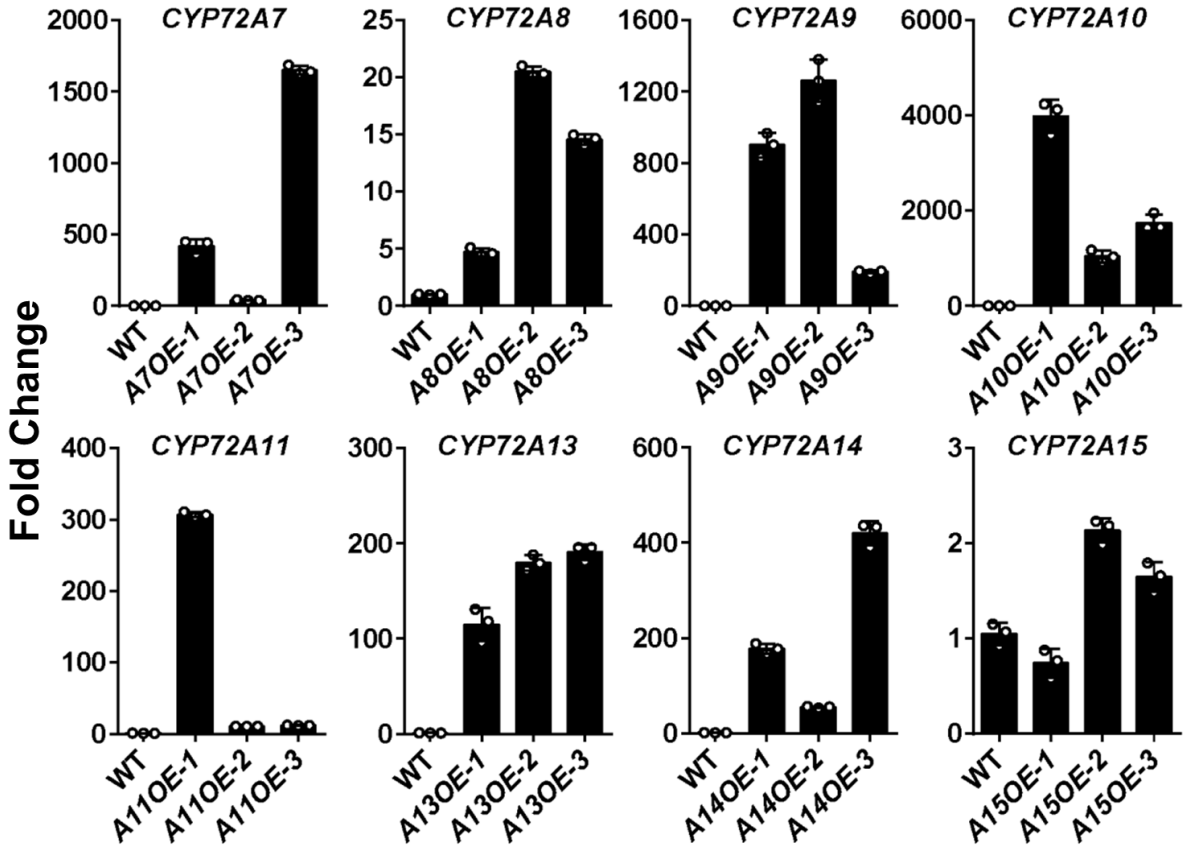
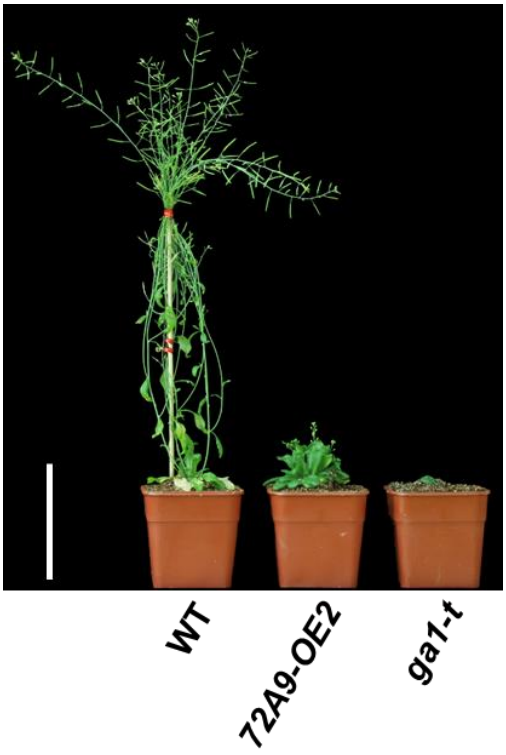
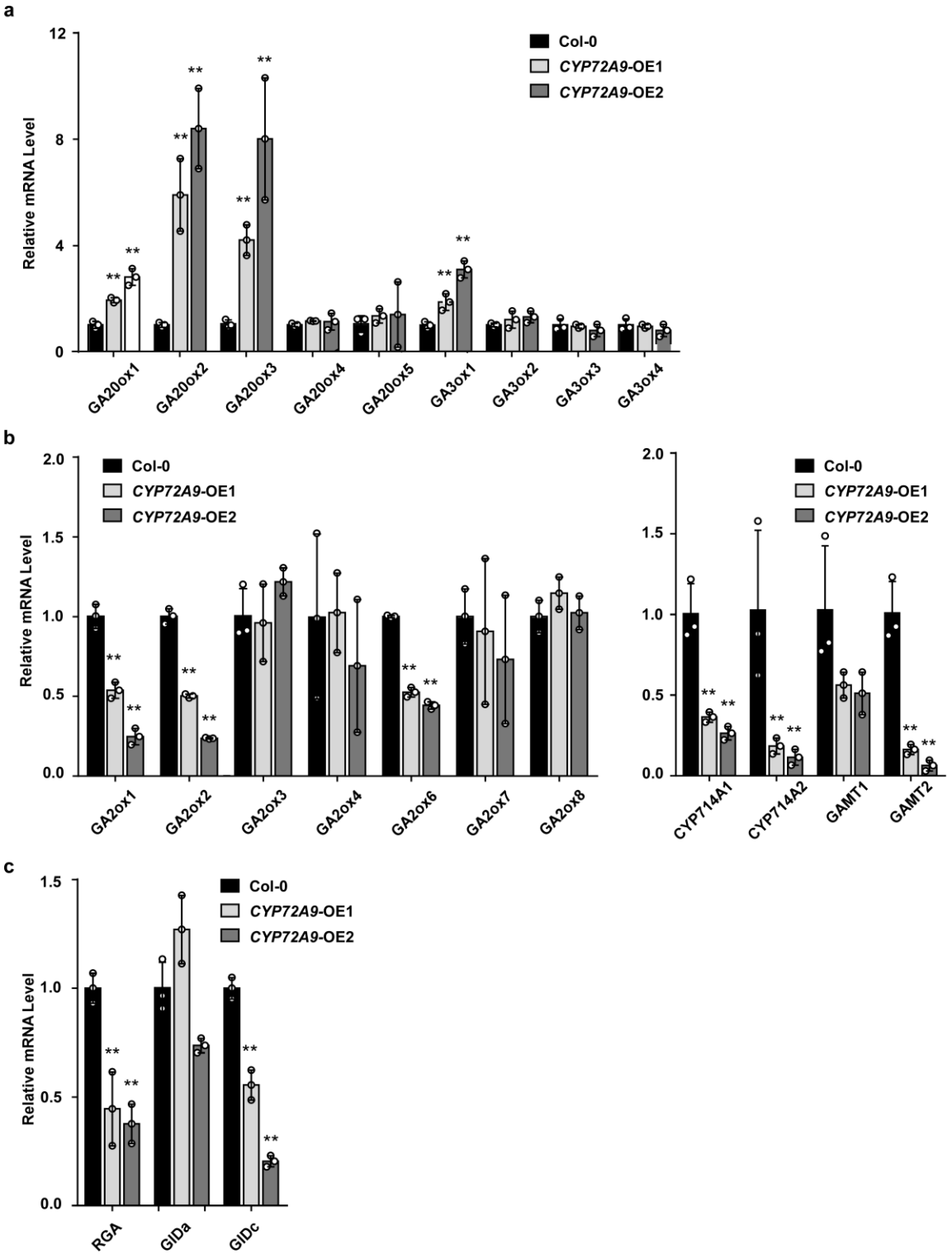
Supplementary Data



