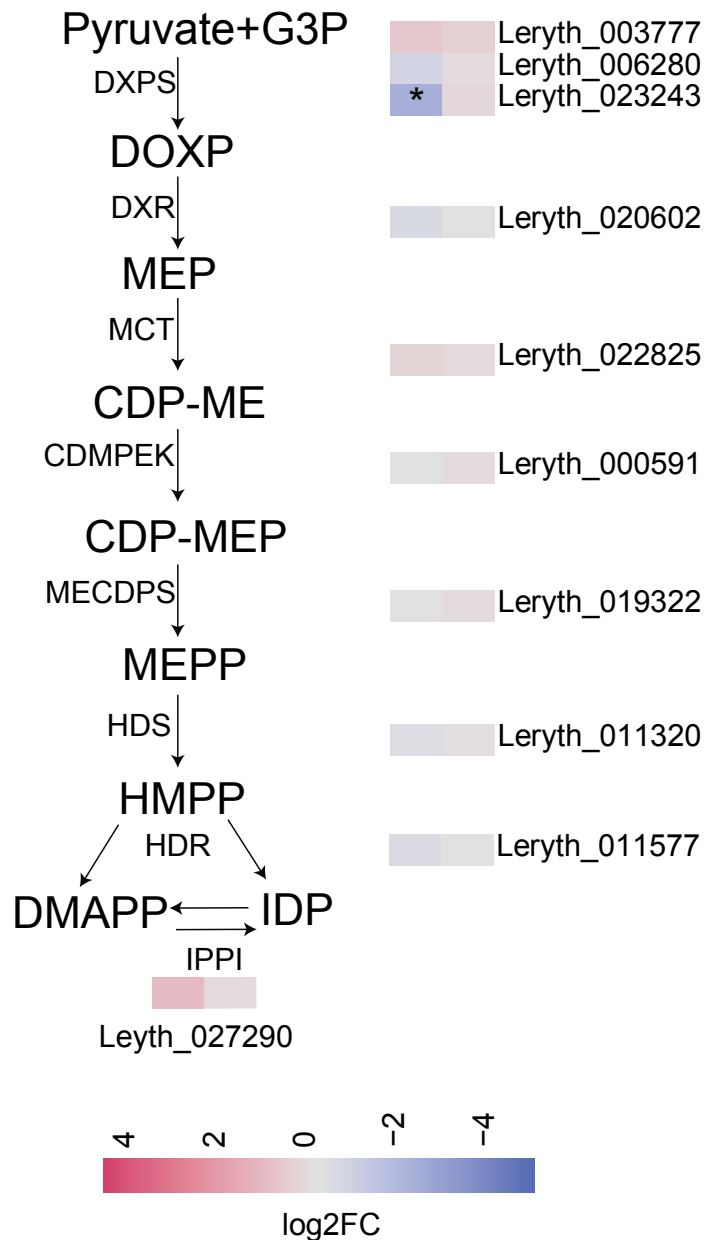


Supplemental Figure S1: Comparison of growth phenotypes between the treatments on three time points. A) Diagram of the evolution of the shoot dry weight of the plants from the different treatments at 4, 6 and 8 wpi. **B)** Diagram of the evolution of the shoot length of the plants from the different treatments at 4, 6 and 8 wpi.

MEP pathway



Supplemental Figure S2. Effect of methyl jasmonate (MeJA) and salicylic acid (SA) on the expression of genes involved in the plastidal methylerythritol phosphate (MEP) pathway. The mean log2 fold-change in expression level of MeJA and SA treated roots as compared to control in the methylerythritol phosphate (MEP) pathway. * Denotes differentially expressed gene at log2fold > |1| and FDR < 0.05. Abbreviations: G3P, D-glyceraldehyde 3-phosphate, DXPS, 1-deoxy-D-xylulose-5-phosphate synthase; DOXP, 1-deoxy-D-xylulose 5-phosphate, DXR, 1-deoxy-D-xylulose-5-phosphate reductoisomerase; MEP, 2-methylerythritol 4-phosphate, MCT, 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase; CDP-ME, 4-Diphosphocytidyl-2-C-methylerythritol; CDMPEK, 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol 2-phosphokinase; CDP-MEP, 4-diphosphocytidyl-2-C-methylerythritol 2-phosphate, MECDPS, 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase;

MEPP, methylerythritol cyclodiphosphate; HDS, 1-hydroxy-2-methyl-2-butenyl-diphosphate synthase; HMPP, (E)-1-hydroxy-2-methylbut-2-enyl 4-diphosphate; HDR, 1-hydroxy-2-methyl-2-(*E*)-butenyl-4-diphosphate reductase; DMAPP, Dimethylallyl pyrophosphate; IDP, isopentenyl diphosphate; IPPI, isopentenyl pyrophosphate isomerase

	10	20	30	40
Consensus	MAEILXANX-SQTX	XXXSSQXYPXWYSPKTGIYH	SKHTSXXLPTEPFX	
At4CLL6	MAATHLHIP-PNPK	TQTSHQNPPFWFSSKTGIYTSK	FPSLHLPVDPNL	
Leryth_018919-t1	MGEILKANE-SQTIT	TPSSQAYPSWYSPKTGIYH	SKHTSMNLPTEPFA	
Leryth_018919_complete	MGENLKANE-SQTIT	TPSSQAYPSWYSPKTGIYH	SKHTSMNLPTEPFA	
Leryth_004695-t1	-----			
Leryth_004695_Complete	MAEILRAFPQTSSK	TFSEASYPYWYSPETGIYQ	SKHTPVALPTEPFV	
Leryth_000173-t1_Complete	MAELFRA----	DAQTFSEDRSYPYWYSPETGIYH	SKHAKVALPIEPFV	
Leryth_000173-t1	-----			

	50	60	70	80	90
Consensus	DAVSYIFSHKHGXTALID	SSTGVSIPYSQLYXSVKAXASGLHH-MGV			
At4CLL6	DAVSALFSHKHHGDTALID	SLTGFSISHTELQIMVQ	SMAAGIYHVLGV		
Leryth_018919-t1	DVVSYIFSQKHEGENALVD	SSTGVSIPYSQLYPSVKAVASGLHH-MGV			
Leryth_018919_complete	DVVSYIFSQKHEGENALVD	SSTGVSIPYSQLYPSVKAVASGLHH-MGV			
Leryth_004695-t1	-----				
Leryth_004695_Complete	DAVSYIFSHKHDGVTALID	SSSGVSIPYSQLYSSVKAIASGLHQ-MGV			
Leryth_000173-t1_Complete	DAVSYIFSHKHDGVTALID	STTGVSIPYSQLYSSVKAIASGLHQ-MGV			
Leryth_000173-t1	-----MGV				

	100	110	120	130	140
Consensus	KQGDVVLISLPNSIIFPIIFL	GVLSJGAIVAPMNPVSNPLEIKKQ	TKD		
At4CLL6	RQGDVVSIVLPLNSVYFPMIF	LSLISLGAIVTTMNPSSSLGEIKKQ	VSE		
Leryth_018919-t1	KQGDVVLILLPNSIIFPIIFL	GVLSLGATIAPMNPVSNPLEIKKQ	TKD		
Leryth_018919_complete	KQGDVVLILLPNSIIFPIIFL	GVLSLGATIAPMNPVSNPLEIKKQ	TKD		
Leryth_004695-t1	-----				
Leryth_004695_Complete	QQGDVVLISLPNSIIFPIIFL	GVLSIGAIVAPMNPVSNPLEIKKQ	TKD		
Leryth_000173-t1_Complete	KQGDVVLISLPNSIIFPIIFL	GVLSIGAIVAPMNPVSNPLEIKKQ	TKD		
Leryth_000173-t1	KQGDVVLISLPNSIIFPIIFL	GVLSIGAIVAPMNPVSNPLEIKKQ	TKD		

	150	160	170	180	190
Consensus	CKVKXAFTTTPEKVXQXSXA-LNL	PAIPVSENITPGSI-----FHKII			
At4CLL6	CSVGLAFTTSTENVEKLSS--LGV	SVISVSESYDFDSIRIENPKFY	SIM		
Leryth_018919-t1	CEVKLAFTTTPEKVEQLKSAGL	QFPTIPVQENIIPGSI-----FHTII			
Leryth_018919_complete	CKVKLAFTTTPEKVEQLKSAGL	QFPTIPVQENIIPGSI-----FHTII			
Leryth_004695-t1	-----				
Leryth_004695_Complete	CKVKFAFTTTPEKVDQVSKA-LNL	PAIPVSENITPGSI-----FHKII			
Leryth_000173-t1_Complete	CKVKFAFTTTPEKVDQVSKA-LNL	QAIPVSENITPGSI-----FHKII			
Leryth_000173-t1	CKVKFAFTTTPEKVDQVSKA-LNL	QAIPVSENITPGSI-----FHKII			

