

Supplemental Figure 1. UV/Vis Spectra of Colorless Chl Catabolites Identified in this Study

(A) On-line UV/Vis spectra of five At-NDCCs observed in senescent leaves of Arabidopsis.

(B) On-line UV/Vis spectra of the five *At*-NCCs observed in senescent leaves of the Arabidopsis *cyp89a9-1* mutant.

(C) On-line UV/Vis spectra of FDCCs observed as products of the assay with recombinant CYP89A9/ATR1 and using *epi-p*FCC as substrate.

(D) On-line UV/Vis spectra of the *epi-p*NDCCs produced *in vitro* by isomerization of *epi-p*FDCCs at pH 5 (see text for further details).



Supplemental Figure 2. Analysis of Gene Expression in *cyp89a9* and *cyp71b19* Mutants and Colorless Chl Catabolites of *cyp71b19* Mutants.

(A) Gene structures of CYP89A9 and CYP71B19 showing the T-DNA insertion sites of the different mutants studied in this work.

(B) Analysis of gene expression during dark-induced senescence in *cyp89a9-1*, *cyp89a9-2*, *cyp71b19-1* and *cyp71b19-2*. Levels of *ACTIN2* (*ACT2*) gene expression were used as control. Expression was analyzed with nonsaturating numbers of PCR cycles as shown at the right. PCR products were separated on agarose gels and visualized with ethidium bromide.

(C) Colorless catabolites of dark-incubated (8 d) leaves of Col-0 and *cyp71b19* mutants were separated by HPLC. A_{254} is shown. For clarity, only the relevant part of the HPLC traces is shown.



Supplemental Figure 3. Analysis of the *cyp89a9-2* Mutant in the Ler Background, a Natural *mes16* Mutant.

Colorless catabolites accumulating in dark-incubated (8 d) leaves of Ler, *mes16-1, cyp89a9-2* and *mes16-1cyp89a9-1* were separated by HPLC. A_{254} is shown. For clarity, only the relevant part of the HPLC traces is shown. Note that because of the absence of MES16, catabolite patterns are different from patterns in Col-0 (Christ et al., 2012). The catabolites in this figure were solely identified by their respective spectra.

Supplemental Data. Christ et al. (2013). Plant Cell 10.1105/tpc.113.112151



Supplemental Figure 4. Colorless Catabolites Accumulating in Dark-Incubated (8 d) Leaves of Col-0, *cyp89a9-1* and Col-0/PPH_{TP}-MES16.

Colorless catabolites were separated by HPLC. $\rm A_{_{254}}$ is shown. For clarity, only the relevant part of the traces is shown.

Supplemental Table 1. Search for Co-Expressed Genes in Senescent Leaves, Cauline Leaves, Petals and Sepals. Expression analysis was performed using the Genes Search Tool "Anatomy" of Genevestigator (Zimmermann et al., 2004). For reference, see main paper.

ARRAY ELEMENT	LOCUS IDENTIFIER	ANNOTATION ^a	SCORE K ^b
259766_at	At1g64360	unknown protein; Has 6 Blast hits to 6 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 6; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	0.55
264261_at	At1g09240	ATNAS3_NAS3nicotianamine synthase 3	0.48
254189_at	At4g24000	ATCSLG2_CSLG2_cellulose synthase like G2	0.44
254574_at	At4g19430	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	
264899_at	At1g23130	Polyketide cyclase/dehydrase and lipid transport superfamily protein	0.4
266292_at	At2g29350	SAG13senescence-associated gene 13	0.37
259058_at	At3g03470	CYP89A9cytochrome P450, family 87, subfamily A, polypeptide 9	
254174_at	At4g24120	ATYSL1_YSL1YELLOW STRIPE like 1	0.32
256300_at	At1g69490	ANAC029_ATNAP_NAPNAC-like, activated by AP3/PI	0.3
254564_at	At4g19170	CCD4_NCED4nine-cis-epoxycarotenoid dioxygenase 4	0.3
249850_at	At5g23240	DNAJ heat shock N-terminal domain-containing protein	0.29
255630_at	At4g00700	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein	0.28
255626_at	At4g00780	TRAF-like family protein	
265913_at	At2g25625	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: LP.06 six leaves visible, LP.04 four leaves visible, 4 anthesis, petal differentiation and expansion stage; Has 24 Blast hits to 24 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 24; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	0.27
254153_at	At4g24450	ATGWD2_GWD3_PWDphosphoglucan, water dikinase	0.26
250435_at	At5g10380	ATRING1_RING1RING/U-box superfamily protein	0.26
249996_at	At5g18600	Thioredoxin superfamily protein	0.26
249454_at	At5g39520	Protein of unknown function (DUF1997)	0.26
262281_at	At1g68570	Major facilitator superfamily protein	
266078_at	At2g40670	ARR16_RR16_response regulator 16	
250259_at	At5g13800	CRN1_PPHpheophytinase	0.24
259765_at	At1g64370	unknown protein; Has 773 Blast hits to 375 proteins in 118 species: Archae - 0; Bacteria - 97; Metazoa - 421; Fungi - 108; Plants - 31; Viruses - 0; Other Eukaryotes - 116 (source: NCBI BLink).	0.23
∠J4JUJ_dl	AL4822200	AKIZ_AKIZ/S_AKIS_KIZ/SPOLASSIUIII (TAIISPOTE 2/3	0.25

247800_at	At5g58570	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes -	0.23
		2996 (source: NCBI BLink).	
258925_at	At3g10420	SPD1_P-loop containing nucleoside triphosphate hydrolases	0.22
245205 -+	4+4-14020	superfamily protein	0.22
245385_at	At4g14020	Rapid alkalinization factor (RALF) family protein	0.22
253382_at	At4g33040	Inioredoxin superfamily protein	0.22
260155_at	At1g52870	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family	
260410 at	At1g69870	NRT1.7 nitrate transporter 1.7	0.21
246302 at	At3g51860	ATCAX3 ATHCX1 CAX1-LIKE CAX3 cation exchanger 3	0.21
250054 at	At5g17860	CAX7 calcium exchanger 7	0.21
256497_at	Δt1g31580	CXC750 ECS1	0.21
251360_at	At3g61210	S-adenosyl-L-methionine-dependent methyltransferases	0.2
231300_at	AUSGOIZIO	superfamily protein	0.2
245346 at	At4g17090	BAM3 BMY8 CT-BMY chloroplast beta-amylase	0.2
	At4g25000	AMY1 ATAMY1 alpha-amylase-like	0.2
	At5g06530	ABCG22 AtABCG22 ABC-2 type transporter family protein	0.2
	At1g23090	AST91 SULTR3:3 sulfate transporter 91	0.19
266572 at	At2g23840	HNH endonuclease	0.19
259129 at	At3g02150	PTF1 TCP13 TFPD plastid transcription factor 1	0.19
254299 at	At4g22920	ATNYE1 NYE1 non-vellowing 1	0.19
250446 at	At5g10770	Eukarvotic aspartyl protease family protein	0.19
245901 at	At5g11060	KNAT4 KNOTTED1-like homeobox gene 4	0.19
248566 s at	At5g49730	ATERO6 FRO6 FRO6 ferric reduction oxidase 6	0.19
	At5g49740		
248153_at	At5g54250	ATCNGC4_CNGC4_DND2_HLM1cyclic nucleotide-gated	0.19
		cation channel 4	
260007_at	At1g67870	glycine-rich protein	0.18
262232_at	At1g68600	Aluminium activated malate transporter family protein	0.18
266938_at	At2g18950	ATHPT_HPT1_TPT1_VTE2homogentisate phytyltransferase 1	0.18
266291_at	At2g29320	NAD(P)-binding Rossmann-fold superfamily protein	0.18
255795_at	At2g33380	AtCLO3 CLO-3 CLO3 RD20 Caleosin-related family protein	
267076_at	At2g41090	Calcium-binding EF-hand family protein	
263497_at	At2g42540	COR15 COR15A cold-regulated 15a	
257634_s_at	At3g26170	CYP71B19cytochrome P450, family 71, subfamily B,	0.18
	At3g26180	polypeptide 19	
254833_s_at	At4g12280	copper amine oxidase family protein	0.18
	At4g12290		
253779_at	At4g28490	HAE_RLK5Leucine-rich receptor-like protein kinase family protein	0.18
249797_at	At5g23750	Remorin family protein	
262626_at	At1g06430	FTSH8FTSH protease 8	
259943_at	At1g71480	Nuclear transport factor 2 (NTF2) family protein	
260774_at	At1g78290	SNRK2-8_SNRK2.8_SRK2CProtein kinase superfamily 0.	
257222 -+	A+2 ~27025	protein Degl DECD1 DegD protecto 1	0 17
777777 AT	AL382/925	Degt_Deget_Dege blorease t	0.17