Supplementary Fig. 1 qRT-PCR analysis of each *AtCYP72* gene in the 10-day-old seedlings of the corresponding *AtCYP72A*-overexpressing Arabidopsis. Three independent homozygous lines for each *AtCYP72A* gene were analyzed, and *Actin 2* (*At3g18780*) was used as a reference gene in the analysis. The expression level of each *AtCYP72* in WT was set as 1.0. Error bars represent means ± SDs (n = 3 biologically independent samples).



Supplementary Fig. 2 Phenotypes of adult plants (8 weeks old) of WT, *72A9*-OE2, and *ga1-t*. Scale bar = 10 cm. This experiment was repeated three times with similar results.



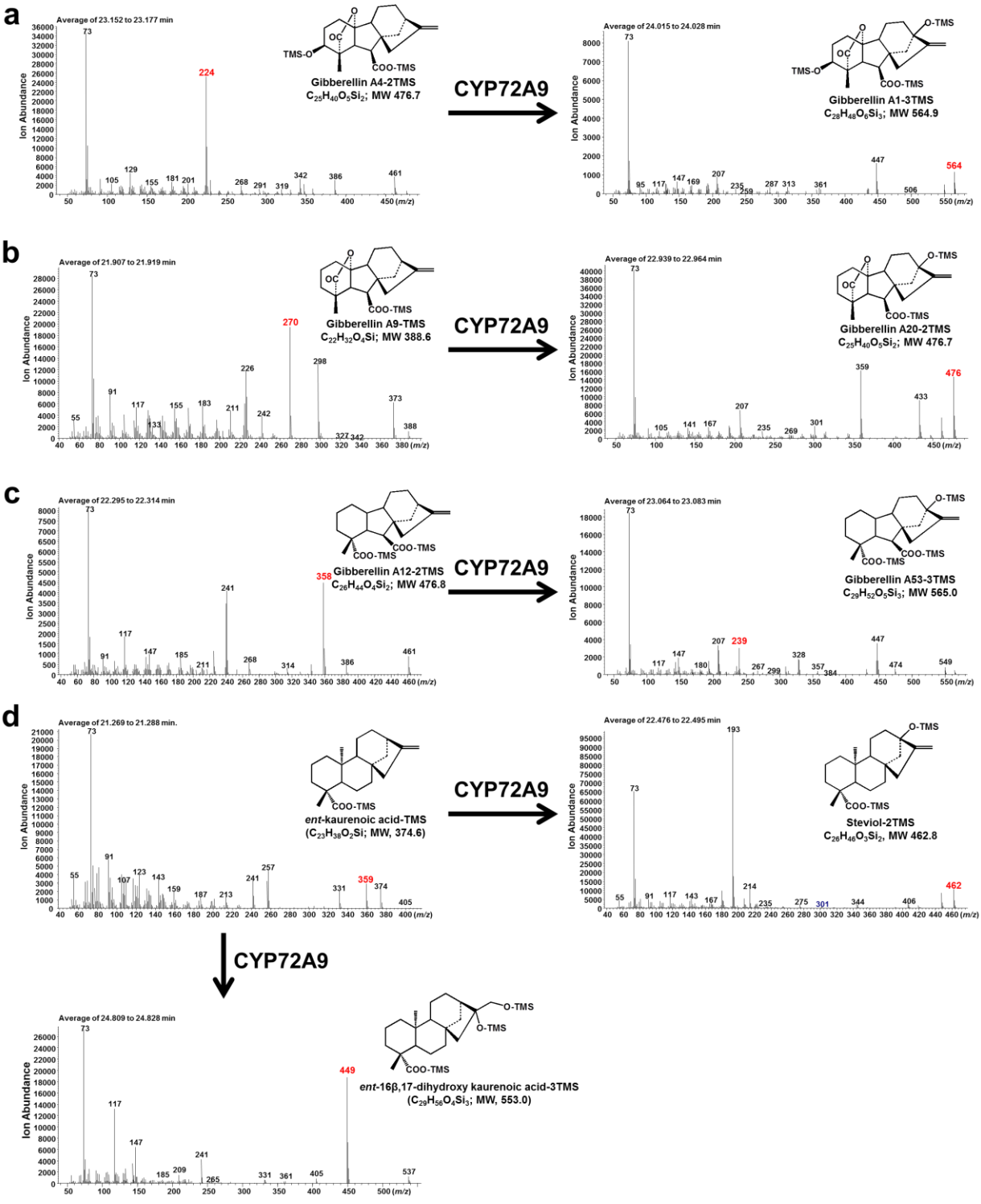
Supplementary Fig. 3 Quantitative RT-PCR (qRT-PCR) analysis of GA metabolism and signaling genes in WT and *CYP72A9*-OE lines. The plant samples (rosette leaves of 4-week-old Arabidopsis) used here were the same as those used in Fig. 2c. *At1g13320*, *At4g26410*, and *At5g46630* were used as reference genes in this analysis. The values are presented as the means ± SDs (n = 3 biologically independent samples). The transcript level of each

tested gene in WT was set as 1.0. **, $P < 0.01$ (two-tailed Student's *t*-test), significantly different from wild-type (Col-0).