	200	210	220	230	240
Consensus	SSDPNXAPKPRINQEDTAAIMF	SSGTTGACKGVVLTHXNFIXMVALFV			
At4CLL6	KESFGFVFPKPLIKQDDVAAIMY	SSGTTGASKGVLLTHRNLIASME	LFV		
Leryth_018919-t1	TSDPNFAPKPIINQEHA	AAAIMFSSGTTGACKGVVLTHKNFIAMVALFI			
Leryth_018919_complete	TSDPNFAPKPIINQEHA	AAAIMFSSGTTGACKGVVLTHKNFIAMVALFI			
Leryth_004695-t1	-----MFSSGTTGACKGVVLTHRNFISMVALFV				
Leryth_004695_Complete	SSDPNLAPKPRISQEDTAAIMF	SSGTTGACKGVVLTHRNFISMVALFV			
Leryth_000173-t1_Complete	SSDPNLAPKPRINQEDTAAIMF	SSGTTGACKGVVLTHKNFISMVALFV			
Leryth_000173-t1	SSDPNLAPKPRINQEDTAAIMF	SSGTTGACK-----			

	250	260	270	280	
Consensus	-----:----- -----:----- -----:----- -----:----- -----:-----	RFEXSQY-EFTPSKNVYLAVLPMFHIFGLAQFVTGLLSLGTTIVVMKK			
At4CLL6		RFEASQY-EYPGSSNVYLAALPLCHIYGLSLFVMGLLSLGSTIVVMKKR			
Leryth_018919-t1		RFEASQYKELSPSKNVYLAVLPMFHIFGLAQFVTGLLSLGTTIIVMKK			
Leryth_018919_complete		RFEASQYKELSPSKNVYLAVLPMFHIFGLAQFVTGLLSLGTTIIVMKK			
Leryth_004695-t1		RFESSQY-SFTPSKNVYIAVLPMFHIFGLAQFVTGLLSLGTTIVVMKK			
Leryth_004695_Complete		RFESSQY-SFTPSKNVYIAVLPMFHIFGLAQFVTGLLSLGTTIVVMKK			
Leryth_000173-t1_Complete		RFESSQY-PFTPSKNVYLAVLPMFHIFGLAQFVTGLLSLGTTIVVMKK			
Leryth_000173-t1		-----AQFVTGLLSLGTTIVVMKK			

	290	300	310	320	330
Consensus	- -----:----- -----:----- -----:----- -----:----- -----:-----	FDPDEMVKAIIEKFGVTHFPVVPPLMTALTKKAKSXDVKXGNFLRSLKQ			
At4CLL6		FDASDVNVNIEFRKITHFPVVPPLMALTTKKAKGVC---GEVFKSLKQ			
Leryth_018919-t1		FDPEEMIRAIIEKFRVTHFPVVPPLMNALTKKARTLP-NSSEILKSLKQ			
Leryth_018919_complete		FDPEEMIRAIIEKFRVTHFPVVPPLMNALTKKARTLP-NSSEILKSLKQ			
Leryth_004695-t1		FNPDEMVKAIKAKYGVTHFPVVPPLMTALTKKAKSMDVKKGNFLRSLKQ			
Leryth_004695_Complete		FNPDEMVKAIKAKYGVTHFPVVPPLMTALTKKAKSMDVKKGNFLRSLKQ			
Leryth_000173-t1_Complete		FHPDEMVKAIISRFVTHFPVVPPLMTALTKKAKSEDVKNANFLRSLKQ			
Leryth_000173-t1		FHPDEMVKAIISRFVTHFPVVPPLMTALTKKAKSEDVKNANFLRSLKQ			

	340	350	360	370	380
Consensus	--- -----:----- -----:----- -----:----- -----:----- -----:-----	VSSGAAPLTTKLIQEFVQALPHVDFIQGYGMTETTAVATRGYNTKELK			
At4CLL6		VSSGAAPLSRKFIEDFLQTLPHVDLIQGYGMTTESTAVGTRGFNSEKLS			
Leryth_018919-t1		VSSGAAPLTTKAIQEFVQALPHVDFIQGYGMTETTAVATRGFNTNELK			
Leryth_018919_complete		VSSGAAPLTTKAIQEFVQALPHVDFIQGYGMTETTAVATRGFNTNELK			
Leryth_004695-t1		VSSGAAPLTTKLIQELVQALPHVDFIQGYGMTETTAVATRGYNTKDLK			
Leryth_004695_Complete		VSSGAAPLTTKLIQELVQALPHVDFIQGYGMTETTAVATRGYNTKDLK			
Leryth_000173-t1_Complete		VSSGAAPLTTKLIQEFVQALPHVDFIQGYGMTETTAVATRGYNTKELK			
Leryth_000173-t1		VSSGAAPLTTKLIQEFVQALPHVDFIQGYGMTETTAVATRGYNTEELK			

	390	400	410	420	430
Consensus	:----- -----:----- -----:----- -----:----- -----:----- -----:-----	NYTSVGLLAPNSEAKVVDVSVSGAXMPPGGVGELWLRSPGVMKGYLNNI			
At4CLL6		RYSSVGLLAPNMQAKVVDWSSGSFLPPGNRGELWIQGPVMKGYLNNP			
Leryth_018919-t1		NYTSVGLLAPNSEAKVVDWVSGESMPPGGVGELWLRSPGVMKCYLKNP			
Leryth_018919_complete		NYTSVGLLAPNSEAKVVDWVSGESMPPGGVGELWLRSPGVMKCYLKNP			
Leryth_004695-t1		NYTSVGLLAPNSEAKVVDVSVSGATMPPGGVGELWLRSPGVMNGYLNNI			
Leryth_004695_Complete		NYTSVGLLAPNSEAKVVDVSVSGATMPPGGVGELWLRSPGVMNGYLNNI			
Leryth_000173-t1_Complete		NYTSVGLLAPNSRAKVIDFVSGAAPPVGGVGELWLRSPGVMKGYLNNI			
Leryth_000173-t1		NYTSVGLLAPNSQAKVIDFVSGAAPPVGGVGELWLRSPGVMKGYLNNI			

	440	450	460	470	480
Consensus	--:----- -----:----- -----:----- -----:----- -----:----- -----:-----	KETMSTVDTEGWLHTGDIVYFDQDGYLYVIDRLKEVIKYKGFQISPAD			
At4CLL6		KATQMSIVEDSWLRTGDIAYFDEDGYLFIVDRIKEIIKYKGFQIAPAD			
Leryth_018919-t1		EETINNVDKDGWLHTGDIVYFDQDGYLYVI---RKVIK-----			
Leryth_018919_complete		EETINNVDKDGWLHTGDIVYFDQDGYLYVIDRLKEVIKYKGFQISPAD			
Leryth_004695-t1		KETMSTVDTEGWLHTGDIVYFDQDGYLYVIDRLKEVIKYKGFQISPAD			
Leryth_004695_Complete		KETMSTVDTEGWLHTGDIVYFDQDGYLYVIDRLKEVIKYKGFQISPAD			
Leryth_000173-t1_Complete		QETMSTVDTEGWLHTGDIVYFDQEGYLYIIDRLKEVIKYKGFQISPAD			
Leryth_000173-t1		KETMSTVDTEGWLHTGDIVYFDQEGYLYIIDRLKEVIKYKGFQISPAD			

	490	500	510	520
Consensus	-----:----- -----:----- -----:----- -----:----- -----:-----	LESVLMSHPEVADA	AAVTAVTDEEAGEI	PVAFVVRKKGSELSEESLMDF
At4CLL6	LEAVLVSHPLI	IDA	AAVTAAAPNEECGEI	PVAFVVRQRQETTLSEEDVISY
Leryth_018919-t1	-----	-----	-----	-----
Leryth_018919_complete	LESVLMSHPEV	VDA	AAVTAVTDEEAGEI	PVAFVVRKKGSKLSETSLMDF
Leryth_004695-t1	LESVLMSHPEV	A	AAVTAVTDEEAGEI	PVAFVVRKKGSELSEESLMDF
Leryth_004695_Complete	LESVLMSHPEV	A	AAVTAVTDEEAGEI	PVAFVVRKKGSELSEESLMDF
Leryth_000173-t1_Complete	LESVLMSHPEV	A	AAVTAVTDEEAGEI	PVAFVVRKKGSELSEESLMDF
Leryth_000173-t1	LESVLMSHPEV	A	AAVTAVTDEEAGEI	PVAFVVRKKGSELSEESLMDF