252648_at	At3g44630	Disease resistance protein (TIR-NBS-LRR class) family	0.17	
246335_at	At3g44880	ACD1_LLS1_PAOPheophorbide a oxygenase family protein 0.17		
		with Rieske [2Fe-2S] domain		
252485_at	At3g46530	RPP13NB-ARC domain-containing disease resistance protein	0.17	
252462_at	At3g47250	Plant protein of unknown function (DUF247) 0.17		
254764_at	At4g13250	NYC1NAD(P)-binding Rossmann-fold superfamily protein	0.17	
253358_at	At4g32940	GAMMA-VPE_GAMMAVPEgamma vacuolar processing enzyme	0.17	
249754_at	At5g24530	DMR62-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	0.17	
247356_at	At5g63800	BGAL6_MUM2Glycosyl hydrolase family 35 protein	0.17	
261077_at	At1g07430	HAI2highly ABA-induced PP2C gene 2	0.16	
259661_at	At1g55265	Protein of unknown function, DUF538	0.16	
262875_at	At1g64970	G-TMT_TMT1_VTE4gamma-tocopherol methyltransferase	0.16	
261120_at	At1g75410	BLH3BEL1-like homeodomain 3	0.16	
267336_at	At2g19310	HSP20-like chaperones superfamily protein	0.16	
266673_at	At2g29630	PY_THICthiaminC	0.16	
263478_at	At2g31880	EVR_SOBIR1Leucine-rich repeat protein kinase family protein	0.16	
263956_at	At2g35940	BLH1_EDA29BEL1-like homeodomain 1	0.16	
258223_at	At3g15840	PIFIpost-illumination chlorophyll fluorescence increase	0.16	
258181_at	At3g21670	Major facilitator superfamily protein	0.16	
256766_at	At3g22231	PCC1pathogen and circadian controlled 1	0.16	
256754_at	At3g25690	AtCHUP1_CHUP1 Hydroxyproline-rich glycoprotein family	0.16	
_	_	protein		
257611_at	At3g26580	Tetratricopeptide repeat (TPR)-like superfamily protein	0.16	
251218_at	At3g62410	CP12-2CP12 domain-containing protein 2		
251221_at	At3g62550	Adenine nucleotide alpha hydrolases-like superfamily protein	0.16	
254551_at	At4g19840	ATPP2-A1_ATPP2A-1_PP2-A1phloem protein 2-A1 (
247304_at	At5g63850	AAP4amino acid permease 4		
247025_at	At5g67030	ABA1_ATABA1_ATZEP_IBS3_LOS6_NPQ2_ZEPzeaxanthin 0.16 epoxidase (ZEP) (ABA1)		
261569_at	At1g01060	LHY_LHY1Homeodomain-like superfamily protein	0.15	
261581_at	At1g01140	CIPK9_PKS6_SnRK3.12CBL-interacting protein kinase 9		
261084_at	At1g07440	NAD(P)-binding Rossmann-fold superfamily protein		
255957_at	At1g22160	Protein of unknown function (DUF581)		
262916_at	At1g59700	ATGSTU16_GSTU16glutathione S-transferase TAU 16		
260012_at	At1g67865	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G67860.1); Has 13 Blast hits to 13 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 13; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	0.15	
267115_s_at	At2g32530 At2g32540	ATCSLB03_ATCSLB3_CSLB03cellulose synthase-like B3	0.15	
256997_at	At3g14067	Subtilase family protein 0.15		
257965_at	At3g19900	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro	0.15	

		DOMAIN/s: Protein of unknown function DUF3067	
		(InterPro:IPR021420); Has 276 Blast hits to 276 proteins in 83	
		species: Archae - 0; Bacteria - 112; Metazoa - 0; Fungi - 2;	
		Plants - 59; Viruses - 0; Other Eukaryotes - 103 (source: NCBI	
		BLink).	
251272_at	At3g61890	ATHB-12_ATHB12_HB-12homeobox 12	0.15
255127_at	At4g08300	nodulin MtN21 /EamA-like transporter family protein	0.15
254998_at	At4g09760	Protein kinase superfamily protein	0.15
255016_at	At4g10120	ATSPS4FSucrose-phosphate synthase family protein	0.15
254573_at	At4g19420	Pectinacetylesterase family protein	0.15
248333_at	At5g52390	PAR1 protein	0.15
Terrete, concernent leaves, coulies leaves, notals and concle. Deave all tissues, Limit, 400 nones,			

Targets: senescent leaves, cauline leaves, petals and sepals. Base: all tissues. Limit: 100 genes. Rows with genes of interest are shaded in grey.

^a Gene annotation was performed using the online tool http://www.bar.utoronto.ca/ntools/cgibin/ntools_agi_converter.cgi.

^b For information about the calculation of the expression score K, see

https://www.genevestigator.com/userdocs/manual/biomarker.html.