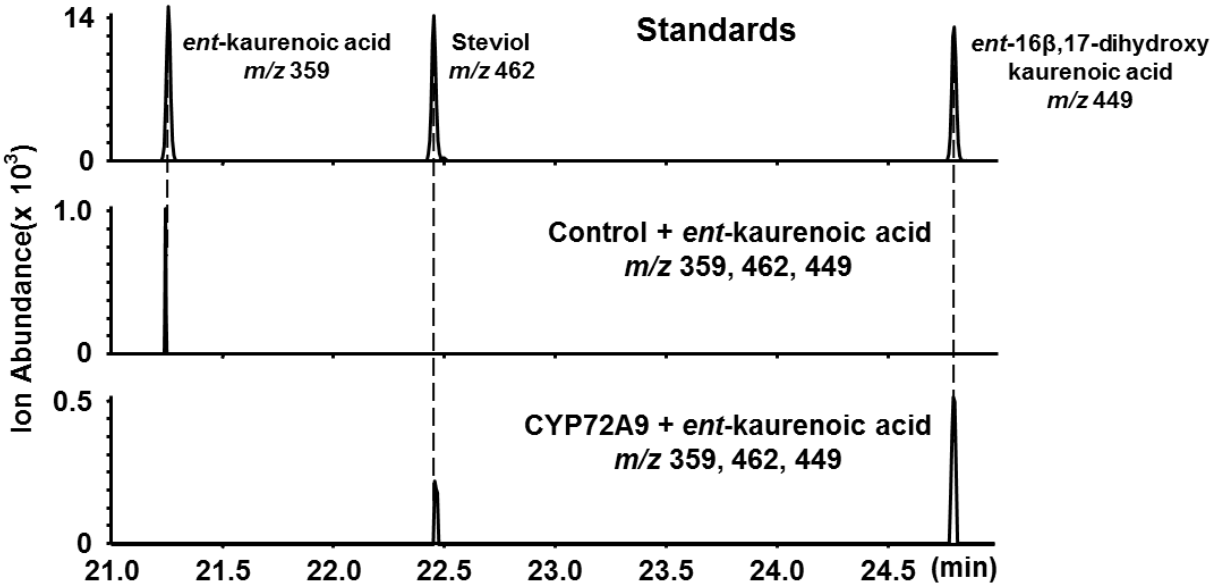
A. qRT-PCR analysis of GA biosynthesis genes (*GA20ox1, At4G25420; GA20ox2, At5G51810; GA20ox3, At5G07200; GA20ox4, At1G60980; GA3ox1, At1G15550; GA3ox2, At1G80340; GA3ox3, At4G21690; GA3ox4, At1G80330*) in the WT and two *CYP72A9*-OE lines.

B. qRT-PCR analysis of GA deactivation genes (*GA2ox1, At1G78440; GA2ox2, At1G30040; GA2ox3, At2G34555; GA2ox4, At1G47990; GA2ox6, At1G02400; GA2ox7, At1G50960; GA2ox8, At4G21200; CYP714A1, At5G24910; CYP714A2, At5G24900; GAMT1, At4G26420; GAMT2, At5G56300*) in the WT and two *CYP72A9*-OE lines.

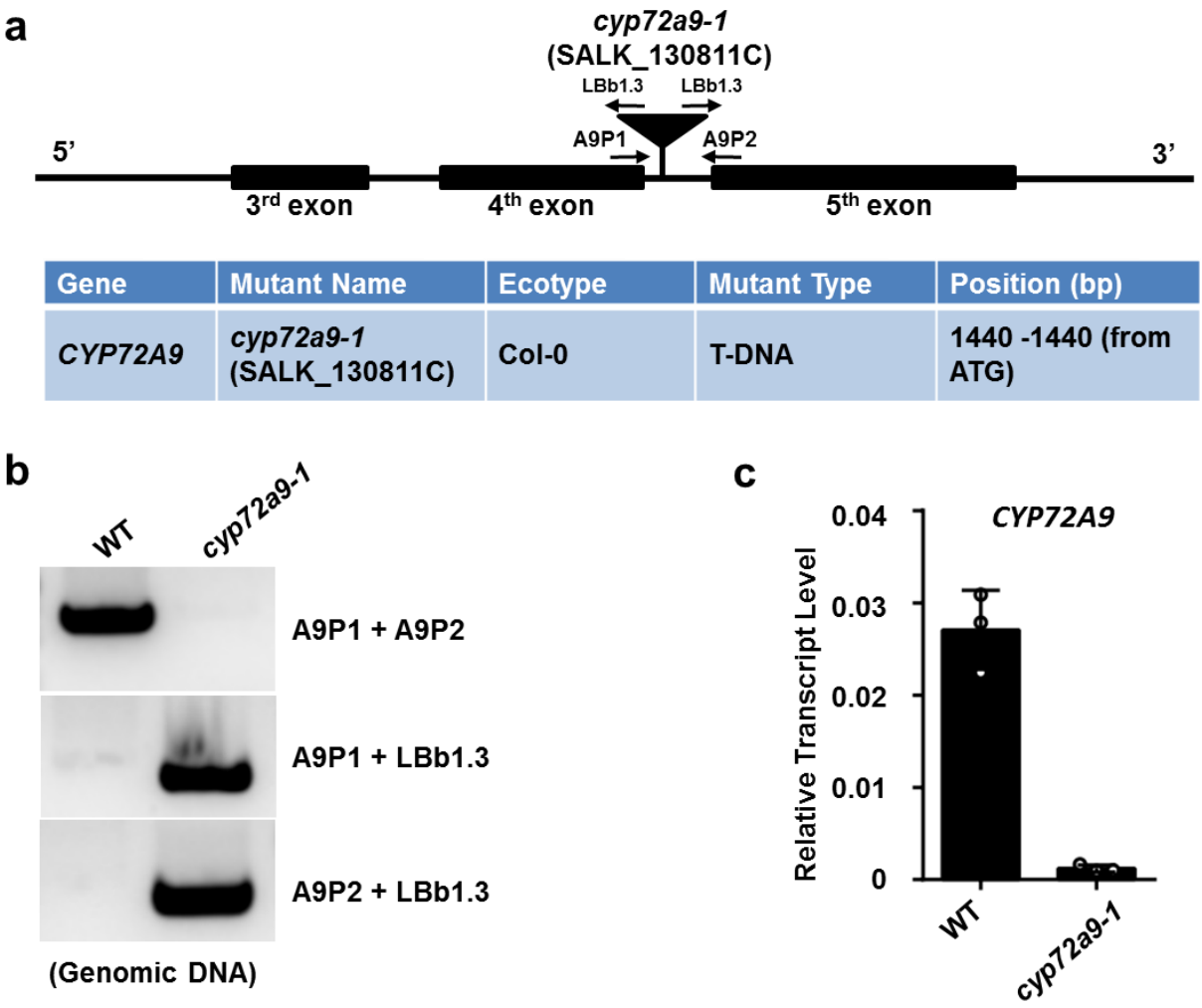
C. qRT-PCR analysis of GA signaling genes (*RGA, At2G01570; GID1a, At3G05120; GID1c, At5G27320*) in the WT and two *CYP72A9*-OE lines.



Supplementary Fig. 4 Mass spectra (GC-MS) of the trimethylsilyl esters of the chemical standards used in this study. The *m/z* number used in SIM scanning of different chemicals is marked in red. This experiment was repeated three times with similar results.



Supplementary Fig. 5 CYP72A9 oxidizes *ent*-kaurenoic acid to produce steviol and *ent*-16β,17- dihydroxy kaurenoic acid. Chromatogram of selected ions of *m/z* 359 for *ent*-kaurenoic acid, *m/z* 462 for steviol, and *m/z* 449 for *ent*-16β,17- dihydroxy kaurenoic acid (see Supplementary Fig. 4d). It is noteworthy that the *y* axis scale for each reaction is arbitrary and provided for clarity. This experiment was repeated three times with similar results.