	530	540	550	560	570	
Consensus	- -----:----- -----:----- -----:----- -----:----- -----:-----	VATKVS	SPYKKVRKVCFT	NSVPRSAAGKII	RRRELKMIL----	P
At4CLL6	VASQV	APYRKVRKVV	MVNSIPKSPTG	KILRKELKRILT	NSVS	SRL
Leryth_018919-t1	-----	-----	-----	-----	-----	-----
Leryth_018919_complete	VATKVS	SPYKKVRKVCFT	NSVPRSAAGKII	RRRELKNIL----	P	SRL
Leryth_004695-t1	VATKVS	SPYKKVRKVCFT	NSVPRSAAGKII	RRRELKMIL----	P	SRL
Leryth_004695_Complete	VSTKV	SPYKKVRKVCFT	NSVPRSAAGKII	RRRELKMIL----	P	SRL
Leryth_000173-t1_Complete	VATKVS	SPYKKVRKVCFT	SSVPRSAAGKII	RRRELKMIL----	P	SRL
Leryth_000173-t1	VATKVS	SPYKKVRKVCFT	SSVPRSAAGKII	RRRELKMIL----	P	SRL

Supplemental Figure S3. Amino acid sequence comparison of putative *L. officinale* 4-coumarate ligases-like genes recovered in coexpression network (4CLL; Leryth_000173, Leryth_004695 and Leryth_018919) with the characterised 4CLL from *Arabidopsis thaliana* (At4CLL6). The amino acid alignments were computed using the MUSCLE algorithm implemented in Geneious. The pink highlighted sequence is the peroxisomal targeting sequence I (PTS I), predicted by PSORT (<https://www.psort.org/>).

	10	20	30	40
	-----:----- -----:----- -----:----- -----:----- -----:-----			
Consensus	MXGSMVKPTV	TMEVGXDGVAVITXINPPVNXLAIPI	IEGLKEKFKEAE	
Leryth_018504-t1	----MVAPT	VTMEVG-----	-----I	IEGLTEKFKEAE
PtCHD1	----MAKPHVT	TMEVGNDGVAVVTLINPPVNALAIPI	IAGLKEKFDEAT	
PtCHD2	MEGSRTKGR	TTIEVGADGVALITII	INPPVNSLSFDVLYSLKDSFEQAL	
PtCHD3	MKGSRTKGT	TTTTIEVGADGVALITLINPPVNALSSDVLSLKDSEYEQAL		
PhCHD	----MAQVKVT	TMEVGTDGVAVITIFNPPVNALAIPI	INALKEKWTEAT	
Leryth_020735-t2	----MVPPT	VTMEVGSDGVAVITMSNPPVNSLAIPI	IEGLTGKFKEAE	
Leryth_020735-t1	----MVPPT	VTMEVGSDGVAVITMSNPPVNSLAIPI	IEGLTGKFKEAE	

	50	60	70	80	90
	- -----:----- -----:----- -----:----- -----:----- -----:-----				
Consensus	RRNDVKAIVLTGKGG	RFSGGFDINVFQLVHKTGD	ISXXPD-VSVEXVV		
Leryth_018504-t1	RRNDVKAIVLTGKGG	KFSGGFDINVFQLVHKTGD	ISHLPD-VSVS	FVN	
PtCHD1	RRNDVKALVLTGKGG	RFSGGFDINVFQKVHATGD	ISLMPD-VS	VELVV	
PtCHD2	RRDDVKAIVITGAKG	KFSGGF	DISSFGGVQGGKSNEPKPGFIS	VEILS	
PtCHD3	RRDDVKAIVITGAKG	KFSGGADISSFEEVQEGKVN	EPKPDFIFSEVLG		
PhCHD	IRNDVKAIVLTGNGG	RFSGGFDINVFQKVHGTGD	ISQMPD-VS	VDLVV	
Leryth_020735-t2	RRSDVKAIVLTGKGG	RFSGGFDINVFQLVHKTG	-----V		
Leryth_020735-t1	RRSDVKAIVLTGKGG	RFSGGFDINVFQLVHKTG	-----V		

	100	110	120	130	140
	--- -----:----- -----:----- -----:----- -----:----- -----:-----				
Consensus	NTXEDCKKPX	VAAIEGLALGGGLELAMACHARI	AAPXAQLGLPELXLG		
Leryth_018504-t1	NIVEDSKKPA	VAAVEGLALGGGLELAMACHARI	AAPKTQLGLPELTLG		
PtCHD1	NTIEDCKKPV	VAAVEGLALGGGLELAMGCHARI	AAPKTQLGLPELTLG		
PtCHD2	DTVEAAKKPS	VAAIDGLALGGGLEVAMACHARI	STSTAQLGLPELQLG		
PtCHD3	DTLEAAKKPS	VAAIDGLALGGGLEVAMACHARI	STPTAQLSLPELQLG		
PhCHD	NTMEDCKKPA	VAAIEGLALGGGLELAMGCHARI	AAPRAQLGLPELSLG		
Leryth_020735-t2	PCKDCCTKNT	-----AGSLLCESCC	-----		
Leryth_020735-t1	PCKDCCTKNT	-----AGSLLCESCC	-----		

	150	160	170	180	190
	:----- -----:----- -----:----- -----:----- -----:----- -----:-----				
Consensus	XIPGFGGTQRLPRLXGLXKA	IEMMXXSKPIMSEE	GEKLG	LIDAVVPSX	
Leryth_018504-t1	IIPGFGGTQRLPRLVGLPKA	IEMMVFSKPIMSEV	GEKLG	LIDAVVPSG	
PtCHD1	VIPGFGGTQRLPRLGLSKA	IEIMLLSKPIMSEE	GKLG	LIDAIVPSQ	
PtCHD2	LIPGFGGTQRLPRLVGISKAL	EMMLTSKPVKGEEAH	GLVD	AVVSPN	
PtCHD3	LIPGFGGTQRLPRLVGITKAL	EMMLTSKPVKGEEAH	GLVD	AVVSPN	
PhCHD	VMPGFGGTQRLPRLIGLSKAV	EMMTSKPIMSEE	GKLG	LIDAIVPSS	
Leryth_020735-t2	----FKQTQRLPRLIGL	PKAIEVMVFSKPIMSEE	GEKLG	LIDVVVPSK	
Leryth_020735-t1	----FKQTQRLPRLIGL	PKAIEVMVFSKPIMSEE	GEKLG	LIDVVVPSK	

	200	210	220	230	240
	--:----- -----:----- -----:----- -----:----- -----:-----				
Consensus	ELLNVARQWALDIAEXRKP	WXRSLHKTDKIGSLSEARE	ILKGARQQVK		
Leryth_018504-t1	DLLNVARRWALDIADKHKP	WIRSLHKTDKIGSISEAH	NILQGARQQVK		
PtCHD1	ELLKVSQWALDISERRKP	WLRLHRTDKIGSLSEARE	VLKAARQQAK		
PtCHD2	ELVSTARQWALDILERRRP	WIASLYKTEKLDLSEARE	IFKFAREQVR		
PtCHD3	ELVSTARQWALDIFECRRP	WIASLYKTEKLDLSEARE	IFKFARAQAQ		
PhCHD	ELLKVSQWALDIAERRKP	WMRSLHKTDKIGSLSEARE	VLKVARQQVK		
Leryth_020735-t2	DLLNVARKWALDIAEKRP	WMRSLHKTDKIGSISEAH	KILQGARQQVK		
Leryth_020735-t1	DLLNVARKWALDIAEKRP	WMRSLHKTDKIGSISEAH	KILQGARQQVK		

	250	260	270	280
	----:----- -----:----- -----:----- -----:----- -----:-----			
Consensus	KTAXNXXHHQLCIDVI	EXGIVHGGYHGLLKE	TKXFNXLVLS	SDXXKGLI