T-DNA confirmation mes16-1 MES16-1-RP GTTGAAGAAAAGAAACCGCAC MES16-1-LP CTGAGCCGTAATTCACTTTG cyp89a9-1 CYP89A9-1-RP TACGACAAATAAGCCCAATGG cyp89a9-2 CYP89A9-1-LP GCTCTGATGTGTTCGGAGAG cyp89a9-2 CYP89A9-2-RP CTCACGATCTCCGAGTCACTC cyp71b19-1 CYP71B19-1-RP ACGATGACCAAAATAAACAAG cyp71b19-2 CYP71B19-1-LP CCACTAGACCATTGCTTCGTGCTC cyp71b19-2 CYP71B19-2-RP CTCTCGGATATGCTTAAGG cyp71b19-2 CYP71B19-2-LP CCAACTTTCTCTCCCGAATC SALK T-DNA LBb1.3 ATTTTGCCGAATTGCCTAAAGG JIC SM T-DNA Spm32 TACGAATAAGAGCG CCATTTAACAATACA JIC GT T-DNA Ds3-1 ACCCGGACTCGTATCGGT CYP89A9 CYP89A9_FL_S TCCGACACCACCTTCTGTTAA CYP71B19 CYP71B19_FL_S TCTCATCATCTGGGAC ACT2 ACT2-S TGGAAACATCATCATCTGGAC CYP71B19_FL_S TCTCACCACGAGGACAACCTA ACT2 ACT2-S TGCGAACCATCACGAGACAACCTA ACT2 ACT2-S TGGAATCACCGGATTCCTGGAC	GENE / MUTANT	PRIMER NAME	SEQUENCE (5'→3')	
mes16-1 MES16-1-RP GTTGAAGAAAAGAAACCGCAC wBsi6-1 MES16-1-LP CTGAGCCCGTAATTCACTTTG cyp89a9-1 CYP89A9-1-RP TACGACAAATAAGCCCAATGG cyp89a9-2 CYP89A9-2-RP GCTCTGATGTGTTTCGGAGAG cyp71b19-1 CYP71B19-1-RP GCGTGGACCAAAATAACAAG cyp71b19-2 CYP71B19-1-RP ATCGATGATGTCTTCGTGCTC CYP71B19-2-RP CCACTAGACCATTGCGTATGC CYP71B19-2-RP cyp71b19-2 CYP71B19-2-RP CCACTGGAACC SALK T-DNA LBb1.3 ATTTGCCGATTTCCGAAC SALK T-DNA LBb1.3 ATTTGCCGATTTCCCCAAATTACCAATTACA JIC ST T-DNA LB2 GCTTCCTATTATATCTCCCCAAATTACCAATACA JIC ST T-DNA LB2 GCTTCGATTAGCCTTAGGCT CYP89A9 CYP89A9-FL_S TCGGAAACATCATCAGGGT CYP71B19 CYP89A9-FL_S TCGGAACCATCATCAGGGT CYP71B19_FL_S TCTCATCACCATCGGCTTAA CYP71B19_FL_S TCTGATCACCATCAGGACCACCA ACT2 ACT2-S TGGAAACCATCACCACTAGGCC CYP71B19_FL_S TCCCCCCGGGATGCAGATTCACCACTATC CVP89A9_CYP89A9-Xmal-S TCCCCCCCGG		T-	DNA confirmation	
MES16-1-LPCTGAGCCCGTAATTCACTTTGcyp89a9-1CYP89A9-1-RPTACGACAAATAAGCCCAATGGcyp89a9-2CYP89A9-2-RPCTCACGATCTCCGAGTCACTCcyp89a9-2CYP89A9-2-LPGCGTGGACCAAAATAAACAAGcyp71b19-1CYP71B19-1-RPATCGATGATGTCTTCGTGCTCcyp71b19-2CYP71B19-1-RPCCACTAGACATTGGCTTTTTCcyp71b19-2CYP71B19-2-RPCCACTAGACCATTGCCTAAAGGsALK T-DNALB1.3ATTTGCCGATTCCCGGAATCSALK T-DNALB2GCTTCCTATTATATCTTCCCGAATCJIC SM T-DNASp32TACGAAACAGAGCG CCATTTAGAGTGAJIC GT T-DNADS3-1ACCCGACCGGATCGTATGGCTTAACYP71B19_FL_STCGGAAACATCATCTGGCTTAACYP71B19_FL_STCCGACACCGGATCATCACCCYP71B19_CYP71B19_FL_STCCGACACCGGACCACCTACYP71B19_CYP71B19_FL_STCCGACACGGACAACCTACYP71B19_CYP71B19_FL_STCCGACAGGACAACCTACYP71B19_CYP71B19_FL_STCCCCCCGGGATGGACCACCTACYP71B19_CYP71B19_FL_STCCCCCCGGGATGGACACCCTACYP71B19_CYP71B19_FL_STCCCCCCGGGATGGACACCCTACYP71B19_CYP71B19_FL_STCCCCCCGGGATGGACACCACTACCACCACTACCYP89A9CYP89A9-Xmal-STCCCCCCGGGATGGAGATCACCACCACTATCCYP89A9CYP89A9-Xmal-SCCCCCCGGGATTGGAGATCACCACCACTATCCCCYP89A9CYP89A9-EcoRI-SCCGGGATTCATGGAGATCACCACCTATCCATTCCCYP89A9CYP89A9-EcoRI-SCCGGGATTCATGAGAACCACCACTATCATATTCCCYP89A9CYP89A9-EcoRI-SCCGGGAATTCATGAGAAAGGGAGAACACCACTATCATATTCCCYP89A9CYP89A9-EcoRI-SCCGGGAATTCATGACACCACTATCATATCCAAGGGAAAGGTGAGGTACCCCGATR-1	mes16-1	MES16-1-RP	GTTGAAGAAAAGAAACCGCAC	
cyp89a9-1CYP89A9-1-RPTACGACAAATAAGCCCAATGGcyp89a9-2CYP89A9-1-LPGCTCTGATGTGTTTCGGAGAGcyp89a9-2CYP89A9-2-RPCTCACGATCTCCCGAGTCACTCCYP71b19-1CYP71B19-1-RPATCGATGATGTCTTCGTGCTCcyp71b19-2CYP71B19-1-LPCCACTAGACCATTGGCTTTTCcyp71b19-2CYP71B19-2-RPCCTCTCGGATATGCCTAAAGGcyp71b19-2CYP71B19-2-LPCCACATGCCTTTCCCGAATCSALK T-DNALB2GCTTCCTATTATCTTCCCCAAATTACCAATACAJIC SM T-DNASpm32TACGAATAAGAGCG CCATTTTAGGAACJIC GT T-DNADs3-1ACCCGACCGGATCGTATCGGTRT-PCRCYP89A9_FL_SCGAACACATCATCTGGCTTAACYP89A9_FL_SCCGAACCATCATCTGGCTTAACYP89A9_FL_SCGAAACATCATCTCGGCTTAACYP89A9_FL_SCGAAACATCATCATCGGCTTAACYP89A9_FL_SCCGACACACACCATCACTCGTTCGTCYP89A9_FL_SCCGACCCGGATCGACACCACACAACT2CYP89A9_FL_STCGAAACATCATCGGACACCCACTACCYP89A9_CYP1B19_FL_SCCATCACACCACACACCACCACCACCACCACCACCACCAC		MES16-1-LP	CTGAGCCCGTAATTCACTTTG	
CYP89A9-1-LPGCTCTGATGTGTTTCGGAGAGcyp89a9-2CYP89A9-2-RPCTCACGATCTCCGAGTCACTCcyp71b19-1CYP71B19-1-RPATCGATGATGTCTTCGTGCTCcyp71b19-2CYP71B19-1-RPCCCACTAGACCATTGCTTTTTCcyp71b19-2CYP71B19-2-LPCCAACTTTCTCTTCCCGAATCSALK T-DNALBb1.3ATTTTGCCGATTTCGGACCSALK T-DNALB2GCTTCCTATTATATCTTCCCAAATTACCAATACAJIC GT T-DNASpm32TACGAATAAGAGCG CCATTTAGAGTGAJIC GT T-DNADs3-1ACCCGACCGGATCGTATCGGTCYP79B9A9CYP89A9_FL_STCGGAAACATCATCTGGCTTAACYP79B19CYP71B19_FL_STCTCACCTTCGTTTCATGACCCYP71B19CYP71B19_FL_STCTCACACCTCAGGACAACACCAACT2ACT2-STGGAATCCACGAGACAACCTAACT2ACT2-STGGAATCCACGAGACAACCTAACT2-ASTTCTGTGAACGATTCCTGGACCYP89A9CYP89A9-Stmal-STCCCCCGCGGATGGAGACACCCACATATCCYP89A9CYP89A9-Stmal-STCCCCCCGGGATGGAGATCACCACCATATCCYP89A9CYP89A9-Stmal-STCCCCCGCGGATGGAGATCACCACTATCCVP89A9CYP89A9-Stmal-STCCCCCCGGGATGGAGATCACCACTATCCVP89A9CYP89A9-Stmal-SCCCCGGGATTCATGGAGATCACCACTATCATCVP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCVP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATATCCCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGAGAAACACACTCTTGAGGCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGAGAAACACACACTATCATATCCCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGAGAAACACACCACTATCATCYP89A9CYP89A9-EcoRI-S </td <td>cyp89a9-1</td> <td>CYP89A9-1-RP</td> <td>TACGACAAATAAGCCCAATGG</td>	cyp89a9-1	CYP89A9-1-RP	TACGACAAATAAGCCCAATGG	