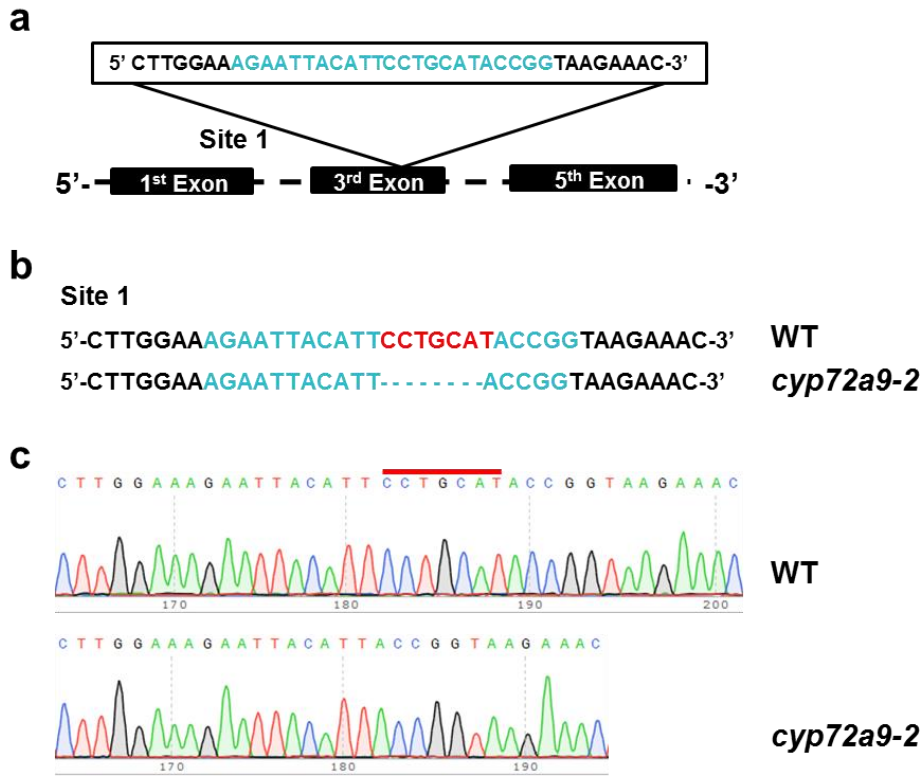
Gene	Mutant Name	Ecotype	Mutant Type	Position (bp)
CYP72A9	*cyp72a9-1* (SALK_130811C)	Col-0	T-DNA	1440 -1440 (from ATG)

Supplementary Fig. 6 Characterization of the *CYP72A9* T-DNA insertion mutant.

a. The positions of T-DNA insertions, which are marked on the gene model of *CYP72A9*.

b. Characterization of *cyp72a9-1* at the genomic level. This experiment was repeated two times with similar results.

c. qRT-PCR analysis of *CYP72A9* in the developing seeds/siliques of WT and the *cyp72a9-1* mutant. The values are presented as the means ± SDs (n = 3 biologically independent samples).

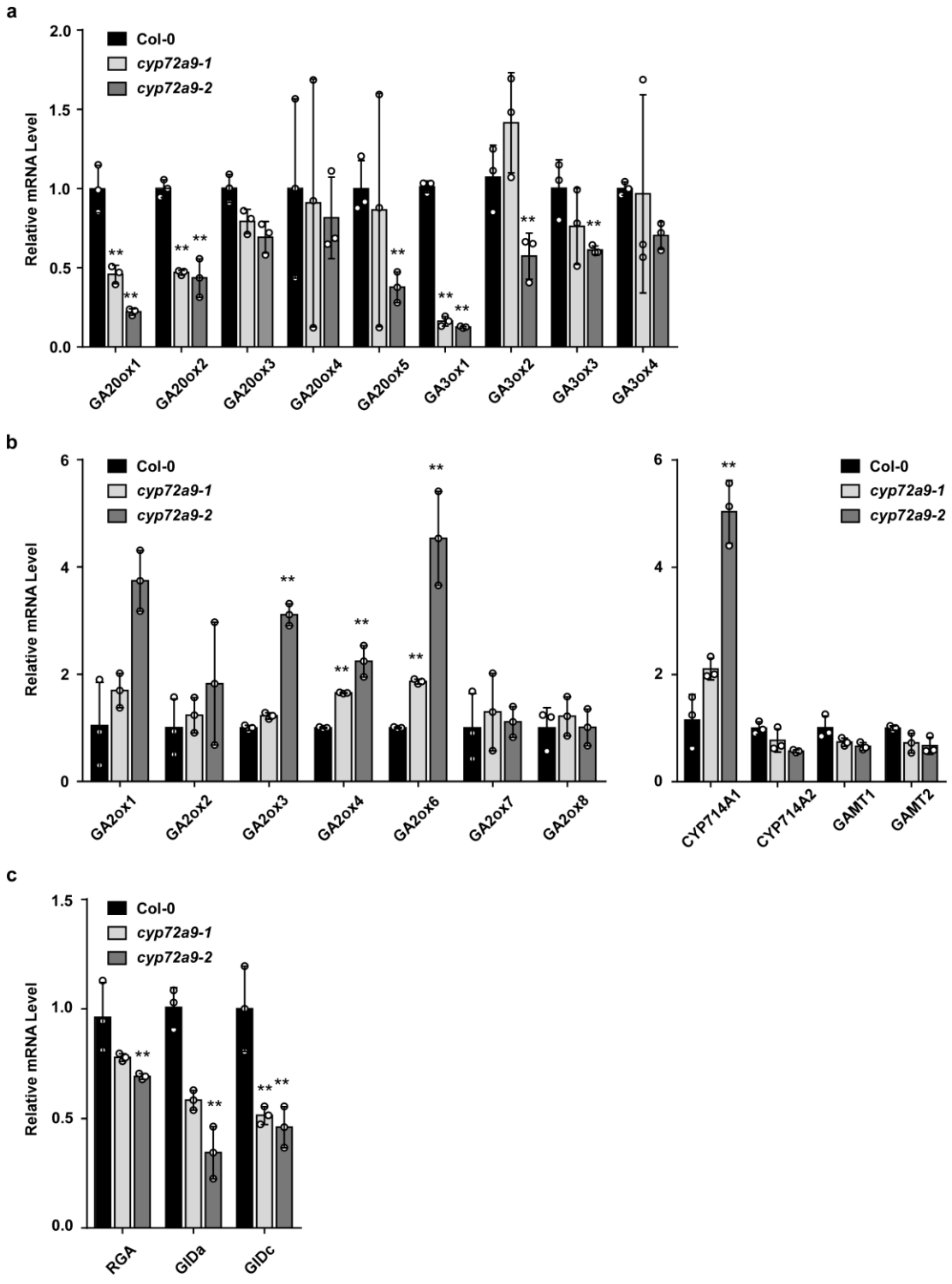


Supplementary Fig. 7 *cyp72a9-2* mutant generated via CRISPR/Cas9.

a. Schematic of the ssDNA template-mediated HDR (homology-directed repair) in *CYP72A9*. The target sequence is indicated in blue.

b. Representative sequences of WT and the *cyp72a9-2* mutant.

c. The DNA sequencing peaks showed evidence of successful gene editing in the target region of *CYP72A9*. Seven deleted base pairs are highlighted by a red line.