Leryth_018504-t1	KTFRNLVHHQLCISVMEDGIVHGGYHGVLEETKTFNKLVLSDNAKGLI
PtCHD1	KIAPNVPQHQAALLDVMEEGI IHGGYNGVLKEAKVFKELVLTETSKGLV
PtCHD2	KRAPNLTHPIVCIDVIEHGIVSGPRDGLYKELESFHELVRSDTCKSLI
PtCHD3	KRAPNLLHPIVCINVVEHGIVSGPRAGLYKEFESFQELVRSDISKSLV
PhCHD	QTAKNMPQHVACIDVIEEGI IHGGYAGVLKEAKVFKDLVLSETSKGLV
Leryth_020735-t2	QTFRNMFHHQLCLDAIEAGIVHGGYHGLLEETKIFNKLVLSDNAKGLI
Leryth_020735-t1	QTFRNMFHHQLCLDAIEAGIVHGGYHGLLEETKIFNKLVLSDNAKGLI
	290 300 310 320 330
	- ----:---- ----:---- ----:---- ----:---- ----:-
Consensus	HIFFAQRATSKVPNVTDVGLKPRPXKKVAVIGGGLMGSGIATALILSN
Leryth_018504-t1	HIFFSQRATSKVPNVTDVGLKPNPAKKVAVIGGGLMGSGIATALVLNN
PtCHD1	HVFFAQRMSTKIPKVTDVGLKPRHIKKVAVIGGGLMGSGIATALIVSN
PtCHD2	HIFFAQRGTTKVPGITDLGLVPRRVKKVAVLGGGLMGSGIATALVLSN
PtCHD3	HIFFALRGTTKVPGITDLGFVPRLVKKVAVLGGGLMGSGIATALILSN
PhCHD	HVFFAQRATSKVPNVTDIGLKPRTVKKVAVIGGGLMGSGIATALALSN
Leryth_020735-t2	HIFFSQRATSKVPNVTDVGLKPNPAKKVAVIGGGLMGSGIATALILNN
Leryth_020735-t1	HIFFSQRATSKVPNVTDVGLKPNPAKKVAVIGGGLMGSGIATALILNN
	340 350 360 370 380
	--- ----:---- ----:---- ----:---- ----:---- ----
Consensus	IXVVLKEINSEYLQKGIKSVEANVRSLVXRKKLTQEKADKALSMLKGX
Leryth_018504-t1	INVVLKEINSDYLLKGIQSVEANVKSMVLRKKLTQEKANKALSLLKGV
PtCHD1	IHVVLKEINSEYLQKGTKTIEANVRSLVTRGKLTRDKADKALSMLKGA
PtCHD2	YPVILKEVNNQFLQAGIGRVRANLQSRVKKGRMTQEKFEKTMSLLKGA
PtCHD3	YPVILKEVNDQFLQAGIGRVRANLQSRVKKGKMTQEKFEKTMSLLKGS
PhCHD	TFVVLKEINSEYLQKGMKAIEANVRGLVARKKL PQDKADKALSMVKGA
Leryth_020735-t2	IYVVLKEINSEYLLKGIKSVEANVRSLVSRKKLTQEKGDKALSMLKGV
Leryth_020735-t1	IYVVLKEINSEYLLKGIKSVEANVRSLVSRKKLTQEKGDKALSMLKGV
	390 400 410 420 430
	:---- ----:---- ----:---- ----:---- ----:---- ---
Consensus	LDYSEFKDVMVIEAVIENVSLKQKIFSELEKICPPHCILASNTSTID
Leryth_018504-t1	LDYSEFKDVMVIEAVIENISLKQKIFGELEKICPPHCVLASNTSTID
PtCHD1	LDYSDFKDVMVIEAVIESVPLKQKIFSEIEKICPPHCILATNTSTID
PtCHD2	LDYESFKDVMVIEAVIENVSLKQQIFSDLEKYCPPHCILASNTSTID
PtCHD3	LDYESFKDVMVIEAVIENVSLKQQIFSDLEKYCPPHCILASNTSTID
PhCHD	LDYSDFKDVMVIEAVIESVPLKQKIFSEIEKVCPPHCILASNTSTID
Leryth_020735-t2	LDYSEFADVMVIEAVIENISLKQKIFGELEKICPPHCVLASNTSTID
Leryth_020735-t1	LDYSEFADVMVIEAVIENISLKQKIFGELEKICPPHCVLASNTSTID
	440 450 460 470 480
	--:---- ----:---- ----:---- ----:---- ----:----
Consensus	LNLVGENTXSQDRIIGAHFFSPAHVMPLEIVRTEKTSXQVILDLMTV
Leryth_018504-t1	LNLVGEKTRSQDRIIGAHFFSPAHVMPLEIVRTEKTSSQVILDLMTV
PtCHD1	LNLVGEKTSSQDRIIGAHFFSPAHVMPLEIVRTEKTSQAAILDLMTV
PtCHD2	LNLIGKQTKSQDRIIGAHFFSPAHVMPLEIVRTKQTSQPQVIVDLLDV
PtCHD3	LNLIGKQTKSQDRIIGAHFFSPAHVMPLEIVRTKQTSQPQVIVDLLDV
PhCHD	LNIIGENTRSKDRIIGAHFFSPAHVMPLEIVRTEKTSTQAAILDLMAV
Leryth_020735-t2	LNLVGENTISQDRIIGAHFFSPAHVMPLEIVRTEKTSQGQVVDLMTV
Leryth_020735-t1	LNLVGENTISQDRIIGAHFFSPAHVMPLEIVRTEKTSQGQVVDLMTV
	490 500 510 520
	-----:---- ----:---- ----:---- ----:---- -----:---
Consensus	GKTIKKVPVVVG NCTGFAVNR TFFPY TQSALFLVNL GVDLFRIDQLIS
Leryth_018504-t1	GKTIKKVPVVVG NCTGFAVNR TFFPY TQSALFLVNL GVDLFRIDQLIS
PtCHD1	GKTIKKVPVVVG NCTGFAVNR AFFPY TQSALILVHL GVADVFRIDKLIS
PtCHD2	GKKIRKTPVVVG NCTGFAVNR MFFPY TQAALLLVEH GADLYQIDKVIT

PtCHD3	GKKIRKTPVVVG	NCTGFAVNR	MFFPYTQAAI	FLVEHGV	DLYQIDRVIT
PhCHD	GKAIKKVPVVVG	NCTGFAVNR	TFFPYSQGAH	ILVNLGV	DAYRIDAQIT
Leryth_020735-t2	GKTIKKVPVVVG	NCTGFAVNR	TFFPYTQSAL	FLVNLGV	DLFRIDQLIS
Leryth_020735-t1	GKTIKKVPVVVG	NCTGFAVNR	TFFPYTQSAL	FLVNLGV	DLFRIDQLIS

	530	540	550	560	570
	- ----	:-----	-----	-----	-----
Consensus	SFGLPMGPFQLQ	DLSGYGVAIAVG	KEFAXAFPDR	TLKSPLIELMIK	SG
Leryth_018504-t1	NFGLPMGPFQLQ	DVSGYGVAIAVG	KEFASAFPDR	TLSPLIELMIK	SG
PtCHD1	SFGLPMGPYQLQ	DLSGYGVALAVE	KEFANAFPDR	TFSPLIHLLVK	SG
PtCHD2	KFGMPMGPFRLV	DLVGFGVAIATG	TQFVVNFPER	TYKSMLIPLMQ	EDK
PtCHD3	KFGMPMGPFRLA	DLVGFGVAIATG	MQFVENFPER	TYKSMLLPLMQ	EDK
PhCHD	SFGLPMGPLQLQ	DLTGYGVAIVAV	GKEFGSAFSD	RTFKSPLIDLLI	KSG
Leryth_020735-t2	SFGLPMGPFQLQ	DVSGYGVAIAVG	KEFATAFPDR	TLRSPLIELMIK	NG
Leryth_020735-t1	SFGLPMGPFQLQ	DVSGYGVAIAVG	KEFATAFPDR	TLRSPLIELMIK	NG

	580	590	600	610	620
	--- -----	:-----	-----	-----	-----
Consensus	RNGKXNGKGYI	IEKGSKPKPD	PSVQSIIEES	SRRLTNAMP	GGK-----
Leryth_018504-t1	RNGKSNGKGYI	IEKGSKPKPD	PSVQSIIEES	SRRLTNAMV	GGKVRLHP
PtCHD1	RNGKTNGKGYI	IEKGSKPRPD	PSVLPPIIEE	SRRLANIMP	NGK-----
PtCHD2	RAGETTRKGFY	LYDDRRKAKPD	PELRKYIEKA	RNISGVAND	PK-----
PtCHD3	RGETTTCCKGF	LYDDRRKAKPD	PELRKYIEKA	RSISGVAVD	PK-----
PhCHD	RNGKNNGKGFY	IEKGSKPRPD	LSVLPPIIEE	SRRLTNIMP	GGK-----
Leryth_020735-t2	RNGKSNGKGYI	IEKGSKPKPD	LSVQSIIEE	SRRLTNAMP	GGK-----
Leryth_020735-t1	RNGKSNGKGYI	IEKGSKPKPD	LSVQSIIEE	SRRLTNAMP	GGK-----