cyp89a9-2CYP89A9-2-RPCTCACGATCTCCGAGTCACTCCYP89A9-2-LPGCGTGGACCAAAATAAACAAGcyp71b19-1CYP71B19-1-RPATCGATGATGTCTTCGTGCTCCYP71B19-1-LPCCACTAGACCATTGGCTTTTTCcyp71b19-2CYP71B19-2-RPCCTCTCGGATATGCCTAAAGGSALK T-DNALBb1.3ATTTTGCCGATTTCCCGAATCSALK T-DNALB2GCTTCCTATTATATCTTCCCCAAATTACCAATACAJIC GT T-DNALB2GCTTCCTATTATATCTTCCCCAAATTACCAATACAJIC GT T-DNASpm32TACGAAACATCATCGGTJIC GT T-DNADs3-1ACCCGACCGGATCGTATCGGTCYP89A9CYP89A9_FL_STCGGAAACATCATCTGGCTTAACYP71B19CYP71B19_FL_STCTCATCACCTTCGTTCGTCYP71B19CYP71B19_FL_STCTCATCACCATCAGAACT2ACT2-STGGAATCCACGAGACAACCTAACT2-ASTTCTGTGAACGATCCTGGACCYP89A9CYP89A9-Mnel-ASCTCACCACGAGAGACACCTAACT2-ASTCCCCCCGGGATGGAGATCACCACTATCCYP89A9CYP89A9-and ATR-1 in pFastbac1 and pFastbac DUALCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATTTCCCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGTCACCACATATATTCCCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGTCACCACATATCATCCCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGTCACCACATATCATCCCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGAGACCCACCATATCATCYP89A9 </td <td></td> <td>CYP89A9-1-LP</td> <td>GCTCTGATGTGTTTCGGAGAG</td>		CYP89A9-1-LP	GCTCTGATGTGTTTCGGAGAG	
CYP89A9-2-LPGCGTGGACCAAAATAAACAAGcyp71b19-1CYP71B19-1-LPATCGATGATGTCTTCGTGCTCcyp71b19-2CYP71B19-1-LPCCACTAGACCATTGGCTTTTCcyp71b19-2CYP71B19-2-LPCCACTAGACCATTGCCTAAAGGSALK T-DNALBb1.3ATTTTGCCGATTCCGAATCSALK T-DNALB2GCTTCCTATTATATCTTCCCAAATTACCAATACAJIC SM T-DNAB2GCTTCCTATTATAGAGTGAJIC GT T-DNADs3-1ACCCGACCGGATCGTATCGGTCYP89A9CYP89A9_FL_STCGGAAACATCATCTGGCTTAACYP71B19FL_STCTCATCACTCTGGCTTAACYP71B19FL_STCTCATCACCTCGTTTCGTCYP71B19FL_STCTCATCACCCACGAGACACCTAACT2ACT2-STGGAATCACGATTCCTGGACCYP89A9CYP89A9.FL_ASTCTTTATGTGTCATCCCACCACCACTAACT2-ASTTCTGTGAACGATTCCTGGACCYP89A9CYP89A9.Stmal-STCCCCCCGGGATGGAGATCACCACTATCCYP89A9CYP89A9.stmal-SCCCCCCGGGATGGAGATCACCACTATCCYP89A9CYP89A9.ecoRI-SCCGGGATTCATGGAGATCACCACTATCATCCYP89A9CYP89A9.ecoRI-SCCGGGATTCATGGAGATCACCACTATCATCYP89A9CYP89A9.ecoRI-SCCGGGATTCACCACTATCATAAACYP89A9CYP89A9.ecoRI-SCCGGGATTCACCACTATCATAAAACYP89A9CYP89A9.ecoRI-SCCGGGATTCACCACTATCATAAAACYP89A9CYP89A9.ecoRI-SCCGGGATTCACCACTATCATAAAACYP89A9CYP89A9.ecoRI-SCCGGGATTCACCACTATCATAAAACYP89A9CYP89A9.ecoRI-SCCGGGATTCACCACTATCATAAAAAAAAAAAAAAAAAAA	сур89а9-2	CYP89A9-2-RP	CTCACGATCTCCGAGTCACTC	
cyp71b19-1CYP71B19-1-RP CYP71B19-1-LPATCGATGATGTTCTCGTGCTC CYP71B19-1-LPcyp71b19-2CYP71B19-1-LPCCACTAGACCATTGGCTTATCcyp71b19-2CYP71B19-2-RPCCTCTCGGATATGCCTAAAGG CYP71B19-2-LPCCAACTTTCTTTCTTCCCGAATCSALK T-DNALBb1.3ATTTTGCCGATTCGGAAC SALL T-DNAJIC GT T-DNAB2GCTTCCTATTATATCTTCCCCAAATTACCAATACA JIC GT T-DNAJIC GT T-DNADs3-1ACCCGGACCGGATCGTATCGGTCYP89A9CYP89A9_FL_STCGGAAACATCATCTGGCTTAA CYP89A9_FL_SCYP89A9CYP89A9_FL_STCCGGAAACATCATCTGGCTTAA CYP89A9_FL_SCYP71B19CYP71B19_FL_STCTCATCACCTTCGTTCGT CYP71B19_FL_SCYP71B19CYP71B19_FL_STCTCATCACCAGGACAACCTA ACT2-ASACT2ACT2-STGGAATCCACGGAGACAACCTA ACT2-ASCloning of CYP89A9-GFPCVP89A9-Xmal-S CCCCCCGGGATGGAGATCACCACTATC CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCAT CCGGAATTCATGCGAGACACCACTATCAT CYP89A9-EcoRI-SCYP89A9CYP89A9-EcoRI-S CCGGAATTCATGGAGATCACCACTATCATATTCC CYP89A9-KpnI-SCCGGGATTCATGGAGATCACCACTATCAT CCGGAATTCATGGAGATCACCACTATCATATTCC CCGGAATTCATGGAGATCACCACTATCATATTCC CYP89A9-KpnI-SCGGGGTACCATGGAGATCACCACTATCATATTCC CCGGAATTCATCACGAGCATCCTGGAT CCGGAATTCATGAGACACCACTATCATATTCC ATR-1-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATATTCC CCGGAATTCATGAGACTCACCACTATCAT CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCAT CYP89A9-EcoRI-SCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCAT CYP89A9-CORI-ASCCGGAATTCATGGAGATCACCACTATCAT CCGGAATTCATGGACTCACCACTATCATCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGACTCCTGAG<		CYP89A9-2-LP	GCGTGGACCAAAATAAACAAG	
CYP71B19-1-LPCCACTAGACCATTGGCTTTTTCcyp71b19-2CYP71B19-2-RPCCTCTCGGATATGCCTAAAGGSALK T-DNALBb1.3ATTTTGCCGATTCGGAACSALK T-DNALB2GCTTCCTATTATATCTTCCCAAATTACCAATACAJIC SM T-DNASpm32TACGAATAAGAGCG CCATTTTAGAGTGAJIC GT T-DNADs3-1ACCCGACCGGATCGTATCGGTRT-PCRCYP89A9CYP89A9_FL_SCCGGAAACATCATCAGCTTTGAAAGGGTTTTTCATGACCCYP89A9_FL_SCCACTCGCATCGGTTTAACYP89A9_FL_SCCACCCGGAACCATCATCAGCCCCCGACCGATCGGCTTAACYP89A9_FL_SCCGGAAACATCATCACCATCAGCYP89A9_FL_SCCACTCACCCCCGGATCGCCCCCCGGCATCGCCCCCCCGGCATCGCCCCCCCC	cyp71b19-1	CYP71B19-1-RP	ATCGATGATGTCTTCGTGCTC	