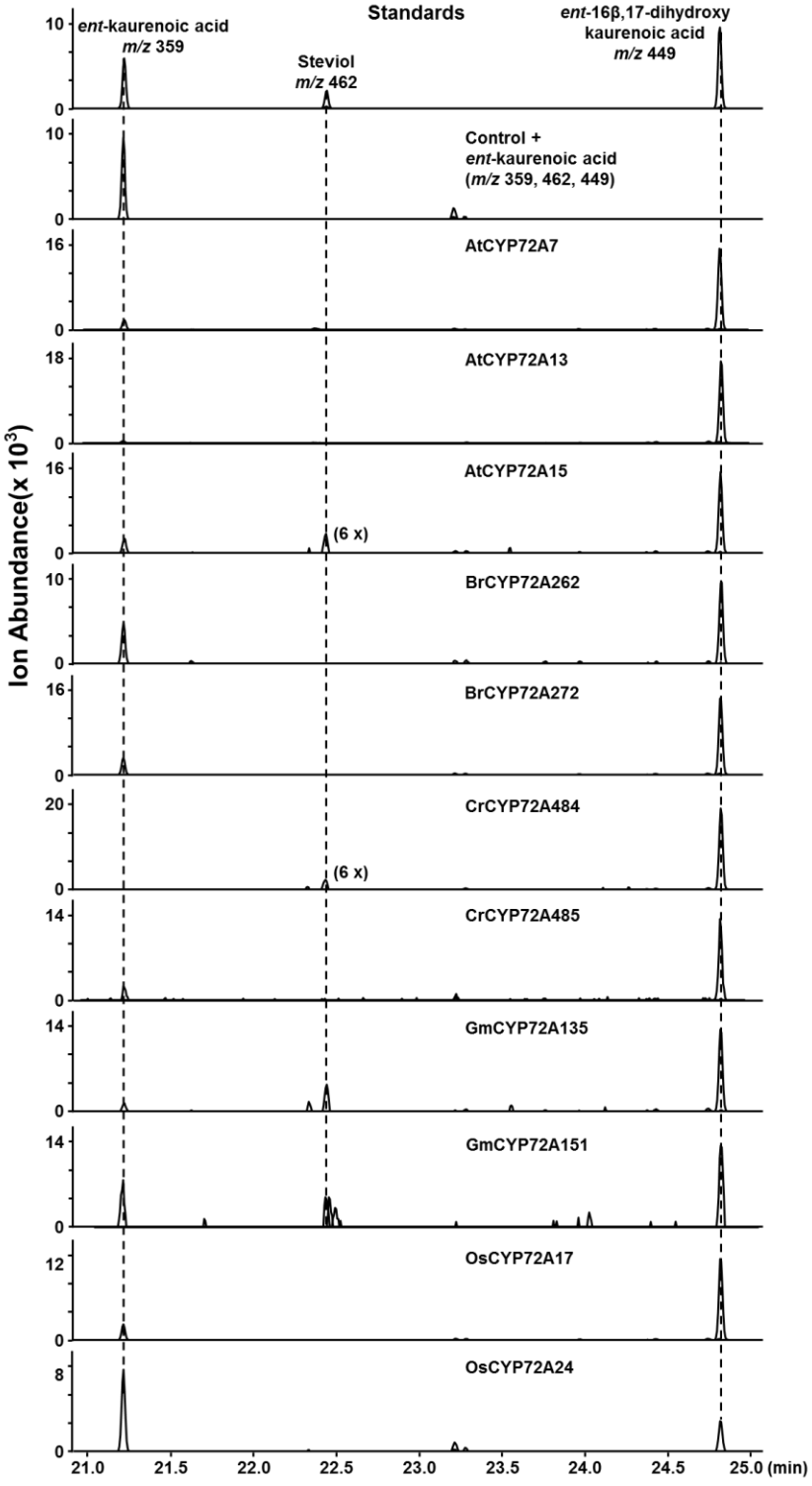
Supplementary Fig. 8 Quantitative RT-PCR (qRT-PCR) analysis of GA metabolism and signaling genes in the WT and *cyp72a9* mutants. The plant samples (developing seeds/siliques) used herein were the same as those used in Fig. 4d. *At1g13320*, *At4g26410*, and *At5g46630* were used as reference genes in this analysis. The values are

presented as the means ± SDs (n = 3 biologically independent samples). The transcript level of each tested gene in WT was set as 1.0. **, $P < 0.01$ (two-tailed Student's t-test), significantly different from wild-type (Col-0).

A. qRT-PCR analysis of GA biosynthesis genes (*GA20ox1, At4G25420; GA20ox2, At5G51810; GA20ox3, At5G07200; GA20ox4, At1G60980; GA3ox1, At1G15550; GA3ox2, At1G80340; GA3ox3, At4G21690; GA3ox4, At1G80330*) in WT and *cyp72a9* mutants.

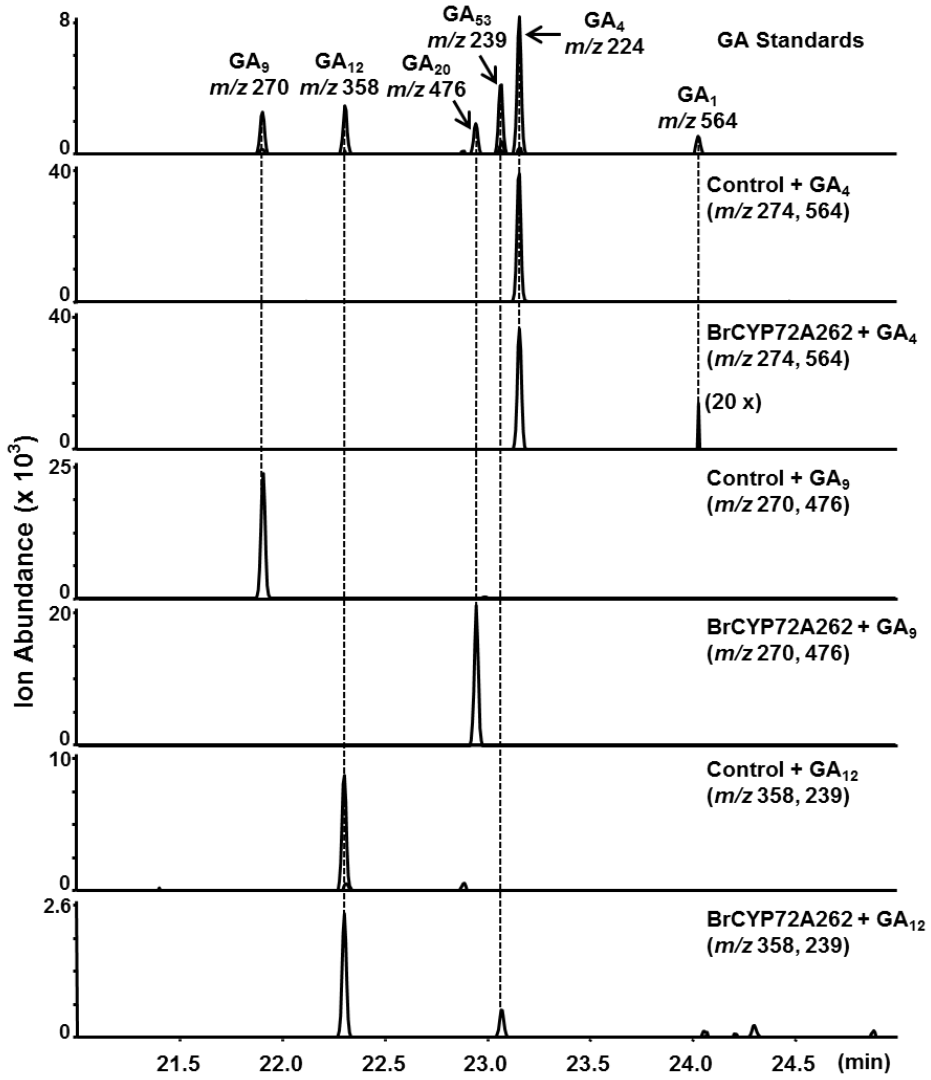
B. qRT-PCR analysis of GA deactivation genes (*GA2ox1, At1G78440; GA2ox2, At1G30040; GA2ox3, At2G34555; GA2ox4, At1G47990; GA2ox6, At1G02400; GA2ox7, At1G50960; GA2ox8, At4G21200; CYP714A1, At5G24910; CYP714A2, At5G24900; GAMT1, At4G26420; GAMT2, At5G56300*) in WT and *cyp72a9* mutants.