	630	640	650	660	670
	:-----	-----	-----	-----	-----
Consensus	-----	PIXVSDQEIV	EMILFPVVNEA		
Leryth_018504-t1	PHMNSLCYTSWY	KFHETNNTFTF	QWLQPIVISD	QEVVEMILFP	VVNEA
PtCHD1	-----	-----	PINITDKEIV	EMVLFPPVNEA	
PtCHD2	-----	-----	LAKLPEKDIV	EMIFFPPVNEA	
PtCHD3	-----	-----	LAKLPEKDIV	EMIFFPPVNEA	
PhCHD	-----	-----	PISVTDQEIV	EMILFPVVNEA	
Leryth_020735-t2	-----	-----	PIAVSDQEVV	DMILFPVVNEA	
Leryth_020735-t1	-----	-----	PIAVSDQEVV	DMILFPVVNEA	

	680	690	700	710	720
	--:-----	-----	-----	-----	-----
Consensus	CRVMDEGIVVRAS	DLDVASVLGMG	FPSYRGGIVF	WADLVGAXHIY	XSLS
Leryth_018504-t1	CRVMDEGIVIRAS	DLDVASVLGMG	FPSYR-----	-----	L
PtCHD1	CRVLDEGVVVRAS	DLDTASVLGMS	FPSYRGGIVF	WADLVGPKHVD	SL
PtCHD2	CRVFAEGIAVKA	ADLDISSLMGMG	FPPYRGGIMF	WADSLGSKYIY	SRL
PtCHD3	CRVFAEGIAVKA	ADLDIASLMGMG	FPPYRGGIMF	WADSFGSKYIY	SRL
PhCHD	CRVLDEGIVVRAS	DLDVASVLGMS	FPSYRGGIVF	WADTVGAGHIY	KSL
Leryth_020735-t2	CRVMDEGIVIRAS	DLDVASVLGMG	FPSYRGGIVF	WADLVGAGHIY	ESL
Leryth_020735-t1	CRVMDEGIVIRAS	DLDVASVLGMG	FPSYRGGIVF	WADLVGAGHIY	ESL

	730	740	750	760
	-----:-----	-----	-----	-----
Consensus	KKWSEVYGDFYK	PSRFLEERATX	GIPLSAPASXS	SSXSRL-SRL
Leryth_018504-t1	KKWSEVYGDFYK	PSRFLEQRAA	AGIPLSAPASS	SSSSSSRS-SRL
PtCHD1	KKWSQRFGDFYK	PSKFLEERAT	TGGIPLSAPASS	SSSGSR-SRM
PtCHD2	EEWSKTYGEFFK	PCAFLAERA	AKGAPLSSPVD	QAK----SRL
PtCHD3	EEWSKTYGEFFE	PCAFLAERGA	KGAPLSSPVEQ	AK----SRL
PhCHD	TKWSELYGNFFK	PSRFLEERAT	KGIALSAPATAS	SASR-SRM
Leryth_020735-t2	KKWSEVYGDFYK	PSRFLEQRAT	AGIPLSAPTST	SSSSRS-SRL

Leryth_020735-t1 KKWSEVYGDFYKPSRFLEQRATAGIPLLSKIFS-----

Supplemental Figure S4. Amino acid sequence comparison of putative *L. officinale* cinnamoyl-CoA hydratase (CHD; Leryth_018504, and Leryth_020735) gene recovered in our coexpression network with gene annotated as CHD in the genome and the characterized CHD genes from *Petunia hybrida* (PhCHD) and *Poplar trichocarpa* (PtCHD1, PtCHD2 and PtCHD3). The amino acid alignments were computed using the MUSCLE algorithm implemented in Geneious. The pink highlighted sequence is the peroxisomal targeting sequence I (PTS I), predicted by PSORT (<https://www.psort.org/>). The predictive hydratase and dehydrogenase domains are highlighted by yellow and green colours, respectively. These domains were predicted by ProSite (<https://prosite.expasy.org/scanprosite/>).

	10	20	30	40
	----	----	----	----
Consensus	MYMLMEKA-----	IX	RQRVLLZHL	RPSX
Leryth_003297-t2	----MEKA-----	IN	RQRVLLGHL	QPSS
Leryth_016775-t1	MYMLHKKCYGLSPIIGHNYNLDVIGPVIDVGILVKRVKAMVEFAKDPS			
Leryth_002701-t1	----MEKA-----	IQ	RQRVLLQHL	RPS-
Leryth_002701-t3	----MEKA-----	IQ	RQRVLLQHL	RPS-
Leryth_002701-t2	----MEKA-----	IQ	RQRVLLQHL	RPS-
Leryth_016775-t2	----MEKA-----	IE	RQRVLLHHL	KPCH
Leryth_016775-t3	----MEKA-----	IE	RQRVLLHHL	KPCH
PtKAT2	----MEKA-----	IN	RQRVLLLEHL	RPSS
PtKAT3	----MEKA-----	SN	RQRVLLGHL	RRSS
PtKAT1	----MEKA-----	FN	RQKVLLLAHL	QPT-
PhKAT1	----MEKA-----	IQ	RQRVLLLEHL	QPIR

	50	60	70	80	90
	- -----	----	----	----	----
Consensus	-----LNNM----	DSNLSASVCAAGDSAS	YQRTSVYGDDVVIVA	AAYRSPL	
Leryth_003297-t2	SDD-HQNY---	ISNVSPSICLAEGG---	KLKAPSGDDVVIVA	AAYRTPL	
Leryth_016775-t1	STIHEKELLGKENQFASVCAAGDSAS	YQRTSVYGDDVVIVA	AAYRSPL		
Leryth_002701-t1	-----LNNM----	DSNLSASVCAAGDSAS	YQRTSVYGDDVVIVA	AAYRSPL	
Leryth_002701-t3	-----LNNM----	DSNLSASVCAAGDSAS	YQRTSVYGDDVVIVA	AAYRSPL	
Leryth_002701-t2	-----LNNM----	DSNLSASVCAAGDSAS	YQRTSVYGDDVVIVA	AAYRSPL	
Leryth_016775-t2	TSSPLENI---	DSSLASVCAAGDSAS	YQRTSVYGDDVVIVA	AAYRSPL	
Leryth_016775-t3	TSSPLENI---	DSSLASVCAAGDSAS	YQRTSVYGDDVVIVA	AAYRSPL	
PtKAT2	----SHNF----	ESTLSASACLAGDSA	AYQRTSAYGDDVVIVA	AAYRTPQ	
PtKAT3	S---YNNH---	ESSLSASACLAGGS-----	AACGDDVVVVA	AAYRTPL	
PtKAT1	-----SP---	SPLLSASICAAGDSA	AYHRTAAFGDDIVIVA	AAYRTAI	
PhKAT1	HH--THDH---	SSSLTTSICAAGDSA	AYQRTAAFGDDVVIVA	AAYRTAI	

	100	110	120	130	140
	--- -----	----	----	----	----
Consensus	CKAKRGGLKDTYXDDL	LAPVLRALIEKTNLDPSE	VGDIVVGSVLAPGS		
Leryth_003297-t2	CKAKRGGFKDTHPDDL	LA AVLKALIDKTHVKPTE	VGDIVVGSVLAPGS		
Leryth_016775-t1	CKAKRGGLKDTYPDDL	LAPVLRALIEKTNVDPSE	IGDIVVGSVLAAGS		
Leryth_002701-t1	CKAKRGGLKDTYADDLL	LAPVLRALIEKTNLDPSE	VGDIIVGSVLAPGS		
Leryth_002701-t3	CKAKRGGLKDTYADDLL	LAPVLRALIEKTNLDPSE	VGDIIVGSVLAPGS		
Leryth_002701-t2	CKAKRGGLKDTYADDLL	LAPVLRALIEKTNLDPSE	VGDIIVGSVLAPGS		
Leryth_016775-t2	CKAKRGGLKDTYPDDL	LAPVLRALIEKTNVDPSE	IGDIVVGSVLAAGS		
Leryth_016775-t3	CKAKRGGLKDTYPDDL	LAPVLRALIEKTNVDPSE	IGDIVVGSVLAAGS		
PtKAT2	CKSKRGGFKDTHADDLL	LAPVLRALIEKTNLDPRE	VGDIVVGSVLAPGS		
PtKAT3	CKSKRGGFKDTHADDLL	LAPVLRALIEKTNLDARE	VGDIIVGSSLAPGS		
PtKAT1	CKARRGGFKDTFPDDL	LGFVLKAVVEKTNVNPSE	VGDIIVGTVLAPGS		
PhKAT1	CKSKRGGFKDTLSDDL	LAPVLRALIEKTNLDPKE	VGDIIVGTVLAPGS		

