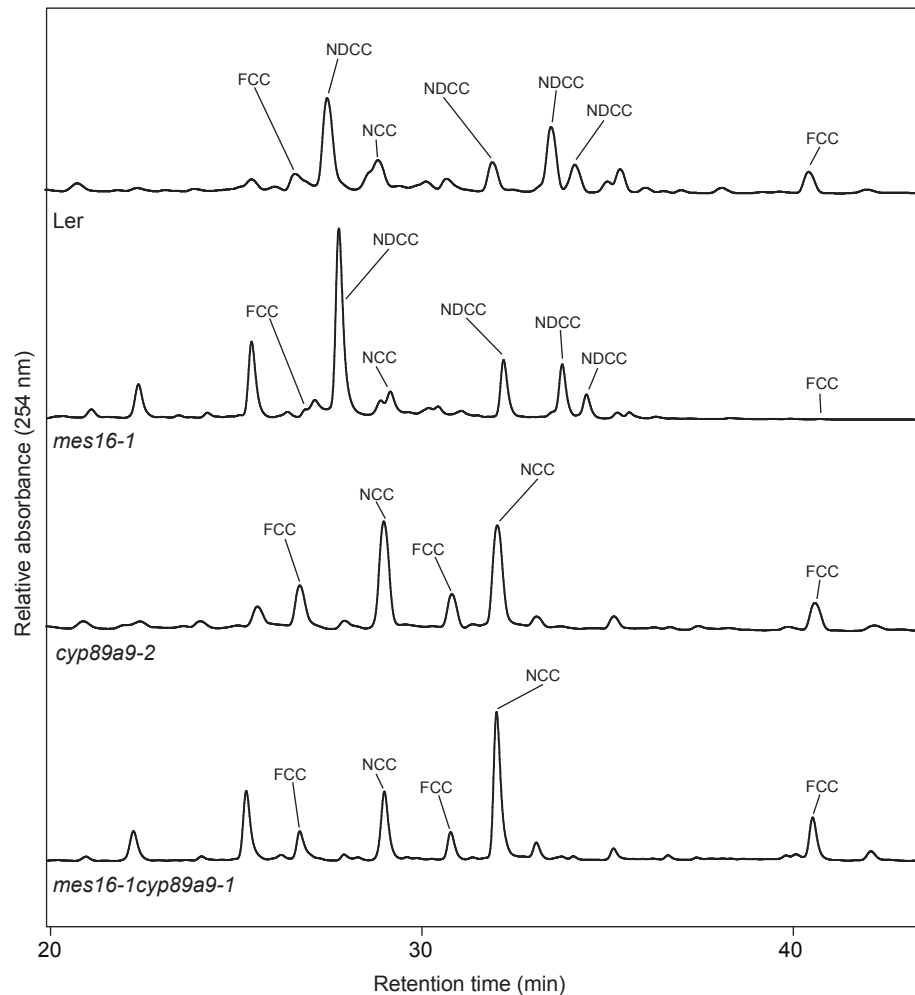


Supplemental Figure 2. Analysis of Gene Expression in *cyp89a9* and *cyp71b19* Mutants and Colorless Chl Catabolites of *cyp71b19* Mutants.