C. qRT-PCR analysis of GA signaling genes (*RGA, At2G01570; GID1a, At3G05120; GID1c, At5G27320*) in WT and *cyp72a9* mutants.

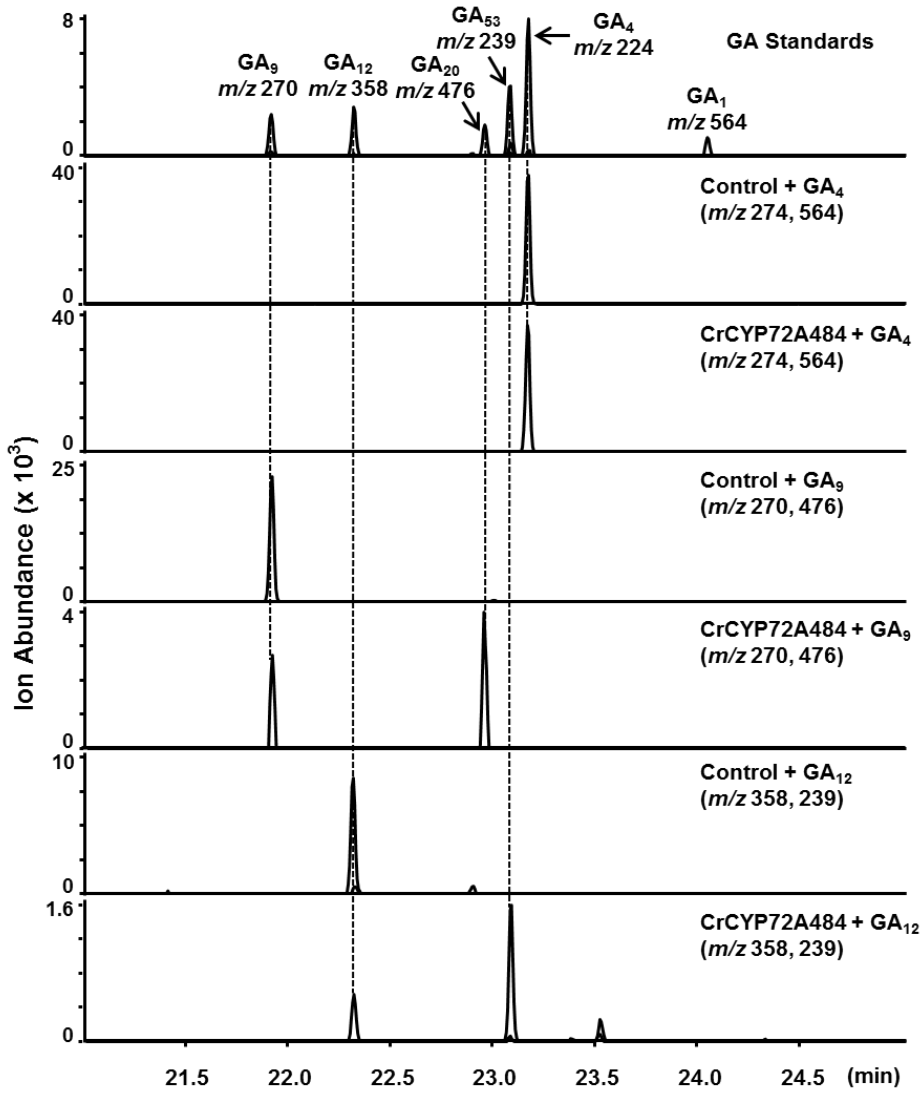


Supplementary Fig. 9 Biochemical screening of CYP72As using *ent*-kaurenoic acid as substrate. Chromatogram of selected ions of *m/z* 359 for KA, *m/z* 462 for steviol, and *m/z* 449 for *ent*-16β,17-dihydroxy KA. It is noteworthy that the *y* axis scale for each reaction is arbitrary and provided for clarity, and the steviol peak has

