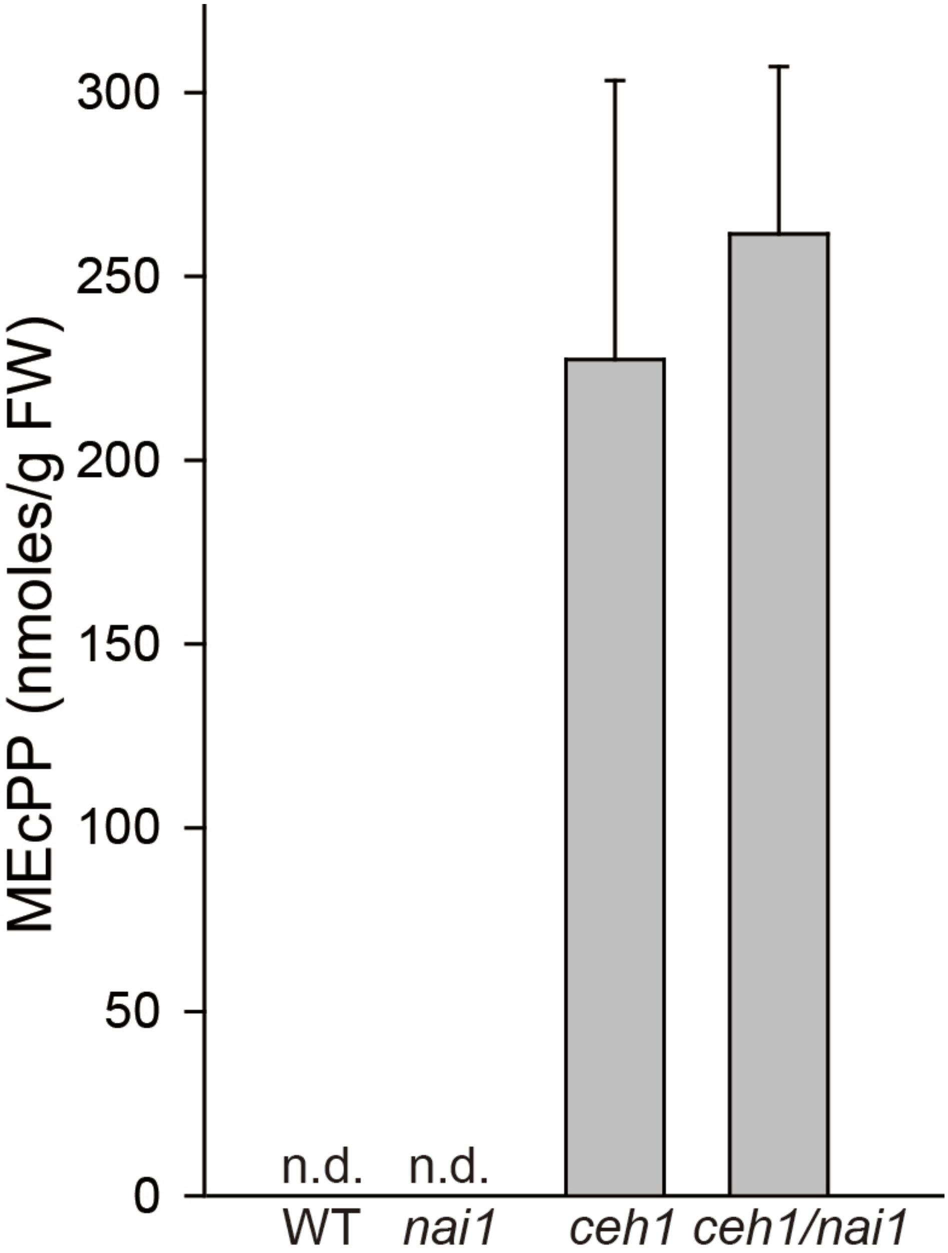


Supplemental Figure 1. Induction of wound inducible ER body genes *TSA1* and *BLGU18* is exclusive to the *ceh1* mutant.