	150	160	170	180	190
	:-----	----	----	----	----
Consensus	QRASECRMAAFYAGFPETVPVRT	VNRQCSSGLQAVADVAAS	IKAGFYD		
Leryth_003297-t2	LRAIEFRMGQFYAGFPATVP	IRT VNRQCSSGLQAVADVAAY	IKAGYYD		
Leryth_016775-t1	QRASECRMAAFYAGFPDTPVP	VRT VNRQCSSGLQAVADVAAS	IKAGFYD		
Leryth_002701-t1	QRASECRMAAFYAGFPETVP	VRT VNRQCSSGLQAVADVAAA	IRAGFYD		
Leryth_002701-t3	QRASECRMAAFYAGFPETVP	VRT VNRQCSSGLQAVADVAAA	IRAGFYD		
Leryth_002701-t2	QRASECRMAAFYAGFPETVP	VRT VNRQCSSGLQAVADVAAA	IRAGFYD		
Leryth_016775-t2	QRASECRMAAFYAGFPDTPVP	VRT VNRQCSSGLQAVADVAAS	IKAGFYD		
Leryth_016775-t3	QRASECRMAAFYAGFPDTPVP	VRT VNRQCSSGLQAVADVAAS	IKAGFYD		
PtKAT2	QRASECRMAAFYAGFPETVP	IRT VNRQCSSGLQAVADVAAS	IKAGFYE		
PtKAT3	QRASECRMAALYAGFPETVP	IRT VNRKCSSGLQAVADVAAS	IKAGFYE		
PtKAT1	ERAIECRMAAFYAGFPDTPV	PLRT VNRQCSSGLQAVADVAAS	IKAGYYD		

PhKAT1	IRAMECRMAAFYAGFPETVP	IR	VR	QC	SS	GL	Q	AV	AD	VA	AS	I	KAGFYD
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		200	210	220	230	240
	--:----	-----	:-----	-----	:-----	-----
Consensus	IGIGAGLESMTXNPM	AWEGSVNPRVK	SMAQAQDC	LLPMGITSEN	VAHR	
Leryth_003297-t2	IGIGAGVECMSIDT	ISNISNP	NPKAQSF	PQAQDC	LLPMGVTS	ENVAQR
Leryth_016775-t1	IGIGAGLESMTTNP	MAWEGSVNPRVK	SMAQAQDC	LLPMGITSEN	VAHR	
Leryth_002701-t1	IGIGAGLESMTANP	MAWEGSVNPRVK	SMAQAQDC	LLPMGITSEN	VAHR	
Leryth_002701-t3	IGIGAGLESMTANP	MAWEGSVNPRVK	SMAQAQDC	LLPMGITSEN	VAHR	
Leryth_002701-t2	IGIGAGLESMTANP	MAWEGSVNPRVK	SMAQAQDC	LLPMGITSEN	VAHR	
Leryth_016775-t2	IGIGAGLESMTTNP	MAWEGSVNPRVK	SMAQAQDC	LLPMGITSEN	VAHR	
Leryth_016775-t3	IGIGAGLESMTTNP	MAWEGSVNPRVK	SMAQAQDC	LLPMGITSEN	VAHR	
PtKAT2	IGIGAGLESMTINQ	MSWDGVDNPK	LKNFQKAQ	DC	LLPMGITSEN	VAHR
PtKAT3	IGIGAGLESMTVNS	RAWVGVDNPK	VKRFQEAQ	DC	LLPMGVTS	ENVAHR
PtKAT1	IGIAAGLECMTVNG	IRSVQVNPR	VEAFQQAR	DC	LLPMGLTS	ENVAQR
PhKAT1	IGIGAGLELMTVDN	IGRVQQRNT	TKVDTFAQ	AR	DC	LLPMGITSEN

		250	260	270	280
	-----	:-----	-----	:-----	-----
Consensus	FGVSRQEQDQAAV	NSHRKAAA	ATASGKFK	DEIIPVNT	KIVDPKTG
Leryth_003297-t2	YGVTREEQDQAAV	ISHKRAAA	ASASGKF	IDEIIPV	STKIVDPK
Leryth_016775-t1	FGVSRQEQDQAAV	NSHRKAAA	ATASGKFK	DEIIPVNT	KIVDPKTG
Leryth_002701-t1	FGVSRQEQDQAAV	NSHRKAAA	ATASGKFK	DEIIPVNT	KIVDPKTG
Leryth_002701-t3	FGVSRQEQDQAAV	NSHRKAAA	ATASGKFK	DEIIPVNT	KIVDPKTG
Leryth_002701-t2	FGVSRQEQDQAAV	C-----			
Leryth_016775-t2	FGVSRQEQDQAAV	NSHRKAAA	ATASGKFK	DEIIPVNT	KIVDPKTG
Leryth_016775-t3	FGVSRQEQDQAAV	NSHRKAAA	ATASGKFK	DEIIPVNT	KIVDPKTG
PtKAT2	FGVSRQEQDQAAV	DSHRKAAA	ATASGRFK	DEIIPVAT	KIVDPKTG
PtKAT3	FSVTRQEQDQAAV	DSHRKAAA	ATASGRFK	DEIIPVAT	KIADPKTG
PtKAT1	YGVTRQDQDQAAV	DSHRKAAA	ARASGKFK	DEIIPVTT	KIVDPETGI
PhKAT1	FGVTRLEQDQAAV	NSHQRAAA	ATASGKFK	DEIIPVLT	KIVDPQTG

		290	300	310	320	330
	- -----	:-----	-----	:-----	-----	:-----
Consensus	PVTISVDDGIRPN	ASVADLAKL	KPVFKKD	GTTTAGN	SSQVSDG	AGAVL
Leryth_003297-t2	PVIIAADDGIRP	TTNLADLAKL	KPAFSKNG	TTTAGN	ASQVTDG	AGGVL
Leryth_016775-t1	PVTISIDDGIRPN	ATVSDLAKL	KPVFKKD	GTTTAGN	SSQVSDG	AGAVL
Leryth_002701-t1	PVTISVDDGIRPN	ASVADLAKL	KPVFKKD	GTTTAGN	SSQVSDG	AGAVL
Leryth_002701-t3	PVTISVDDGIRPN	ASVADLAKL	KPVFKKD	GTTTAGN	SSQVSDG	AGAVL
Leryth_002701-t2	-----					
Leryth_016775-t2	PVTISIDDGIRPN	ATVSDLAKL	KPVFKKD	GTTTAGN	SSQVSDG	AGAVL
Leryth_016775-t3	PVTISIDDGIRPN	ATVSDLAKL	KPVFKKD	GTTTAGN	SSQVSDG	AGAVL
PtKAT2	PIVVSVDGIRP	ETSVAGLGK	LKTVF	FKKD	GTTTAGN	SSQISD
PtKAT3	PIIVSVDDGIRP	NTSLADLGK	LKAVFRK	DGTTTAGN	SSQISD	GAAVL
PtKAT1	VITISEDGIRP	NSNLAE	LSRLKPA	FKKD	GSTTAGN	ASQVSD
PhKAT1	PVVISVDDGIRP	NTNLTSLGK	LKPAFKND	GTTTAGN	ASQVSD	GAAVL

		340	350	360	370	380
	---	-----	:-----	-----	:-----	-----
Consensus	LMKR	SVAMKKGLPXL	GVFRTFA	AVGVDP	AIMGVGP	AVAI
Leryth_003297-t2	LMKR	SVAIKKGLPIL	GVWRSFE	AVGV	EPGVMGIG	PAVAI
Leryth_016775-t1	LMKR	SVAMKKGLPVL	GVFRTFA	AVGVDP	AIMGVGP	AVAI
Leryth_002701-t1	LMKR	SVAMQKGLPVL	GVFR-----			
Leryth_002701-t3	LMKR	SVAMQKGLPVL	GVFR-----			
Leryth_002701-t2	-----					
Leryth_016775-t2	LMKR	SVAMKKGLPVL	GVFRTFA	AVGVDP	AIMGVGP	AVAI
Leryth_016775-t3	LMKR	SVAMKKGLPVL	GVFRTFA	AVGVDP	AIMGVGP	AVAI
PtKAT2	LMKR	SVAVQKGLPIL	GVFRTFA	AVGVDP	AIMGVGP	AVAI

PtKAT3	LMKRSVAMRKGLPILGVFRTFVVVGVDPAIMGVGPAAVAIPAAVKAAGL
PtKAT1	LMKRSLAAQKGLPILGVFRSFAAVGVDPAVMGVGPAAAIIPAAVQAAGL
PhKAT1	LMKRSVAMKKGLPILGVFRSFAAVGVDPAVMGIGPAVAIPPAVKLSAGL