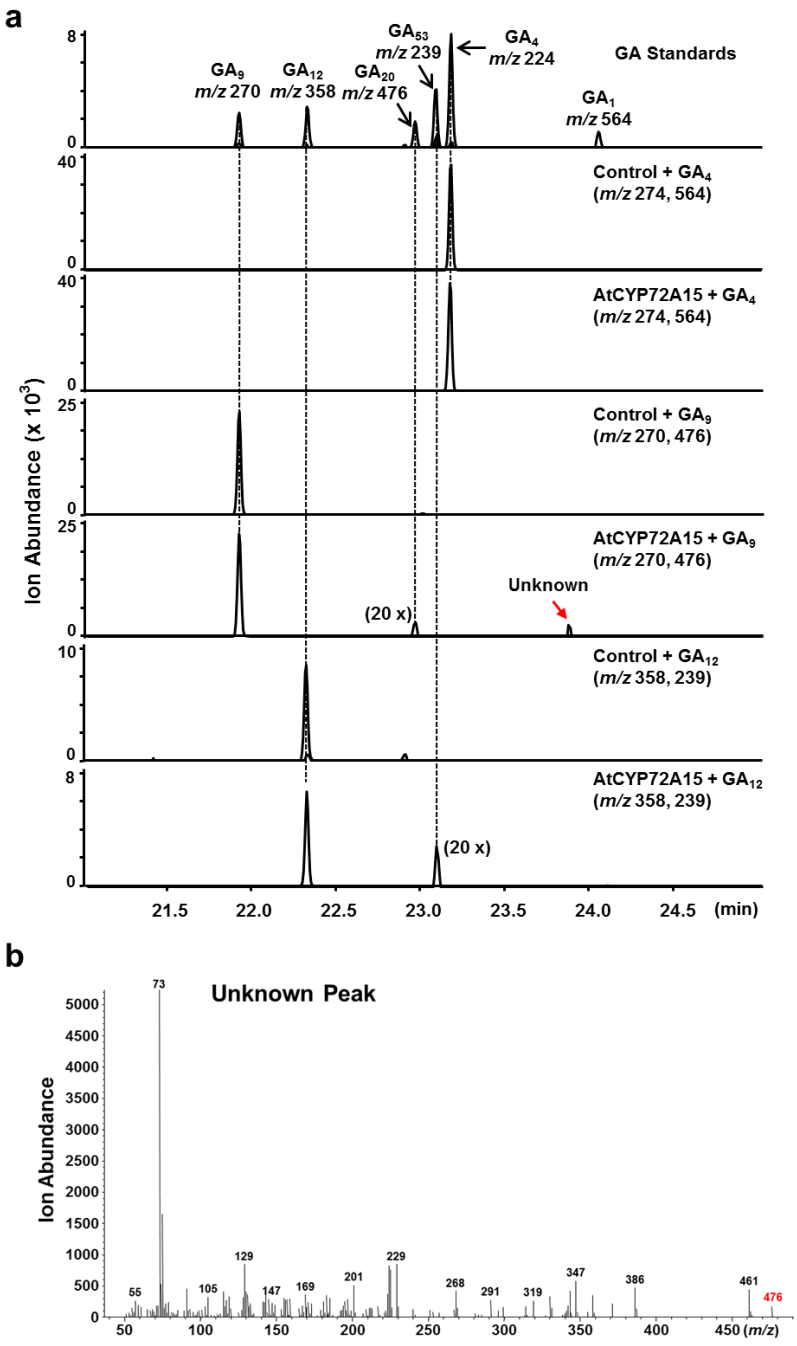
been amplified by 6 times to allow easier visualization. Control, yeast strain harboring pESC-Leu empty vector. This experiment was repeated two times with similar results.



Supplementary Fig. 10 Biochemical assays of CYP72A262 from *Brassica rapa*. CYP72A262 converted GA_4, GA_9, and GA_{12} into GA_1, GA_{20}, and GA_{53}, as verified by comparison to authentic standards. Chromatogram of selected ions of *m/z* 546 for GA_1, *m/z* 224 for GA_4, *m/z* 270 for GA_9, *m/z* 358 for GA_{12}, *m/z* 476 for GA_{20}, and *m/z* 239 for GA_{53}. It is noteworthy that the *y* axis scale for each reaction is arbitrary and provided for clarity and the GA_4 region has been amplified by 20 times to allow easier visualization. Control, yeast strain harboring pESC-Leu empty vector. This experiment was repeated two times with similar results.



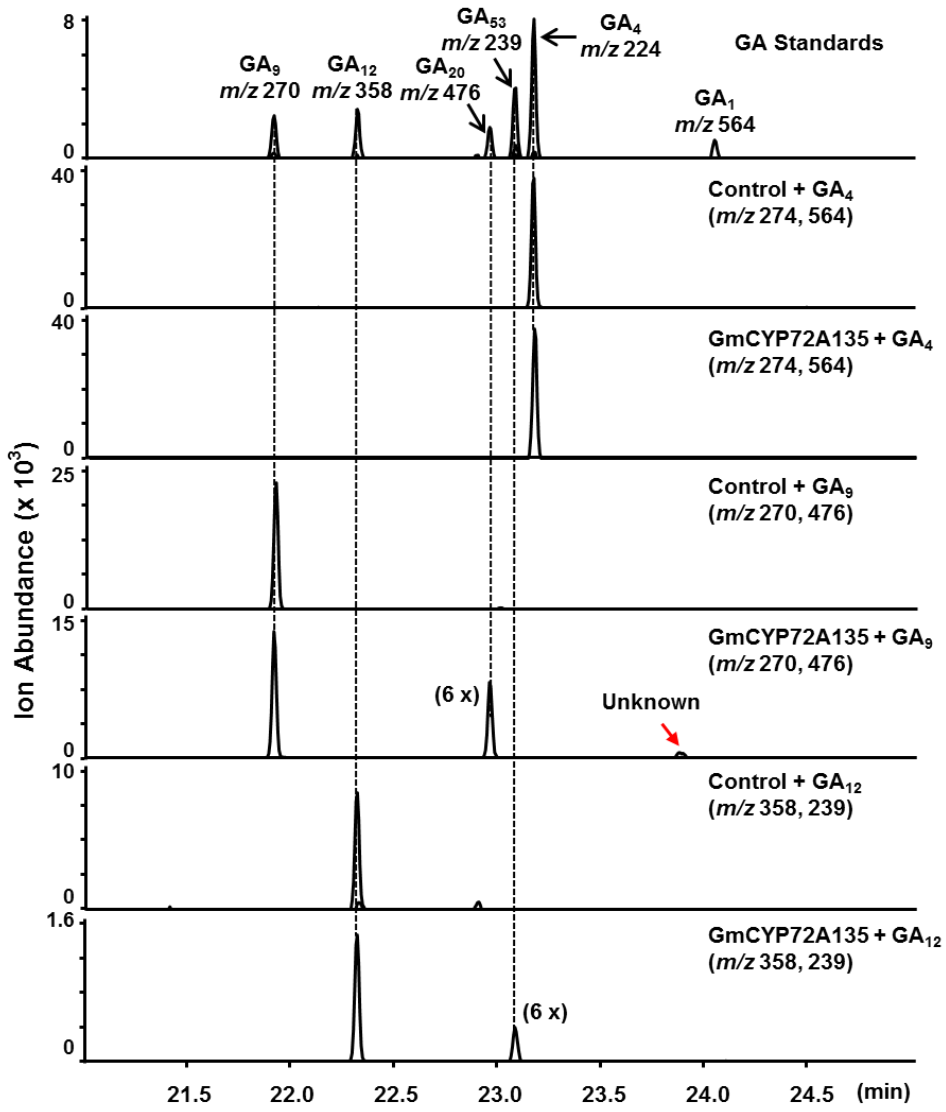
Supplementary Fig. 11 Biochemical assays of CYP72A484 from *Capsella rubella*. CYP72A484 converted GA_9, and GA_{12} into GA_{20}, and GA_{53}, as verified by comparison to authentic standards. Chromatogram of selected ions of *m/z* 546 for GA_1, *m/z* 224 for GA_4, *m/z* 270 for GA_9, *m/z* 358 for GA_{12}, *m/z* 476 for GA_{20}, and *m/z* 239 for GA_{53}. It is noteworthy that the *y* axis scale for each reaction is arbitrary and provided for clarity. Control, yeast strain harboring pESC-Leu empty vector. This experiment was repeated two times with similar results.