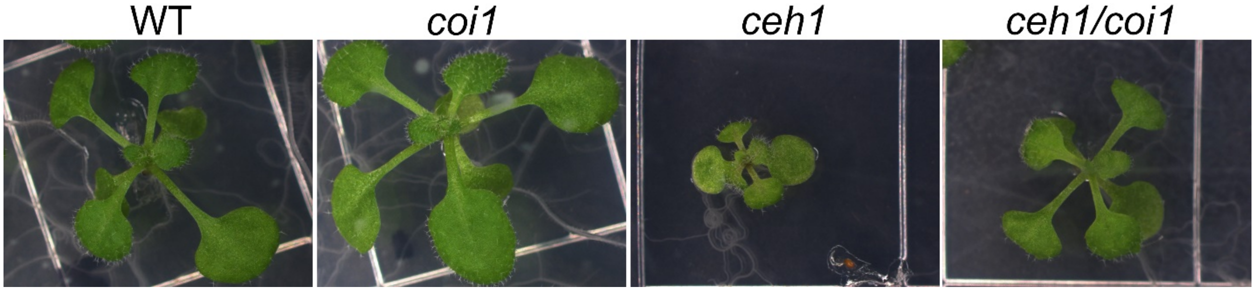
Relative expression levels of wound inducible ER marker genes (*TSA1* and *BGLU18*) in *ceh1* and MEP pathway RNAi lines. Total RNA extracted from these genotypes was subjected to real-time quantitative-PCR analysis. The transcript levels were normalized to *At4g26410* (M3E9) measured in the same samples. Data are mean fold difference ±SD of three biological replicates each with three technical repeats.



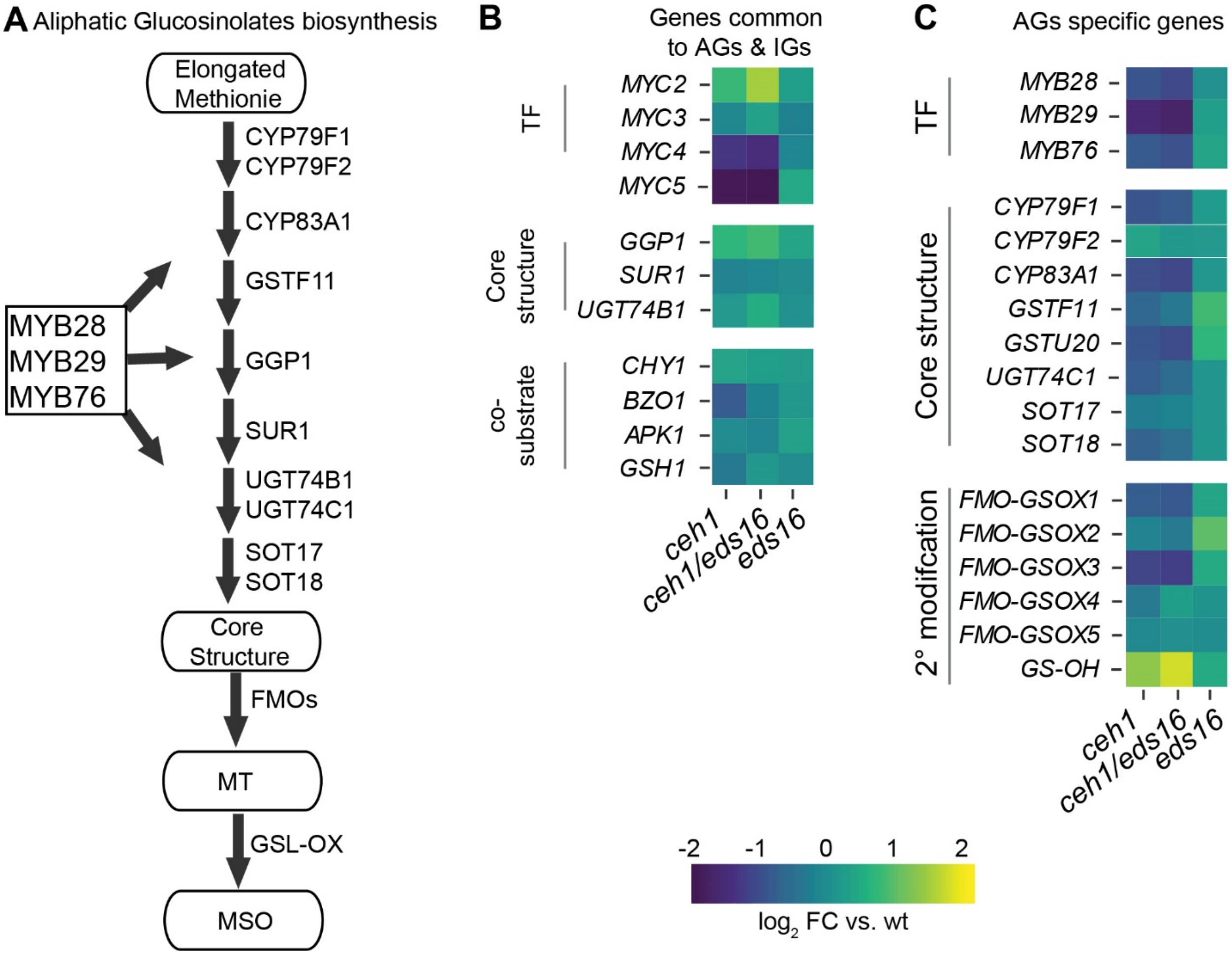
Supplemental Figure 2. Phenotypes of various genotypes (WT, *nai1*, *ceh1* and *ceh1*/*nai1*).