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

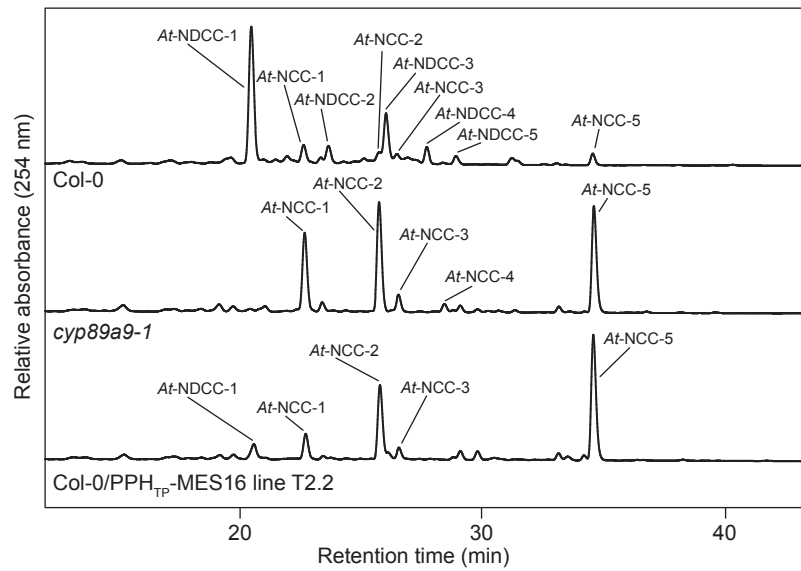
(B) Analysis of gene expression during dark-induced senescence in *cyp89a9-1*, *cyp89a9-2*, *cyp71b19-1* and *cyp71b19-2*. Levels of *ACTIN2* (*ACT2*) gene expression were used as control. Expression was analyzed with nonsaturating numbers of PCR cycles as shown at the right. PCR products were separated 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 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. 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_NAS3__nicotianamine 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).	0.43
264899_at	At1g23130	Polyketide cyclase/dehydrase and lipid transport superfamily protein	0.4
266292_at	At2g29350	SAG13__senescence-associated gene 13	0.37
259058_at	At3g03470	CYP89A9__cytochrome P450, family 87, subfamily A, polypeptide 9	0.33
254174_at	At4g24120	ATYSL1_YSL1__YELLOW STRIPE like 1	0.32
256300_at	At1g69490	ANAC029_ATNAP_NAP__NAC-like, activated by AP3/PI	0.3
254564_at	At4g19170	CCD4_NCED4__nine-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	0.28
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_PWD__phosphoglucan, water dikinase	0.26
250435_at	At5g10380	ATRING1_RING1__RING/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	0.25
266078_at	At2g40670	ARR16_RR16__response regulator 16	0.24
250259_at	At5g13800	CRN1_PPH__pheophytinase	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
254305_at	At4g22200	AKT2_AKT2/3_AKT3_KT2/3__potassium transport 2/3	0.23

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 - 2996 (source: NCBI BLink).	0.23
258925_at	At3g10420	SPD1__P-loop containing nucleoside triphosphate hydrolases superfamily protein	0.22
245385_at	At4g14020	Rapid alkalization factor (RALF) family protein	0.22
253382_at	At4g33040	Thioredoxin superfamily protein	0.22
260155_at	At1g52870	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein	0.21
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	At1g31580	CXC750__ECS1	0.2
251360_at	At3g61210	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	0.2
245346_at	At4g17090	BAM3_BMY8_CT-BMY__chloroplast beta-amylase	0.2
254101_at	At4g25000	AMY1_ATAMY1__alpha-amylase-like	0.2
250690_at	At5g06530	ABCG22_AtABCG22__ABC-2 type transporter family protein	0.2
264901_at	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-yellowing 1	0.19
250446_at	At5g10770	Eukaryotic aspartyl protease family protein	0.19
245901_at	At5g11060	KNAT4__KNOTTED1-like homeobox gene 4	0.19
248566_s_at	At5g49730 At5g49740	ATFRO6_FRO6_FRO6__ferric reduction oxidase 6	0.19
248153_at	At5g54250	ATCNGC4_CNGC4_DND2_HLM1__cyclic nucleotide-gated cation channel 4	0.19
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_VTE2__homogentisate 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	0.18
267076_at	At2g41090	Calcium-binding EF-hand family protein	0.18
263497_at	At2g42540	COR15_COR15A__cold-regulated 15a	0.18
257634_s_at	At3g26170 At3g26180	CYP71B19__cytochrome P450, family 71, subfamily B, polypeptide 19	0.18
254833_s_at	At4g12280 At4g12290	copper amine oxidase family protein	0.18
253779_at	At4g28490	HAE_RLK5__Leucine-rich receptor-like protein kinase family protein	0.18
249797_at	At5g23750	Remorin family protein	0.18
262626_at	At1g06430	FTSH8__FTSH protease 8	0.17
259943_at	At1g71480	Nuclear transport factor 2 (NTF2) family protein	0.17
260774_at	At1g78290	SNRK2-8_SNRK2.8_SRK2C__Protein kinase superfamily protein	0.17
257222_at	At3g27925	Deg1_DEGP1__DegP protease 1	0.17