cyp71b19-2CYP71B19-2-RP CYP71B19-2-LPCCTCTCGGATATGCCTAAAGG CCAACTTTCTCTTCCCGAATCSALK T-DNALBb1.3ATTTTGCCGATTCCGAACSALK T-DNALB2GCTTCCTATTATATCTTCCCCAAATTACCAATACAJIC SM T-DNASpm32TACGAATAAGAGCG CCATTTTAGAGTGAJIC GT T-DNADs3-1ACCCGACCGGATCGTATCGGTRT-PCRCYP89A9CYP89A9_FL_STCGGAAACATCATCTGGCTTAACYP71B19CYP71B19_FL_STCTCATCACCTTCGTTCGTCYP71B19CYP71B19_FL_STCTACACCATCACCATCAGACT2ACT2-STGGAATCCACGAGACAACCTAACT2-ASTTCTGTGAACGATTCCTGGACCYP89A9CYP89A9-Xmal-STCCCCCCGGGATGGAGATCACCACTATCCYP89A9CYP89A9-Xmal-STCCCCCCGGGATGGAGATCACCACTATCCYP89A9CYP89A9-and ATR-1 in pFastbac1 and pFastbac DUALCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-KpnI-SCGGGGTACCATGGAGATCACCACTATCATATTCCCYP89A9CYP89A9-KpnI-SCGGGGTACCATGGAGATCACCACTATCATATTCCCYP89A9CYP89A9-KpnI-SCGGGGTACCATGGAGATCACCACTATCATATTCCCYP89A9CYP89A9-KpnI-SCGGGGATTCATGACTTCTGCTTTGTATGACYP89A9CYP89A9-KpnI-SCGGGAATTCATGACTTCTGCTTGATAGACYP89A9CYP89A9-KpnI-SCGGGAATTCATGACTTCTGCTTGAGACYP89A9CYP89A9-KpnI-SCGGGGAATTCATGACTCTGAGACYP89A9CYP89A9-KpnI-SCGGGAATTCATGACACCACTATCATAGAGTACCCCGATR-1ATR-1-EcoRI-SCCGGAATTCATGAGATCACCACACTTCTGAG <td< td=""><td></td><td>CYP71B19-1-LP</td><td>CCACTAGACCATTGGCTTTTTC</td></td<>		CYP71B19-1-LP	CCACTAGACCATTGGCTTTTTC	
CYP71B19-2-LPCCAACTTTCCTCCCGAATCSALK T-DNALBb1.3ATTTGCCGATTTCGGAACSAIL T-DNALB2GCTTCCTATTATATCTTCCCAAATTACCAATACAJIC SM T-DNASpm32TACGAATAAGAGCG CCATTTTAGAGTGAJIC GT T-DNADs3-1ACCCGACCGGATCGTATCGGTCYP89A9CYP89A9_FL_STCGGAAACATCATCTGGCTTAACYP71B19CYP71B19_FL_STCTCATCACCTTCGTTTCGTCYP71B19CYP71B19_FL_STCTCATCACCTCCATCAGACT2ACT2-STGGAATCCACGAGACAACCTAACT2-ASTTCTGTGAACGATTCCTGGACCYP89A9CYP89A9-xmal-STCCCCCCGGGATGGAGATCACCACTATCCYP89A9CYP89A9-xmal-STCCCCCCGGGATGGAGATCACCACTATCCVP89A9CYP89A9-and ATR-1 in pFastbac1 and pFastbac DUALCYP89A9CYP89A9-EcoRI-SCCGGAATTCACGAGAGACACCCACTATCATCTCCTGGATAAAACYP89A9CYP89A9-EcoRI-SCCGGGATTCACCACTGGAGATCACCACTATCATATTCCCYP89A9CYP89A9-EcoRI-SCGGGGTACCATGGAGATCACCACTATCATATTCCCYP89A9CYP89A9-KpnI-SCGGGGATCCATGGAGATCACCACTATCATATTCCCYP89A9CYP89A9-KpnI-SCGGGGATCCATGGAGATCACCACTATCATATTCCCYP89A9CYP89A9-KpnI-SCGGGGATCCATGGAGATCACCACTATCATATTCCCYP89A9CYP89A9-KpnI-ASCCCGGAATTCATGGACTCTCTGGAGCYP89A9CYP89A9-KpnI-ASCCGGAATTCATGACTTCTGCTTGAGAGTCACCCGATR-1ATR-1-EcoRI-SCCGGAATTCATGGACATCACCACTATCATATTCCCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACATATCATCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACATTCATCATCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGA	cyp71b19-2	CYP71B19-2-RP	CCTCTCGGATATGCCTAAAGG	
SALK T-DNALBb1.3ATTTTGCCGATTTCGGAACSALL T-DNALB2GCTTCCTATTATATCTTCCCAAATTACCAATACAJIC SM T-DNASpm32TACGAATAAGAGCG CCATTTTAGAGTGAJIC GT T-DNADs3-1ACCCGACCGGATCGTATCGGTCYP89A9CYP89A9_FL_STCGGAAACATCATCTGGCTTAACYP89A9CYP89A9_FL_STCGGAAACATCATCTGGCTTAACYP71B19CYP71B19_FL_STCTCATCACCTTCGTTTCGTCYP71B19CYP71B19_FL_STCTCATCACCACGAGACAACCTAACT2ACT2-STGGAATCCACGAGACAACCTAACT2-ASTTCTGTGAACGATTCCTGGACCYP89A9CYP89A9-Xmal-STCCCCCCGGGATGGAGATCACCACTATCCYP89A9CYP89A9-Xmal-STCCCCCCGGGATGGAGATCACCACTATCATCYP89A9CYP89A9-and ATR-1 in pFastbac1 and pFastbac DUALCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATATTCCCYP89A9CYP89A9-KpnI-ASGCAAATATTTATCCAAGGAGAAAGTGAGGTACCCCGATR-1ATR-1-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATATTCCCYP89A9CYP89A9-KpnI-ASGCAAATATTTATCCAAGGAGAAAGTGAGGTACCCCGATR-1ATR-1-EcoRI-SCCGGAATTCATGACTTCTGCTTGATGCATR-1ATR-1-EcoRI-SCCGGAATTCACCACACTATCATGAGCYP89A9CYP89A9-EcoRI-SCCGGAATTCACCACACTCTCTGAGCYP89A9CYP89A9-EcoRI-SCCGGAATTCACCACACTATCATGAGCYP89A9CYP89A9-FL-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACACTATCATCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTTCATCAT <td></td> <td>CYP71B19-2-LP</td> <td>CCAACTTTCTCTTCCCGAATC</td>		CYP71B19-2-LP	CCAACTTTCTCTTCCCGAATC	
SAIL T-DNALB2GCTTCCTATTATATCTTCCCAAATTACCAATACAJIC SM T-DNASpm32TACGAATAAGAGCG CCATTTTAGAGTGAJIC GT T-DNADs3-1ACCCGACCGGATCGTATCGGTRT-PCRRT-PCRCYP89A9CYP89A9_FL_STCGGAAACATCATCTGGCTTAACYP71B19CYP71B19_FL_STCTCATCACCTTCGTTTCGTCYP71B19CYP71B19_FL_STCTCATCACCACGAGACAACCTAACT2ACT2-STGGAATCCACGAGACAACCTAACT2-ASTTCTGTGAACGATTCCTGGACCYP89A9CYP89A9-Nhel-ASTCCCCCCGGGATGGAGATCACCACTATCCYP89A9CYP89A9-Nhel-ASTCCCCCCGGGATGGAGATCACCACTATCCYP89A9CYP89A9-Stmal-STCCCCCCGGGATGGAGATCACCACTATCCYP89A9CYP89A9-Stmal-SCCCGCCCGGGATGGAGATCACCACTATCCYP89A9CYP89A9-Stmal-SCCCCCCCGGGATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-Stmal-SCCGCGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCGGGGTACCATGGAGATCACCACTATCATATTCCCYP89A9CYP89A9-KpnI-SCGGGGTACCATGGAGATCACCACTATCATATTCCCYP89A9CYP89A9-KpnI-SCGGGGAATTCATGGAGATCACCACTATCATATTCCCYP89A9CYP89A9-KpnI-SCCGGAATTCATGACTTCTGCTTTGATAGCATR-1ATR-1-EcoRI-SCCGGAATTCATGACTTCTGCTTTGAGCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCAT	SALK T-DNA	LBb1.3	ATTTTGCCGATTTCGGAAC	