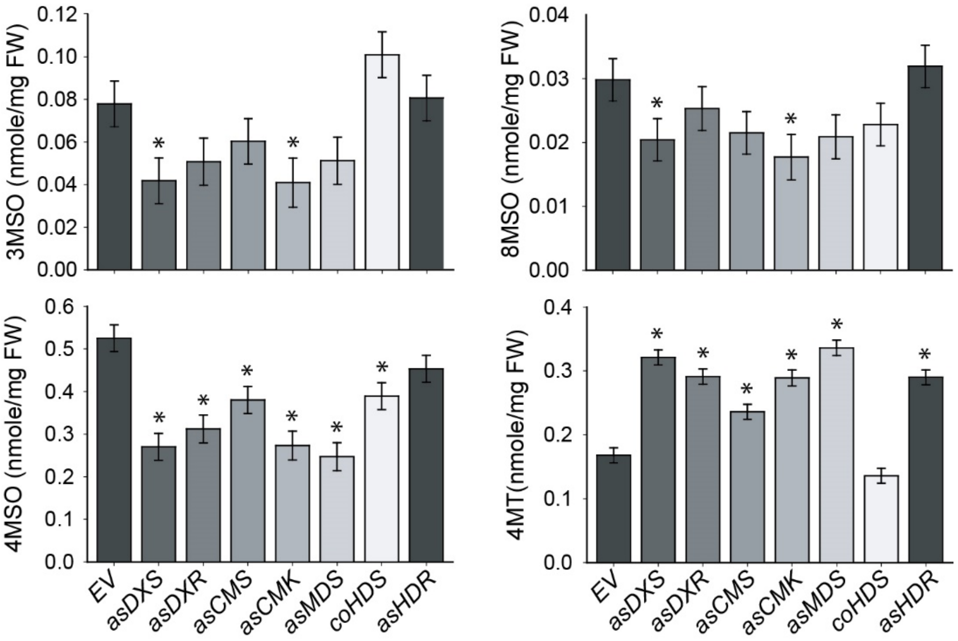
Supplemental Figure 3. MEcPP levels in various genotypes (WT, *nai1*, *ceh1* and *ceh1*/*nai1*).