252648_at	At3g44630	Disease resistance protein (TIR-NBS-LRR class) family	0.17
246335_at	At3g44880	ACD1_LLS1_PAO__Pheophorbide a oxygenase family protein with Rieske [2Fe-2S] domain	0.17
252485_at	At3g46530	RPP13__NB-ARC domain-containing disease resistance protein	0.17
252462_at	At3g47250	Plant protein of unknown function (DUF247)	0.17
254764_at	At4g13250	NYC1__NAD(P)-binding Rossmann-fold superfamily protein	0.17
253358_at	At4g32940	GAMMA-VPE_GAMMAVPE__gamma vacuolar processing enzyme	0.17
249754_at	At5g24530	DMR6__2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	0.17
247356_at	At5g63800	BGAL6_MUM2__Glycosyl hydrolase family 35 protein	0.17
261077_at	At1g07430	HAI2__highly ABA-induced PP2C gene 2	0.16
259661_at	At1g55265	Protein of unknown function, DUF538	0.16
262875_at	At1g64970	G-TMT_TMT1_VTE4__gamma-tocopherol methyltransferase	0.16
261120_at	At1g75410	BLH3__BEL1-like homeodomain 3	0.16
267336_at	At2g19310	HSP20-like chaperones superfamily protein	0.16
266673_at	At2g29630	PY_THIC__thiaminC	0.16
263478_at	At2g31880	EVR_SOBR1__Leucine-rich repeat protein kinase family protein	0.16
263956_at	At2g35940	BLH1_EDA29__BEL1-like homeodomain 1	0.16
258223_at	At3g15840	PIFI__post-illumination chlorophyll fluorescence increase	0.16
258181_at	At3g21670	Major facilitator superfamily protein	0.16
256766_at	At3g22231	PCC1__pathogen and circadian controlled 1	0.16
256754_at	At3g25690	AtCHUP1_CHUP1__Hydroxyproline-rich glycoprotein family protein	0.16
257611_at	At3g26580	Tetratricopeptide repeat (TPR)-like superfamily protein	0.16
251218_at	At3g62410	CP12-2__CP12 domain-containing protein 2	0.16
251221_at	At3g62550	Adenine nucleotide alpha hydrolases-like superfamily protein	0.16
254551_at	At4g19840	ATPP2-A1_ATPP2A-1_PP2-A1__phloem protein 2-A1	0.16
247304_at	At5g63850	AAP4__amino acid permease 4	0.16
247025_at	At5g67030	ABA1_ATABA1_ATZEP_IBS3_LOS6_NPQ2_ZEP__zeaxanthin epoxidase (ZEP) (ABA1)	0.16
261569_at	At1g01060	LHY_LHY1__Homeodomain-like superfamily protein	0.15
261581_at	At1g01140	CIPK9_PKS6_SnRK3.12__CBL-interacting protein kinase 9	0.15
261084_at	At1g07440	NAD(P)-binding Rossmann-fold superfamily protein	0.15
255957_at	At1g22160	Protein of unknown function (DUF581)	0.15
262916_at	At1g59700	ATGSTU16_GSTU16__glutathione S-transferase TAU 16	0.15
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_CSLB03__cellulose 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-12__homeobox 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	ATSPS4F__Sucrose-phosphate synthase family protein	0.15
254573_at	At4g19420	Pectinacetylerase family protein	0.15
248333_at	At5g52390	PAR1 protein	0.15

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/cgi-bin/ntools_agi_converter.cgi.