JIC SM T-DNASpm32TACGAATAAGAGCG CCATTTTAGAGTGAJIC GT T-DNADs3-1ACCCGACCGGATCGTATCGGTRT-PCRRT-PCRCYP89A9CYP89A9_FL_ASGCTTTGAAAGGGTTTTTCATGACCCYP71B19CYP71B19_FL_STCTCATCACCTTCGTTCGTCYP71B19CYP71B19_FL_ASTCTTTATGTGTCATCCCATCAGACT2ACT2-STGGAATCACGAGAGACAACCTAACT2-ASTTCTGTGAACGATTCCTGGACCYP89A9CYP89A9-Xmal-STCCCCCCGGGATGGAGATCACCACTATCCYP89A9CYP89A9-Nhel-ASCTAGCTAGCCTTTCTCCTTGGATAAATATTTGCCloning of CYP89A9 and ATR-1 in pFastbac1 and pFastbac DUALCYP89A9CYP89A9CYP89A9-EcoRI-SCCGGGATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCGGGGATTCCACGAGATCACCACTATCATCYP89A9CYP89A9-Kpnl-SCGGGGATTCCACGAGATCACCACTATCATTCCCYP89A9CYP89A9-Kpnl-SCGGGATTCCAGGAGATCACCACTATCATATTCCCYP89A9CYP89A9-Kpnl-SCGGGATTCCAGGATCACCACTATCATATTCCCYP89A9CYP89A9-Kpnl-SCGGGATTCATGACATGACACACACTATCATATTCCCYP89A9CYP89A9-Kpnl-SCGGGATTCATGACATGACATGACTATCATGAGGTACCCCGATR-1-EcoRI-SCCGGAATTCATGACATCACCACTATCATATTCCCYP89A9CYP89A9-Kpnl-SCGGGAATTCATGACATCACCACTCTCGAGCYP89A9CYP89A9-Kpnl-SCGGGAATTCATGACACCACTATCATATCCCYP89A9CYP89A9-Kpnl-SCGGGAATTCATGACACACACTCTCGAGCYP89A9CYP89A9-Kpnl-SCCGGAATTCATGACACCACTATCATATCCCYP89A9CYP89A9-FindIII-ASCCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-FindIII-ASCCGGAATTCATGGAATCACCACACTATC	SAIL T-DNA	LB2	GCTTCCTATTATATCTTCCCAAATTACCAATACA	
JIC GT T-DNADs3-1ACCCGACCGGATCGTATCGGTRT-PCRCYP89A9CYP89A9_FL_STCGGAAACATCATCTGGCTTAACYP89A9CYP71B19_FL_STCTCATCACCTTCGTTTCATGACCCYP71B19CYP71B19_FL_STCTCATCACCCTCGTTCGTCYP71B19CYP71B19_FL_ASTCTTTATGTGTCATCCCATCAGACT2ACT2-STGGAATCCACGAGACAACCTAACT2-ASTTCTGTGAACGATTCCTGGACCYP89A9CYP89A9-Xmal-SCYP89A9CYP89A9-Nhel-ASCloning of CYP89A9-GFPCYP89A9CYP89A9-Nhel-ASCloning of CYP89A9-CTTCCTTGGATAAATATTTGCCloning of CYP89A9-EcoRI-SCCGGAATTCACGAGTCACCACTATCATCYP89A9CYP89A9-EcoRI-SCCGGAATTCTCACTTCTCCTTGGATAAACYP89A9CYP89A9-EcoRI-SCGGGAATTCACCACCACTATCATTCCCYP89A9CYP89A9-EcoRI-SCGGGAATTCACGAGATCACCACTATCATTCCCYP89A9CYP89A9-EcoRI-SCGGGAATTCACGAGATCACCACTATCATTCCCYP89A9CYP89A9-EcoRI-SCGGGAATTCATGGAGATCACCACTATCATATTCCCYP89A9CYP89A9-EcoRI-SCGGGAATTCATGAGAGAAGTGAGGTACCCCGATR-1ATR-1-EcoRI-SCCGGAATTCATGACTTCTGCTTTGTATGCATR-1ATR-1-EcoRI-SCCGGAATTCACCACACTATCATGAGGCOmplementation of cyp89a9-1, cyp89a9-2 and mes16-1cyp89a9-1CYP89A9-HindIII-ASCYP89A9-HindIII-ASCCCAAGCTTTCACTTTCTCCTTGGATAAAT	JIC SM T-DNA	Spm32	TACGAATAAGAGCG CCATTTTAGAGTGA	
RT-PCRCYP89A9CYP89A9_FL_STCGGAAACATCATCTGGCTTAACYP89A9_FL_ASGCTTTGAAAGGGTTTTTCATGACCCYP71B19CYP71B19_FL_STCTCATCACCTTCGTTCGTCYP71B19CYP71B19_FL_SACT2ACT2-STGGAATCCACGAGACAACCTAACT2-ASTTCTGTGAACGATTCCTGGACCloning of CYP89A9-GFPCYP89A9CYP89A9-Xmal-SCCCCCGGGATGGAGATCACCACTATCCYP89A9CYP89A9-Nhel-ASCTAGCTAGCCTTTCTCCTTGGATAAATATTTGCCloning of CYP89A9 and ATR-1 in pFastbac1 and pFastbac DUALCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCGGGAACCATGGAGATCACCACTATCATATTCCCYP89A9-KpnI-SCGGGGTACCACTGGAGATCACCACTATCATATTCCCYP89A9-KpnI-SCGGGAATTCATGGAGAAGTGAGGGTACCCCGATR-1ATR-1-EcoRI-SCCGGAATTCATGACACATCTTCTGCTTGATGCATR-1ATR-1-EcoRI-SCCGGAATTCATGAGATCACCACTATCATGAGCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGAGACACTCTTGAGGCYP89A9CYP89A9-KpnI-ASCCGGAATTCATGGAGATCACCACTATCATATTCCCYP89A9CYP89A9-KpnI-ASCCGGAATTCATGGAGATCACCACTATCATGGCYP89A9CYP89A9-KpnI-ASCCGGAATTCATGGAGATCACCACTATCATGCCYP89A9CYP89A9-KpnI-ASCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-KpnI-ASCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCCGGAATTCAT	JIC GT T-DNA	Ds3-1	ACCCGACCGGATCGTATCGGT	
CYP89A9CYP89A9_FL_STCGGAAACATCATCTGGCTTAACYP71B19CYP71B19_FL_ASGCTTTGAAAGGGTTTTTCATGACCCYP71B19CYP71B19_FL_STCTCATCACCTTCGTTCGTCYP71B19_FL_ASTCTTTATGTGTCATCCCATCAGACT2ACT2-STGGAATCCACGAGACAACCTAACT2-ASTTCTGTGAACGATTCCTGGACCVP89A9CYP89A9-Xmal-STCCCCCCGGGATGGAGATCACCACTATCCYP89A9CYP89A9-Nhel-ASCTAGCTAGCCTTTCTCCTTGGATAAATATTTGCCloning of CYP89A9 and ATR-1 in pFastbac1 and pFastbac DUALCYP89A9CYP89A9CYP89A9-EcoRI-SCCGGAATTCACGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCGGGGTACCATGGAGATCACCACTATCATCYP89A9CYP89A9-KpnI-SCGGGGTACCATGGAGATCACCACTATCATATTCCCYP89A9CYP89A9-KpnI-SCGGGGTACCATGGAGATCACCACTATCATATTCCCYP89A9CYP89A9-KpnI-SCGGGAATTCATGACTTCTGCTTTGTATGCATR-1ATR-1-EcoRI-SCCGGAATTCATGACTTCTGCTTTGTATGCATR-1-EcoRI-ASCCGGAATTCACCAGACATCTCTGAGComplementation of cyp89a9-1, cyp89a9-2 and mes16-1cyp89a9-1CYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9-HindIII-ASCCCAAGCTTTCACTTTCTCCTTGGATAAAT			RT-PCR	