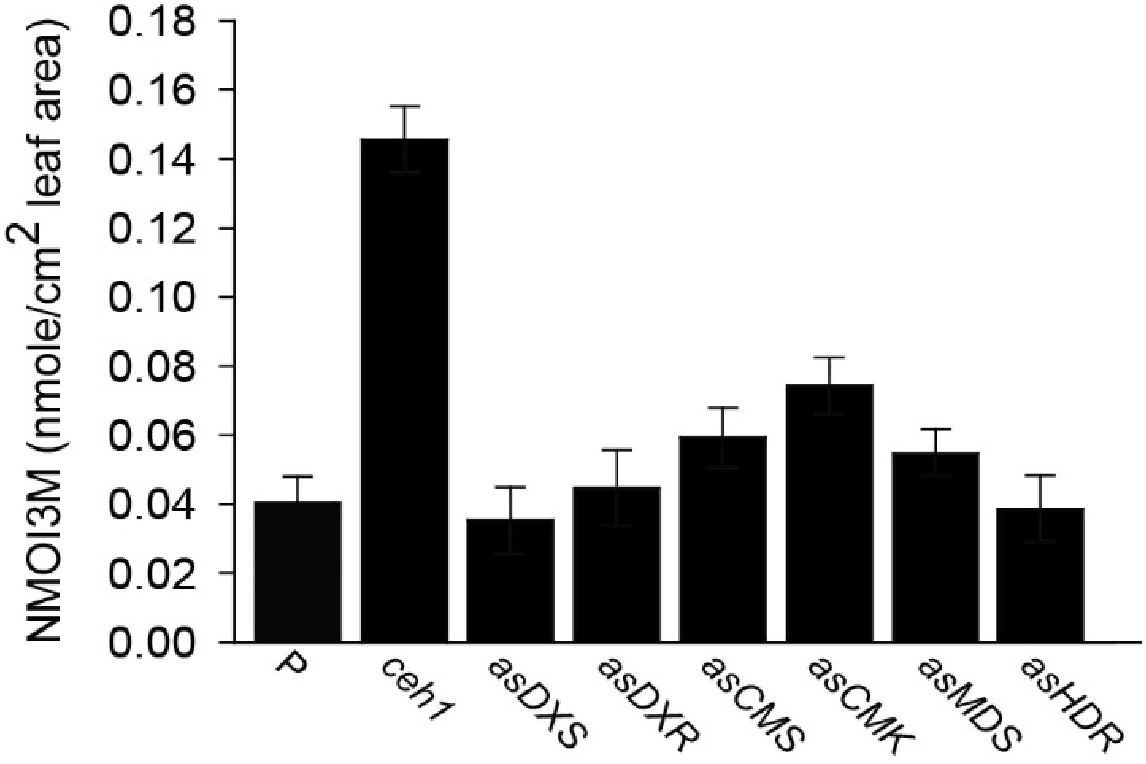
Supplemental Figure 4. Phenotypes of various genotypes (WT, *coi1*, *ceh1* and *ceh1*/*coi1*).



Supplemental Figure 5. MEcPP *does not* induce expression of genes associated with aliphatic glucosinolates (AGs) biosynthesis. (A) Schematic illustration of AGs biosynthesis pathway and their associated transcription factors (boxed) and metabolites (lassoed). (B) Heatmap of the expression levels of genes common to both the AGs and IGs biosynthesis, in *ceh1*, *ceh1/eds16*, *eds16* as compared to the WT levels using RNAseq data. (C) Heatmap of the expression of genes specifically associated with AGs biosynthesis in *ceh1*, *ceh1/eds16*, *eds16* relative to the WT levels using RNAseq data. The $\log_2$-fold change for *ceh1* (left), *ceh1/eds16* (middle), and *eds16* (right) vs WT is represented by color, from -2 (blue) to 2 (yellow).



Supplemental Figure 6. Alteration of aliphatic glucosinolates *is not* specific to MEcPP. Measurement of AGs levels in WT transformed with empty vector (EV), RNAi lines silencing MEP-pathway genes individually and co-suppressed (*csHDS*). Data are mean±SEM; n=3. Asterisks show the significant differences relative to EV (*P* < 0.05). All the statistical analyses were performed using ANOVA.



Supplemental Figure 7. Production of NMOI3M in response to botrytis infection is most prominent in the *ceh1* mutant.

Supplemental Table 1. List of annotated ER body localized or associated proteins.

Gene ID	Name	Reference
AT3G09260	PYK10/BGLU23	(Nagano et al., 2008)
AT1G66270	BGLU21	(Nagano et al., 2008)
AT1G66280	BGLU22	(Nagano et al., 2008)
AT3G16420	PBP1/JAL30	(Nagano et al., 2008)
AT3G16430	JAL31	(Nagano et al., 2008)
AT3G16450	JAL33	(Nagano et al., 2008)
AT3G16460	JAL34	(Nagano et al., 2008)
AT3G16470	JAL35	(Nagano et al., 2008)
AT1G54000	GLL22	(Nagano et al., 2008)
AT2G22770	NAI1	(Matsushima et al., 2004)
AT4G27860	MEB1	(Yamada et al., 2013)
AT5G24290	MEB2	(Yamada et al., 2013)
AT1G52400	BGLU18	(Nakano et al., 2014)
AT5G23820	ML3	(Hakenjos et al., 2013)
AT1G54010	GLL23	(Nakano et al., 2016)
AT1G54030	MVP 1	(Agee et al., 2010; Nakano et al., 2012)
AT3G15950	NAI2	(Yamada et al., 2008)

Supplemental table 2. List of annotated ER body localized or associated proteins altered in *ceh1*.