	390	400	410	420	430
	:--- ---	:--- ---	:--- ---	:--- ---	:--- ---
Consensus	ELEDIDLFEINEAFASQFVYCQKKLELDPEK	INVNGGAMAIGHPLGAT			
Leryth_003297-t2	ELDDISLFEINEAFASQYVYCCKKLNLDPER	VNVNGGAMALGHPLGAT			
Leryth_016775-t1	ELEDIDLFEINEAFASQFVYCQKKLELDPEK	INVNGGAMAIGHPLGAT			
Leryth_002701-t1	-----	-----			
Leryth_002701-t3	-----	-----			
Leryth_002701-t2	-----	-----			
Leryth_016775-t2	ELEDIDLFEINEAFASQFVYCQKKLELDPEK	INVNGGAMAIGHPLGAT			
Leryth_016775-t3	ELEDIDLFEINEVI-----	-----			
PtKAT2	ELEDIDLFEINEAFASQFVYCRKKLELDPQK	INVNGGAMAIGHPLGAT			
PtKAT3	ELEDIDLFEINEAFASQFVYCCKKLELDLQK	INVNGGAIAIGHPLGTT			
PtKAT1	ELNDIDLFEINEAFASQYVYCIKKLELDPEK	VNVNGGAIALGHPLGAT			
PhKAT1	DLDDIDLFEINEAFASQFVYCQKKLNLDPEK	VNVNGGAMALGHPLGAT			

	440	450	460	470	480
	--:--- ---	:--- ---	:--- ---	:--- ---	:--- ---
Consensus	GARCVATLLHEMKRRGXDCRF	GVXSMCIGXGMGAA	AVFERGDGCDEL	C	
Leryth_003297-t2	GARCVATLLHEMKRRGKDCRF	GVISMCIGSGMGAA	AVFERGDF	-----	
Leryth_016775-t1	GARCVATLLHEMKRRGRDCRF	GVVSMCIGTGMGAA	AVFERGDS	CDEL	R
Leryth_002701-t1	-----	-----			
Leryth_002701-t3	-----	-----			
Leryth_002701-t2	-----	-----			
Leryth_016775-t2	GN-----	-----			
Leryth_016775-t3	-----	-----			
PtKAT2	GARCVATLLHEMKRRGRDCRF	GVVSMCIGTGMGAA	AVFERGDGCDEL	C	
PtKAT3	GARCVATILHEMKRRGRDCRF	GVVSMCIGTGMGAA	AVFERGDGCDEL	C	
PtKAT1	GARCVGTLLNEMKRRGKDSRF	GVISMCIGSGMGAA	AVFERGDCV	DALC	
PhKAT1	GARCVATLLHEMKRRGKDCRF	GVISMCIGSGMGAA	AVFERGDAV	DDLC	

	490
	-----:--- -----:---
Consensus	N-ARKVESNNLLSKDAR
Leryth_003297-t2	-----
Leryth_016775-t1	N-ARKIDVNNQLSKDAR
Leryth_002701-t1	-----
Leryth_002701-t3	-----
Leryth_002701-t2	-----
Leryth_016775-t2	-----
Leryth_016775-t3	-----
PtKAT2	NGGRKVESNNLLSRDSR
PtKAT3	N-ARKVESNNLLSKDSR
PtKAT1	N-VRKVGSDLLSKDAR
PhKAT1	N-ARVSNNSFLSKDAK

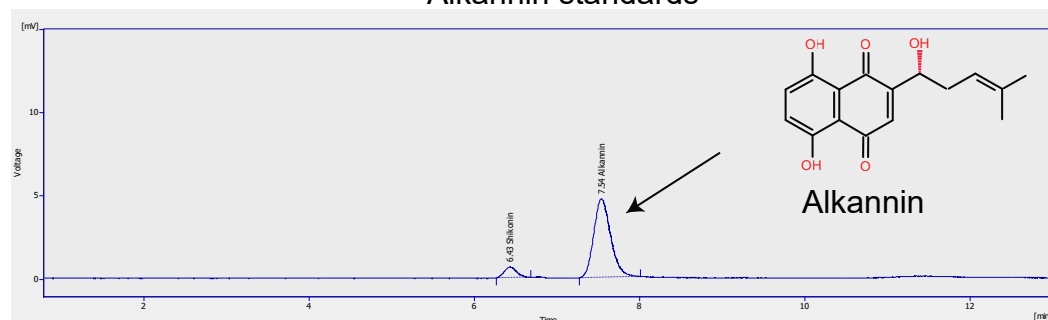
Supplemental Figure S5. Amino acid sequence comparison of putative *L. officinale* 3-ketoacyl-CoA thiolase (KAT: Leryth_003297) gene recovered in our coexpression network, with genes annotated as KAT in the genome and the characterized KAT genes from *Petunia hybrida* (PhKAT1) and *Poplar trichocarpa* (PtKAT1, PtKAT2 and PtKAT3). The amino acid alignments were computed using the MUSCLE algorithm implemented in Geneious. The pink highlighted sequence is the peroxisomal

targeting sequence I (PTS I), predicted by PSORT (<https://www.psort.org/>). The putative regions involved in thiolase activity are highlighted by yellow colours. These domains were predicted by ProSite (<https://prosite.expasy.org/scanprosite/>).

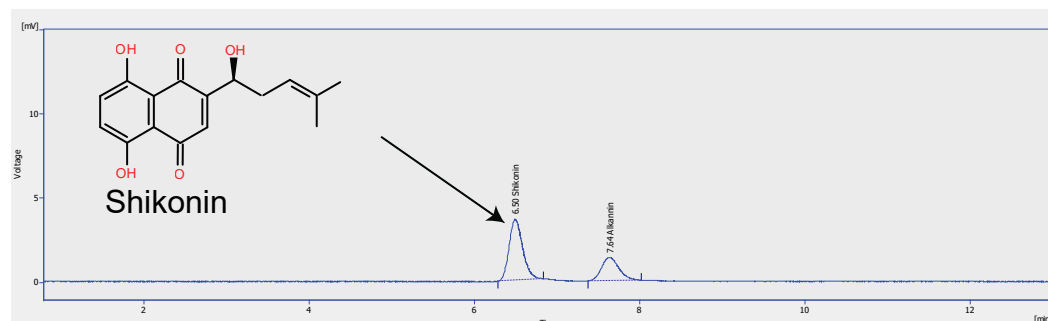
	10	20	30	40
	-----:----- -----:----- -----:----- -----:----- -----:-----			
Consensus	MDX-----XXX-ASSKTXIIDXPLHXLGFEFDELSPTXXXGRLXX			
PhTE1	MKP-----PPLSSSAAGIKIREIDIPLHEIGFEYVEITPHKISGRHLH			
AtDNAT2	MDP-----KSPEFIIDQPLKILGFVDFELSATRVSGHLTL			
Leryth_026039-t1	MDSTRKPEAQSSSSSSSNKTQILDSPLHTLGFEIEELSSNKVTGKLIV			
AtDNAT1	MDS-----ASSNTKAIDPPLHMLGFEFDELSPTTRITGRLPV			
	50	60	70	80
	- -----:----- -----:----- -----:----- -----:----- -----:-----			
Consensus	TEKCCQPFKVLHGGVSALIAESLASMGAHIASGFKRVAGIHLISIXHLK			
PhTE1	TERCCQPFKVLHGGISALIAESLASMGAHIASGFTRVAGVHLSIHHLK			
AtDNAT2	TEKCCQPFKVLHGGVSALIAEALASLGAGIASGFKRVAGIHLISIHHLR			
Leryth_026039-t1	NEKCLQPFRVLHGGVSAVIAEGLASMGAHIASGWRRVAGIHLISINHIK			
AtDNAT1	SPVCCQPFKVLHGGVSALIAESLASMGAHMASGFKRVAGIQLSINHLK			
	100	110	120	130
	--- -----:----- -----:----- -----:----- -----:----- -----:-----			
Consensus	SAXLGDLVFAEATPVSVGKTIQVWEVRLWKXTKXEEEX-NKIXISSSRV			
PhTE1	SAQLGDLVIAEAAAPVNVGQSIQVWEVCLWKIYESNEEEKKTLIASSRV			
AtDNAT2	PAALGEIVFAESFPVSVGKNIQVWEVRLWKAKKTETPDNKIMVSTSRV			
Leryth_026039-t1	SATLGDLVFAEATPVSVGKTIQIWEVRLWKVTKEEE---KSMISSSRV			
AtDNAT1	SADLGDLVFAEATPVSTGKTIQVWEVKLWKTTQKDKA-NKILISSSRV			
	150	160	170	
	:----- -----:----- -----:-----			
Consensus	TLXCNLXPDPNAKDAAAXLKKX-AKL			
PhTE1	TLKTNMFVPENAKDAAVVLKKY-AKL			
AtDNAT2	TLFCGLPIPDHVKDAPDELKKVI-SKL			
Leryth_026039-t1	TLLCNLPVPQDS-DAAPNLRKY-AKL			
AtDNAT1	TLICNLPIPDNAKDAANMLKMOV-AKL			

Supplemental Figure S6. Amino acid sequence comparison of putative *L. officinale* thioesterase (TE: Leryth_026039) gene recovered in our coexpression network with the characterised TE genes from *Petunia hybrida* (PhTE1) and *Arabidopsis thaliana* (AtDNAT1 and AtDNAT2). The amino acid alignment was computed using the MUSCLE algorithm implemented in Geneious. The pink highlighted sequence is the peroxisomal targeting sequence I (PTS I), needed for peroxisomal localization.