CYP89A9_FL_ASGCTTTGAAAGGGTTTTTCATGACCCYP71B19CYP71B19_FL_STCTCATCACCTTCGTTTCGTCYP71B19_FL_ASTCTTTATGTGTCATCCCATCAGACT2ACT2-STGGAATCCACGAGACAACCTAACT2-ASTTCTGTGAACGATTCCTGGACCloning of CYP89A9-GFPCYP89A9CYP89A9-Xmal-STCCCCCCGGGATGGAGATCACCACTATCCYP89A9CYP89A9-Nhel-ASCTAGCTAGCCTTTCTCCTTGGATAAATATTTGCCloning of CYP89A9 and ATR-1 in pFastbac1 and pFastbac DUALCYP89A9CYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCGGGGTACCATGGAGATCACCACTATCATCYP89A9CYP89A9-KpnI-SCGGGGTACCATGGAGATCACCACTATCATATTCCCYP89A9CYP89A9-KpnI-SCGGGGTACCATGGAGATCACCACTATCATATTCCCYP89A9CYP89A9-KpnI-ASGCAAATATTTATCCAAGGAGAAAGTGAGGTACCCCGATR-1ATR-1-EcoRI-SCCGGAATTCCTGCTTTGTATGCATR-1-EcoRI-ASCCGGAATTCCACCAGACATCTTGAGCOmplementation of cyp89a9-1, cyp89a9-2 and mes16-1cyp89a9-1CYP89A9-HindIII-ASCCCAAGCTTTCACTTTCTCCTTGGATAAAT	CYP89A9	CYP89A9_FL_S	TCGGAAACATCATCTGGCTTAA	
CYP71B19CYP71B19_FL_STCTCATCACCTTCGTTTCGTCYP71B19_FL_ASTCTTTATGTGTCATCCCATCAGACT2ACT2-STGGAATCCACGAGACAACCTAACT2-ASTTCTGTGAACGATTCCTGGACCloning of CYP89A9-GFPCYP89A9-Xmal-SCYP89A9CYP89A9-Xmal-STCCCCCCGGGATGGAGATCACCACTATCCYP89A9CYP89A9-Nhel-ASCTAGCTAGCCTTTCTCCTTGGATAAATATTTGCCloning of CYP89A9 and ATR-1 in pFastbac1 and pFastbac DUALCYP89A9CYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCGGGGTACCATGGAGATCACCACTATCATAAACYP89A9CYP89A9-KpnI-SCGGGGTACCATGGAGATCACCACTATCATATTCCCYP89A9CYP89A9-KpnI-SCGGGGATCCATGGAGATCACCACTATCATATTCCATR-1ATR-1-EcoRI-SCCGGAATTCATGACTTCTGCTTTGTATGCATR-1ATR-1-EcoRI-SCCGGAATTCCACGACATCTTGAGCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGACATCTTGAGCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGACATCTTGAGCYP89A9CYP89A9-EcoRI-SCCGGAATTCCACGACATCTTGAGCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9-HindIII-ASCCCAAGCTTTCACTTTCTCCTTGGATAAAT		CYP89A9_FL_AS	GCTTTGAAAGGGTTTTTCATGACC	
CYP71B19_FL_ASTCTTTATGTGTCATCCCATCAGACT2ACT2-STGGAATCCACGAGACAACCTAACT2-ASTTCTGTGAACGATTCCTGGACCloning of CYP89A9-GFPCYP89A9CYP89A9-Xmal-STCCCCCCGGGATGGAGATCACCACTATCCYP89A9CYP89A9-Nhel-ASCTAGCTAGCCTTTCTCCTTGGATAAATATTTGCCloning of CYP89A9 and ATR-1 in pFastbac1 and pFastbac DUALCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCCGGGAATTCCACGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-ASCCGGGAATTCCACGAGATCACCACTATCATAAACYP89A9CYP89A9-KpnI-SCGGGGTACCATGGAGATCACCACTATCATATTCCCYP89A9CYP89A9-KpnI-SCGGGGAATTCATGAGGTACCCCGATR-1ATR-1-EcoRI-SCCGGAATTCATGACTTCTGCTTTGTATGCATR-1ATR-1-EcoRI-SCCGGAATTCATCACCAGACATCTCTGAGComplementation of cyp89a9-1, cyp89a9-2 and mes16-1cyp89a9-1CYP89A9-HindIII-ASCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCAT	CYP71B19	CYP71B19_FL_S	TCTCATCACCTTCGTTTCGT	
ACT2ACT2-STGGAATCCACGAGACAACCTA TTCTGTGAACGATTCCTGGACACT2-ASTTCTGTGAACGATTCCTGGACCloning of CYP89A9-GFPCYP89A9-Xmal-SCYP89A9CYP89A9-Nhel-ASCTAGCTAGCCTTTCTCCTTGGATAAATATTTGCCloning of CYP89A9 and ATR-1 in pFastbac1 and pFastbac DUALCloning of CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCAT CYP89A9CYP89A9-EcoRI-SCCGGGATTCTCACTTTCTCCTTGGATAAACYP89A9CYP89A9-EcoRI-SCGGGGTACCATGGAGATCACCACTATCAT CYP89A9-EcoRI-SCGGGGTACCATGGAGATCACCACTATCATATTCCCYP89A9CYP89A9-KpnI-SCGGGGTACCATGGAGAAAGTGAGGTACCCCGATR-1ATR-1-EcoRI-SCCGGAATTCATGACTTCTGCTTTGTATGC ATR-1-EcoRI-ASComplementation of cyp89a9-1, cyp89a9-2 and mes16-1cyp89a9-1CYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCAT CYP89A9-HindIII-ASCCCAAGCTTTCACTTTCTCCTTGGATAAAT		CYP71B19_FL_AS	TCTTTATGTGTCATCCCATCAG	
ACT2-ASTTCTGTGAACGATTCCTGGACCloning of CYP89A9-GFPCYP89A9CYP89A9-Xmal-SCYP89A9-Nhel-ASCTAGCTAGCCTTTCTCCTTGGATAAATATTTGCCloning of CYP89A9 and ATR-1 in pFastbac1 and pFastbac DUALCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCCGGGATTCTCACTTTCTCCTTGGATAAACYP89A9CYP89A9-EcoRI-ASCGGGGTACCATGGAGATCACCACTATCATAAACYP89A9CYP89A9-KpnI-SCGGGGTACCATGGAGATCACCACTATCATATTCCCYP89A9CYP89A9-KpnI-ASGCAAATATTTATCCAAGGAGAAAGTGAGGTACCCCGATR-1ATR-1-EcoRI-SCCGGAATTCATGACTTCTGAGComplementation of cyp89a9-1, cyp89a9-2 and mes16-1cyp89a9-1CYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9-HindIII-ASCCCAAGCTTTCACTTTCTCCTTGGATAAAT	ACT2	ACT2-S	TGGAATCCACGAGACAACCTA	
Cloning of CYP89A9-GFPCYP89A9CYP89A9-Xmal-STCCCCCCGGGATGGAGATCACCACTATCCYP89A9-Nhel-ASCTAGCTAGCCTTTCTCCTTGGATAAATATTTGCCloning of CYP89A9 and ATR-1 in pFastbac1 and pFastbac DUALCYP89A9CYP89A9-EcoRI-SCYP89A9CYP89A9-EcoRI-SCYP89A9CYP89A9-EcoRI-SCYP89A9CYP89A9-KpnI-SCGGGGTACCATGGAGATCACCACTATCATATTCCCYP89A9-KpnI-ASGCAAATATTTATCCAAGGAGAAAGTGAGGTACCCCGATR-1ATR-1-EcoRI-SCCGGAATTCATCACCAGACATCTCTGAGComplementation of cyp89a9-1, cyp89a9-2 and mes16-1cyp89a9-1CYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9-HindIII-ASCCCAAGCTTTCACTTTCTCCTTGGATAAAT		ACT2-AS	TTCTGTGAACGATTCCTGGAC	