Gene ID	Name	Fold change (log$_2$) Expression	*P* value	Fold change (log$_2$) Protein	*P* value
AT1G52400	BGLU18	2.396541298	0.00299129	1.135421511	0.023237
AT3G09260	PYK10/BGLU23	1.175750063	0.00584943	2.419837605	0.000773
AT3G16420	PBP1/JAL30	n.d.	n.d.	1.222032104	0.003441
AT3G16450	JAL33	1.406667546	0.00579349	1.354872393	0.003285
AT3G16460	JAL34	0.732285878	0.2226334	1.929333173	0.031609
AT3G16470	JAL35	2.158159579	0.04639408	0.621660709	0.026101
AT1G54010	GLL23	n.d.	n.d.	2.344242453	0.026378
AT3G15950	NAI2	1.020693235	0.17069045	1.786527024	0.006863
AT4G27860	MEB1	3.250747779	0.03079126	1.781855467	0.025035
AT5G23820	ML3	1.368483384	0.01896147	0.281228153	0.144649

Supplemental Table 3. Transcriptomics analysis of GSLs synthesis genes in *ceh1* and *ceh1/eds16*.

Glucosinolate		Gene		ceh vs. wt			ceh/eds vs. wt			eds vs. wt		
Ali/Indol	Function	TAIR ID	NAME	log2 FC	q		log2 FC	q		log2 FC	q	
Indolic	Core structure	AT2G22330	CYP79B3	-0.2393	0.181		-0.0575	0.801		0.1242	0.708	
Indolic	Core structure	AT2G30860	GSTF9	1.00816	2E-08	*	1.34414	2E-14	*	0.3424	0.242	
Indolic	Core structure	AT2G30870	GSTF10	1.51315	6E-16	*	2.26044	9E-35	*	-0.008	0.99	
Indolic	Core structure	AT1G24100	UGT74B1	0.11227	0.653		0.47359	0.027		-0.027	0.961	
Indolic	Core structure	AT1G74100	SOT16	0.59503	8E-06		1.10667	5E-18	*	-0.073	0.815	
Indolic	unknown	AT1G76790	AT1G76790	2.64603	3E-30	*	3.88737	1E-65	*	1.4472	2E-07	*
Indolic	Core structure	AT4G31500	CYP83B1	0.77821	3E-12		1.05165	1E-21	*	-0.287	0.093	
Indolic	unknown	AT4G37400	CYP81F3	-0.2013	0.661		-0.8608	0.045		0.1005	0.915	
Indolic	unknown	AT4G37410	CYP81F4	1.37819	0.014	*	1.85363	8E-04	*	0.2978	NA	
Indolic	unknown	AT4G37430	CYP81F1	0.80999	0.013		0.55712	0.127		0.0976	0.905	
Indolic	Core structure	AT4G39950	CYP79B2	1.71285	7E-22	*	2.1347	1E-33	*	-0.02	0.972	
Indolic	Core structure	AT5G05730	ASA1	1.00615	1E-16	*	1.43772	2E-33	*	-0.212	0.343	
Indolic	Secondary Modification	AT1G21100	IGMT1	0.99226	7E-07		2.0832	7E-28	*	-0.248	0.538	
Indolic	Secondary Modification	AT1G21120	IGMT2	1.21815	9E-06	*	2.0722	3E-15	*	-1.049	0.016	*
Indolic	Secondary Modification	AT1G21110	IGMT3	1.20028	2E-06	*	1.9029	6E-15	*	-0.28	0.584	
Indolic	Secondary Modification	AT1G21130	IGMT4	0.8836	1E-07		1.62861	4E-24	*	-0.327	0.229	
Indolic	Core structure	AT5G54810	TSB1	0.48686	6E-04		1.20665	6E-20	*	-0.053	0.877	
Indolic	Core structure	AT5G57220	CYP81F2	2.32941	1E-16	*	3.26757	1E-32	*	-0.635	0.28	
Indolic	Core structure	AT5G05260	CYP79A2	0	NA		0	NA		0.5108	NA	
Aliphatic	Secondary modification	AT1G12140	FMOGS-OX5	-0.1466	0.369		-0.0554	0.78		-0.082	0.794	
Aliphatic	Core structure	AT1G16400	CYP79F2	0.317	0.25		0.09901	0.776		0.1188	0.839	
Aliphatic	Core structure	AT1G16410	CYP79F1	-0.9739	2E-06		-0.8671	3E-05		0.143	0.741	
Aliphatic	Core structure	AT1G18590	SOT17	-0.3329	0.124		-0.2552	0.28		0.0627	0.896	
Aliphatic	Side-chain elongation	AT1G31180	IMDH1	-0.3635	0.006		-0.2598	0.068		0.2077	0.326	
Aliphatic	Secondary modification	AT1G62540	FMOGS-OX2	-0.2485	0.376		-0.4027	0.164		0.9407	9E-04	
Aliphatic	Secondary modification	AT1G62560	FMOGS-OX3	-1.2003	7E-11	*	-1.2947	5E-12	*	0.4138	0.146	
Aliphatic	Secondary modification	AT1G62570	FMOGS-OX4	-0.4049	0.208		0.19558	0.599		0.0302	0.971	
Aliphatic	Secondary modification	AT1G65860	FMOGS-OX1	-0.8613	8E-05		-0.9229	3E-05		0.3327	0.366	
Aliphatic	Core structure	AT1G74090	SOT18	-0.7812	5E-06		-0.5582	0.002		0.0668	0.87	
Aliphatic	Core structure	AT1G78370	GSTU20	-0.9458	7E-06		-1.108	1E-07	*	0.6143	0.033	
Aliphatic	Side-chain elongation	AT1G80560	IMDH2	0.0582	0.727		0.32618	0.018		0.2093	0.336	
Aliphatic	Secondary modificatio	AT2G25450	GSL-OH	1.29853	9E-25	*	1.7338	1E-43	*	0.4221	0.017	
Aliphatic	Core structure	AT2G31790	UGT74C1	-0.8413	2E-05		-0.5995	0.004		0.062	0.896	
Aliphatic	Side-chain elongation	AT2G43100	IPMI2	-0.768	1E-04		-0.9607	1E-06		0.3889	0.208	
Aliphatic	Core structure	AT3G03190	GSTF11	-0.7026	0.003		-0.4274	0.106		0.7727	0.007	
Aliphatic	Side-chain elongation	AT3G19710	BCAT4	-0.4958	0.005		-0.4193	0.024		0.2858	0.314	
Aliphatic	Side-chain elongation	AT3G49680	BCAT3	-0.5933	5E-10		-0.6429	3E-11		0.2755	0.041	
Aliphatic	Side-chain elongation	AT3G58990	IPMI1	-0.6562	0.004		-0.9515	2E-05		0.2845	0.47	