^b For information about the calculation of the expression score K, see <https://www.genevestigator.com/userdocs/manual/biomarker.html>.

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

GENE / MUTANT	PRIMER NAME	SEQUENCE (5'→3')
<i>T-DNA confirmation</i>		
<i>mes16-1</i>	MES16-1-RP	GTTGAAGAAAAGAAACCGCAC
	MES16-1-LP	CTGAGCCCGTAATTCACITTTG
<i>cyp89a9-1</i>	CYP89A9-1-RP	TACGACAAATAAGCCCAATGG
	CYP89A9-1-LP	GCTCTGATGTGTTTCGGAGAG
<i>cyp89a9-2</i>	CYP89A9-2-RP	CTCACGATCTCCGAGTCACTC
	CYP89A9-2-LP	GCGTGGACCAAATAAACAAG
<i>cyp71b19-1</i>	CYP71B19-1-RP	ATCGATGATGTCTTCGTGCTC
	CYP71B19-1-LP	CCACTAGACCATTGGCTTTTTTC
<i>cyp71b19-2</i>	CYP71B19-2-RP	CCTCTCGGATATGCCTAAAGG
	CYP71B19-2-LP	CCAACTTTCTCTTCCCGAATC
SALK T-DNA	LBb1.3	ATTTTGCCGATTTCCGGAAC
SAIL T-DNA	LB2	GCTTCCTATTATATCTTCCCAAATTACCAATACA
JIC SM T-DNA	Spm32	TACGAATAAGAGCG CCATTTTAGAGTGA
JIC GT T-DNA	Ds3-1	ACCCGACCGGATCGTATCGGT
<i>RT-PCR</i>		
<i>CYP89A9</i>	CYP89A9_FL_S	TCGGAAACATCATCTGGCTTAA
	CYP89A9_FL_AS	GCTTTGAAAGGGTTTTTCATGACC
<i>CYP71B19</i>	CYP71B19_FL_S	TCTCATCACCTTCGTTTCGT
	CYP71B19_FL_AS	TCTTTATGTGTCATCCCATCAG
<i>ACT2</i>	ACT2-S	TGGAATCCACGAGACAACCTA
	ACT2-AS	TTCTGTGAACGATTCTGGAC
<i>Cloning of CYP89A9-GFP</i>		
<i>CYP89A9</i>	CYP89A9- <i>Xma</i> I-S	TCCCCCGGGATGGAGATCACCCTATC
	CYP89A9- <i>Nhe</i> I-AS	CTAGCTAGCCTTTCTCCTTGGATAAATATTTGC
<i>Cloning of CYP89A9 and ATR-1 in pFastbac1 and pFastbac DUAL</i>		
<i>CYP89A9</i>	CYP89A9- <i>Eco</i> RI-S	CCGGAATTCATGGAGATCACCCTATCAT
	CYP89A9- <i>Eco</i> RI-AS	CCGGAATTCCTACTTTCTCCTTGGATAAA
<i>CYP89A9</i>	CYP89A9- <i>Kpn</i> I-S	CGGGGTACCATGGAGATCACCCTATCATATTCC
	CYP89A9- <i>Kpn</i> I-AS	GCAAATATTTATCCAAGGAGAAAGTGAGGTACCCCG
<i>ATR-1</i>	ATR-1- <i>Eco</i> RI-S	CCGGAATTCATGACTTCTGCTTTGTATGC
	ATR-1- <i>Eco</i> RI-AS	CCGGAATTCtCACCAGACATCTCTGAG
<i>Complementation of cyp89a9-1, cyp89a9-2 and mes16-1cyp89a9-1</i>		
<i>CYP89A9</i>	CYP89A9- <i>Eco</i> RI-S	CCGGAATTCATGGAGATCACCCTATCAT
	CYP89A9- <i>Hind</i> III-AS	CCCAAGCTTTCCTTTCTCCTTGGATAAAT