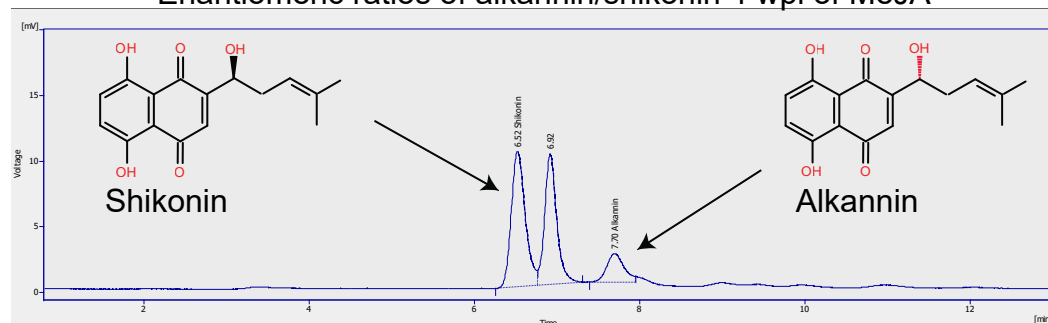
A Alkannin standards



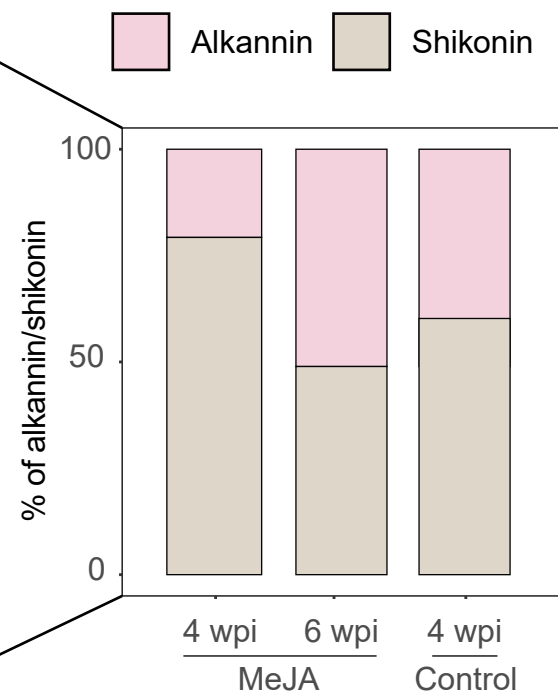
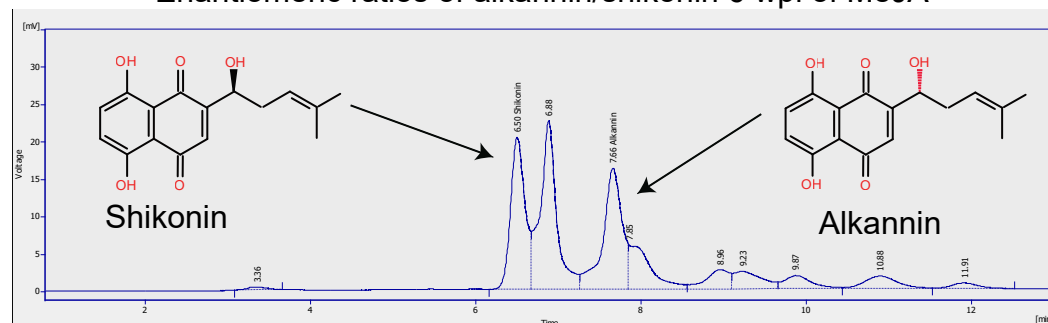
B Shikonin standards



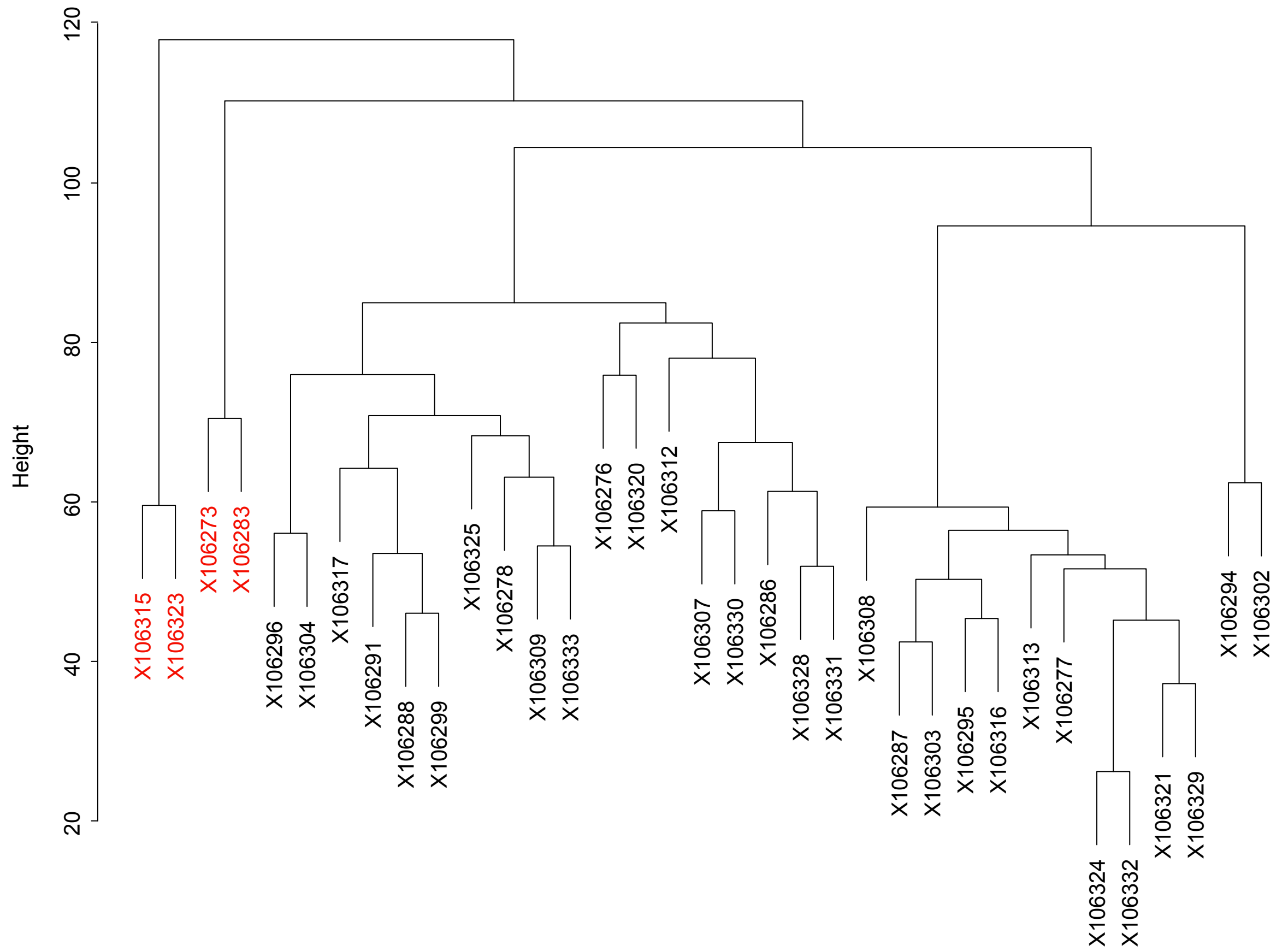
C Enantiomeric ratios of alkannin/shikonin 4 wpi of MeJA



D Enantiomeric ratios of alkannin/shikonin 6 wpi of MeJA



Supplemental Figure S7. Enantiomeric ratios of alkannin/shikonin (A/S) in MeJA treated plants of *L. officinale*. HPLC chromatogram of A) alkannin standards B) shikonin standards C) enantiomeric ratios of alkannin/shikonin at 4 wpi and D) 6 wpi. The inset stacked bar graphs represent percentage composition of alkannin:shikonin in plants of MeJA treatment.



Supplemental Figure S8. Clustering of samples to detect outliers. Samples highlighted in red were removed before coexpression analysis.