Aliphatic	Secondary modification	AT4G03060	AOP2	-0.8702	1E-05		-0.9745	1E-06		0.4443	0.134	
Aliphatic	Side-chain elongation	AT4G12030	BASS5	-1.054	3E-06	*	-1.1129	8E-07	*	0.2665	0.523	
Aliphatic	Side-chain elongation	AT4G13430	IIL1	-0.2764	0.063		-0.2971	0.051		-0.005	0.99	
Aliphatic	Core structure	AT4G13770	CYP83A1	-1.0524	1E-14	*	-1.1667	9E-18	*	0.0811	0.794	
Aliphatic	unknown	AT4G03050	AOP3	0	NA		0.13791	NA		0.1554	NA	
Aliphatic	Side-chain elongation	AT5G14200	IMDH3	-0.9051	6E-10		-0.9231	3E-10		0.5357	0.005	
Aliphatic	Side-chain elongation	AT5G23010	MAM1	-0.641	7E-05		-0.7496	3E-06		0.3623	0.135	
Aliphatic	Core structure	AT5G23020	MAM3	0.65176	9E-04		0.26834	0.257		-1.168	5E-06	*
Aliphatic and indolic	Core structure	AT4G30530	AT4G30530	0.61748	1E-04		0.78052	6E-07		0.3366	0.167	
Aliphatic and indolic	Core structure	AT2G20610	SUR1	-0.221	0.157		-0.1871	0.265		-0.104	0.723	
Aliphatic and indolic	co-substrate	AT4G23100	GSH1	-0.4229	0.004		0.10768	0.559		-0.097	0.753	
Aliphatic and indolic	co-substrate	AT5G65940	CHY1	0.27467	0.08		0.21992	0.198		0.1716	0.531	
Aliphatic and indolic	co-substrate	AT1G65880	BZO1	-0.8681	0.155		-0.2651	0.725		0.1042	NA	
Aliphatic and indolic	co-substrate	AT2G14750	APK1	-0.1153	0.445		-0.1953	0.187		0.2499	0.211	
Aliphatic and indolic	Transcription factor	AT1G32640	MYC2	0.70496	3E-04		1.45388	6E-15	*	0.215	0.563	
Aliphatic and indolic	Transcription factor	AT5G46760	MYC3	-0.158	0.409		0.24509	0.193		-0.292	0.276	
Aliphatic and indolic	Transcription factor	AT4G17880	MYC4	-1.4097	2E-15	*	-1.548	2E-17	*	-0.177	0.616	
Aliphatic	Transcription factor	AT5G61420	MYB28	-0.9735	3E-09		-1.1561	2E-12	*	-0.028	0.952	
Aliphatic	Transcription factor	AT5G07690	MYB29	-1.6437	1E-17	*	-1.7609	2E-19	*	0.2147	0.564	
Aliphatic	Transcription factor	AT5G07700	MYB76	-0.908	0.009		-1.0325	0.005	*	0.3183	0.613	
Indolic	Transcription factor	AT5G60890	MYB34	-0.8344	8E-06		-0.9473	7E-07		0.1147	0.777	
Indolic	Transcription factor	AT1G18570	MYB51	2.09471	1E-36	*	2.83585	5E-67	*	-0.529	0.055	
Indolic	Transcription factor	AT1G74080	MYB122	2.0296	5E-04	*	2.54066	9E-06	*	-0.348	NA	
Indolic	Transcription factor	AT4G17490	ERF6	2.26971	4E-10	*	3.6804	9E-26	*	0.229	0.798	
Unknown	Transcription factor	AT5G46830	MYC5	-1.9652	5E-05	*	-2.1547	3E-05	*	0.3971	NA	