CYP89A9CYP89A9-Xmal-S CYP89A9-Nhel-ASTCCCCCCGGGATGGAGATCACCACTATC CTAGCTAGCCTTTCTCCTTGGATAAATATTTGCCloning of CYP89A9 and ATR-1 in pFastbac1 and pFastbac DUALCYP89A9CYP89A9-EcoRI-S CYP89A9-EcoRI-SCYP89A9CYP89A9-EcoRI-S CYP89A9-EcoRI-ASCYP89A9CYP89A9-KpnI-S CGGGGTACCATGGAGATCACCACTATCATATTCC CYP89A9-KpnI-ASCYP89A9CYP89A9-KpnI-S CGGGGTACCATGGAGATCACCACTATCATATTCC CYP89A9-KpnI-ASATR-1ATR-1-EcoRI-S ATR-1-EcoRI-SCCGGAATTCATGACATCTTCTGCTTTGTATGC ATR-1-EcoRI-ASCOmplementation of cyp89a9-1, cyp89a9-2 and mes16-1cyp89a9-1CYP89A9CYP89A9-EcoRI-S CCGGAATTCATGGAGATCACCACTATCAT CYP89A9-HindIII-AS		Cloni	ing of CYP89A9-GFP	
CYP89A9-Nhel-ASCTAGCTAGCCTTTCTCCTTGGATAAATATTTGCCloning of CYP89A9 and ATR-1 in pFastbac1 and pFastbac DUALCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-ASCCGGGATTCTCACTTTCTCCTTGGATAAACYP89A9CYP89A9-KpnI-SCGGGGTACCATGGAGATCACCACTATCATATTCCCYP89A9-KpnI-ASGCAAATATTTATCCAAGGAGAAAGTGAGGTACCCCGATR-1ATR-1-EcoRI-SCCGGAATTCATGACTTCTGCTTTGTATGCATR-1-EcoRI-ASCCGGAATTCACCAGACATCTCTGAGComplementation of cyp89a9-1, cyp89a9-2 and mes16-1cyp89a9-1CYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9-HindIII-ASCCCAAGCTTTCACTTTCTCCTTGGATAAAT	CYP89A9	CYP89A9- <i>Xma</i> I-S	TCCCCCCGGGATGGAGATCACCACTATC	
Cloning of CYP89A9 and ATR-1 in pFastbac1 and pFastbac DUALCYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9-EcoRI-ASCCGGAATTCTCACTTTCTCCTTGGATAAACYP89A9CYP89A9-KpnI-SCGGGGTACCATGGAGATCACCACTATCATATTCCCYP89A9-KpnI-ASGCAAATATTTATCCAAGGAGAAAGTGAGGTACCCCGATR-1ATR-1-EcoRI-SCCGGAATTCATGACTTCTGCTTTGTATGCATR-1-EcoRI-ASCCGGAATTCACCAGACAATCTCTGAGComplementation of cyp89a9-1, cyp89a9-2 and mes16-1cyp89a9-1CYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9-HindIII-ASCCCAAGCTTTCACTTTCTCCTTGGATAAAT		CYP89A9- <i>Nhe</i> l-AS	CTAGCTAGCCTTTCTCCTTGGATAAATATTTGC	
CYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9CYP89A9-EcoRI-ASCCGGGATTCTCACTTTCTCCTTGGATAAACYP89A9CYP89A9-KpnI-SCGGGGTACCATGGAGATCACCACTATCATATTCCCYP89A9-KpnI-ASGCAAATATTTATCCAAGGAGAAAGTGAGGTACCCCGATR-1ATR-1-EcoRI-SCCGGAATTCATGACTTCTGCTTTGTATGCATR-1-EcoRI-ASCCGGAATTCtCACCAGACATCTCTGAGComplementation of cyp89a9-1, cyp89a9-2 and mes16-1cyp89a9-1CYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9-HindIII-ASCCCAAGCTTTCACTTTCTCCTTGGATAAAT	Cloning of CYP89A9 and ATR-1 in pFastbac1 and pFastbac DUAL			
CYP89A9-EcoRI-ASCCGGAATTCTCACTTTCTCCTTGGATAAACYP89A9CYP89A9-KpnI-SCGGGGTACCATGGAGATCACCACTATCATATTCCCYP89A9-KpnI-ASGCAAATATTTATCCAAGGAGAAAGTGAGGTACCCCGATR-1ATR-1-EcoRI-SCCGGAATTCATGACTTCTGCTTTGTATGCATR-1-EcoRI-ASCCGGAATTCtCACCAGACATCTCTGAGComplementation of cyp89a9-1, cyp89a9-2 and mes16-1cyp89a9-1CYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9-HindIII-ASCCCAAGCTTTCACTTTCTCCTTGGATAAAT	CYP89A9	CYP89A9-EcoRI-S	CCGGAATTCATGGAGATCACCACTATCAT	
CYP89A9CYP89A9-Kpnl-SCGGGGTACCATGGAGATCACCACTATCATATTCCCYP89A9-Kpnl-ASGCAAATATTTATCCAAGGAGAAAGTGAGGTACCCCGATR-1ATR-1-EcoRI-SCCGGAATTCATGACTTCTGCTTTGTATGCATR-1-EcoRI-ASCCGGAATTCtCACCAGACATCTCTGAGComplementation of cyp89a9-1, cyp89a9-2 and mes16-1cyp89a9-1CYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9-HindIII-ASCCCAAGCTTTCACTTTCTCCTTGGATAAAT		<i>CYP89A9-Eco</i> RI-AS	CCGGAATTCTCACTTTCTCCTTGGATAAA	
CYP89A9-Kpnl-AS GCAAATATTTATCCAAGGAGAAAGTGAGGTACCCCG ATR-1 ATR-1-EcoRI-S CCGGAATTCATGACTTCTGCTTTGTATGC ATR-1-EcoRI-AS CCGGAATTCtCACCAGACATCTCTGAG Complementation of cyp89a9-1, cyp89a9-2 and mes16-1cyp89a9-1 CYP89A9 CYP89A9-EcoRI-S CCGGAATTCATGGAGATCACCACTATCAT CYP89A9-HindIII-AS CCCAAGCTTTCACTTTCTCCTTGGATAAAT	CYP89A9	CYP89A9-Kpnl-S	CGGGGTACCATGGAGATCACCACTATCATATTCC	
ATR-1 ATR-1-EcoRI-S ATR-1-EcoRI-AS CCGGAATTCATGACTTCTGCTTTGTATGC CCGGAATTCtCACCAGACATCTCTGAG Complementation of cyp89a9-1, cyp89a9-2 and mes16-1cyp89a9-1 CYP89A9 CYP89A9 CYP89A9-EcoRI-S CYP89A9-HindIII-AS CCGGAATTCATGGAGATCACCACTATCAT CCCAAGCTTTCACTTTCTCCTTGGATAAAT		CYP89A9-Kpnl-AS	GCAAATATTTATCCAAGGAGAAAGTGAGGTACCCCG	
ATR-1-EcoRI-AS CCGGAATTCtCACCAGACATCTCTGAG Complementation of cyp89a9-1, cyp89a9-2 and mes16-1cyp89a9-1 CYP89A9 CYP89A9-EcoRI-S CCGGAATTCATGGAGATCACCACTATCAT CYP89A9-HindIII-AS CCCAAGCTTTCACTTCCCTTGGATAAAT	ATR-1	<i>ATR-1-Eco</i> RI-S	CCGGAATTCATGACTTCTGCTTTGTATGC	
Complementation of cyp89a9-1, cyp89a9-2 and mes16-1cyp89a9-1CYP89A9CYP89A9-EcoRI-SCCGGAATTCATGGAGATCACCACTATCATCYP89A9-HindIII-ASCCCAAGCTTTCACTTTCTCCTTGGATAAAT		ATR-1-EcoRI-AS	CCGGAATTCtCACCAGACATCTCTGAG	
CYP89A9 CYP89A9-EcoRI-S CCGGAATTCATGGAGATCACCACTATCAT CYP89A9-HindIII-AS CCCAAGCTTTCACTTTCTCCTTGGATAAAT	С	complementation of cyp8	9a9-1, cyp89a9-2 and mes16-1cyp89a9-1	
CYP89A9-HindIII-AS CCCAAGCTTTCACTTTCTCCTTGGATAAAT	CYP89A9	CYP89A9-EcoRI-S	CCGGAATTCATGGAGATCACCACTATCAT	
		CYP89A9-HindIII-AS	CCCAAGCTTTCACTTTCTCCTTGGATAAAT	

Supplemental Table 2. List of Primers Used in this Study.