Asterisk (*) denote statistical significance.

Supplemental table 4. List of primers used in this study.

Name	Primer	Note
NAI1-F	ACCATTCTCACTAAGATGGACAACAAATT	qRT Primer
NAI1-R	ACGTTTAACCACTGCGAAATTCACA	qRT Primer
NAI2-F	AACTTGAGTTCGAAGCACATATCAATGA	qRT Primer
NAI2-R	TTCACGTTCAATGGCTTCCAACA	qRT Primer
BGLU18-F	CGAGGTTCGGACTTTACTACATCGAT	qRT Primer
BGLU18-R	TGTCCCGATAGGATTCTTGATCATCT	qRT Primer
BGLU23-F	ACGTTACGAGAAAGAATCCGGCA	qRT Primer
BGLU23-R	TCTTGGTCACTCACAAAGTAAAACATAGGA	qRT Primer
TSA1-F	GGCTGACAAAGAAGAATCTGCAAAGA	qRT Primer
TSA1-R	GTTGGTATAACAATCGAGGAATCTTCGT	qRT Primer
JAL34-F	AAATCCAAGAGAGTTTGTGATTAACCATC	qRT Primer
JAL34-R	GCTGACCTCATAAGTGTTCAAGTTCGT	qRT Primer
GLL23-F	GAACGAATTGGCTAGAACAG	qRT Primer
GLL23-R	GCAACCATAAGCATCATGTG	qRT Primer
MEB1-F	AGGATGCCTTCTGCTTCTGT	qRT Primer
MEB1-R	GAGTGAAACGGGACCTCATT	qRT Primer
ERF6-F	ATTGTCTCCGTTGCCTACTA	qRT Primer
ERF6-R	GGTTTGGTTTCAAATTCAGA	qRT Primer
MYB51-F	AGCTCGTGGACTACCAGGAA	qRT Primer
MYB51-R	GGAGGTTATGCCCTTGTGTG	qRT Primer
MYB122-F	AACTTCATTGATCGGCGTCAC	qRT Primer
MYB122-R	ACCTCTTCGAATCTCCCCATC	qRT Primer
CYP81F2-F	GTCACAGGGAGACGCTACTAC	qRT Primer
CYP81F2-R	CACCACTGTTGTCATTGATGTC	qRT Primer
CYP81F4-F	TTGTTGAACCACCCAAAAGTTT	qRT Primer
CYP81F4-R	GGAGGTAAGGAAGGTTTGCT	qRT Primer
NSP1-F	ACTCCCTTGGGGCCTATGT	qRT Primer
NSP1-R	GCATCTTAGCCCTGGACCTT	qRT Primer
ESM1-F	AACGCCGTTCTTCGTAGGAT	qRT Primer
ESM1-R	TTCGAGTGCACGTTTCCCTT	qRT Primer

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