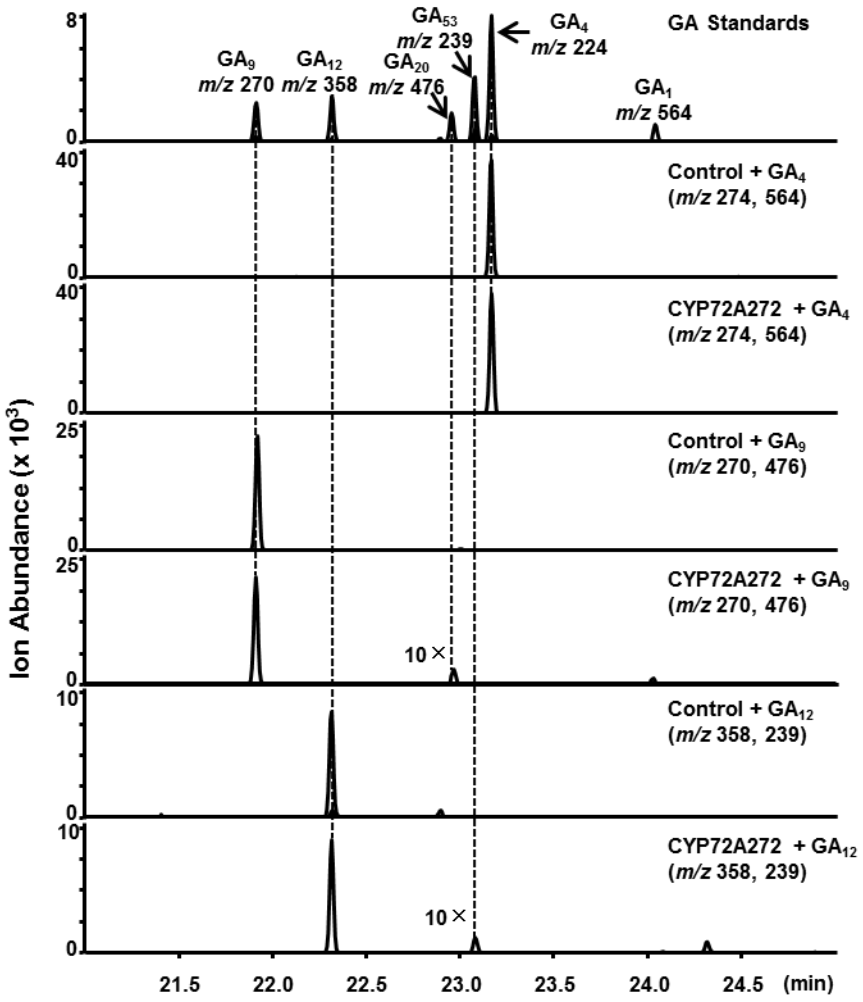
Supplementary Fig. 12 Biochemical assays of CYP72A15 from *Arabidopsis thaliana*.

a. CYP72A15 converted GA_9, and GA_{12} into GA_{20} (and an unknown product) and GA_{53}, as verified by comparison to authentic standards. Chromatogram of selected ions of *m/z* 546 for GA_1, *m/z* 224 for GA_4, *m/z* 270 for GA_9, *m/z* 358 for GA_{12}, *m/z* 476 for GA_{20}, and *m/z* 239 for GA_{53}. It is noteworthy that the *y* axis scale for each reaction is arbitrary and provided for clarity. Control, yeast strain harboring pESC-Leu empty vector. This experiment was repeated two times with similar results.

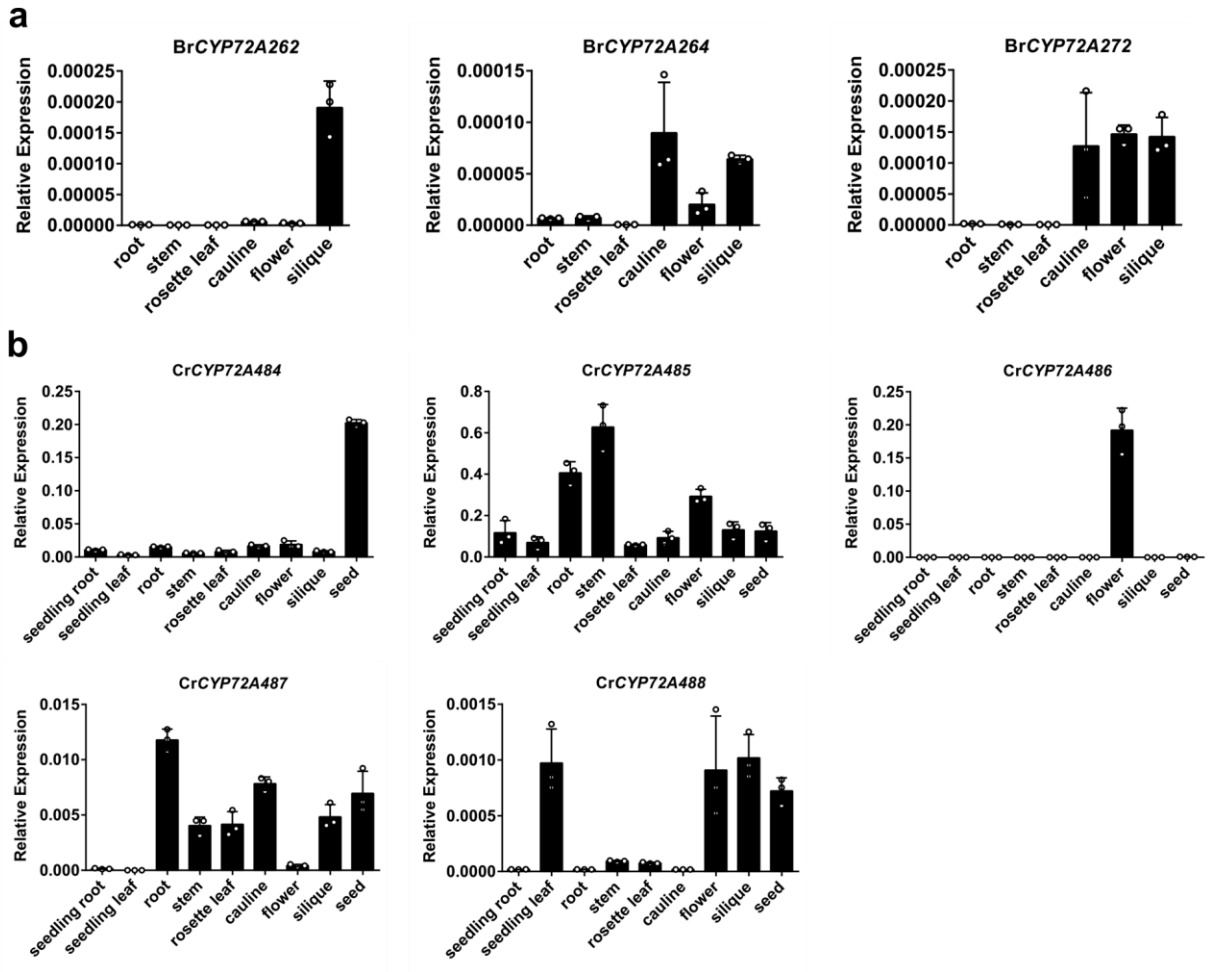
b. The mass spectrum of the unknown product generated from GA_9 by CYP72A15.



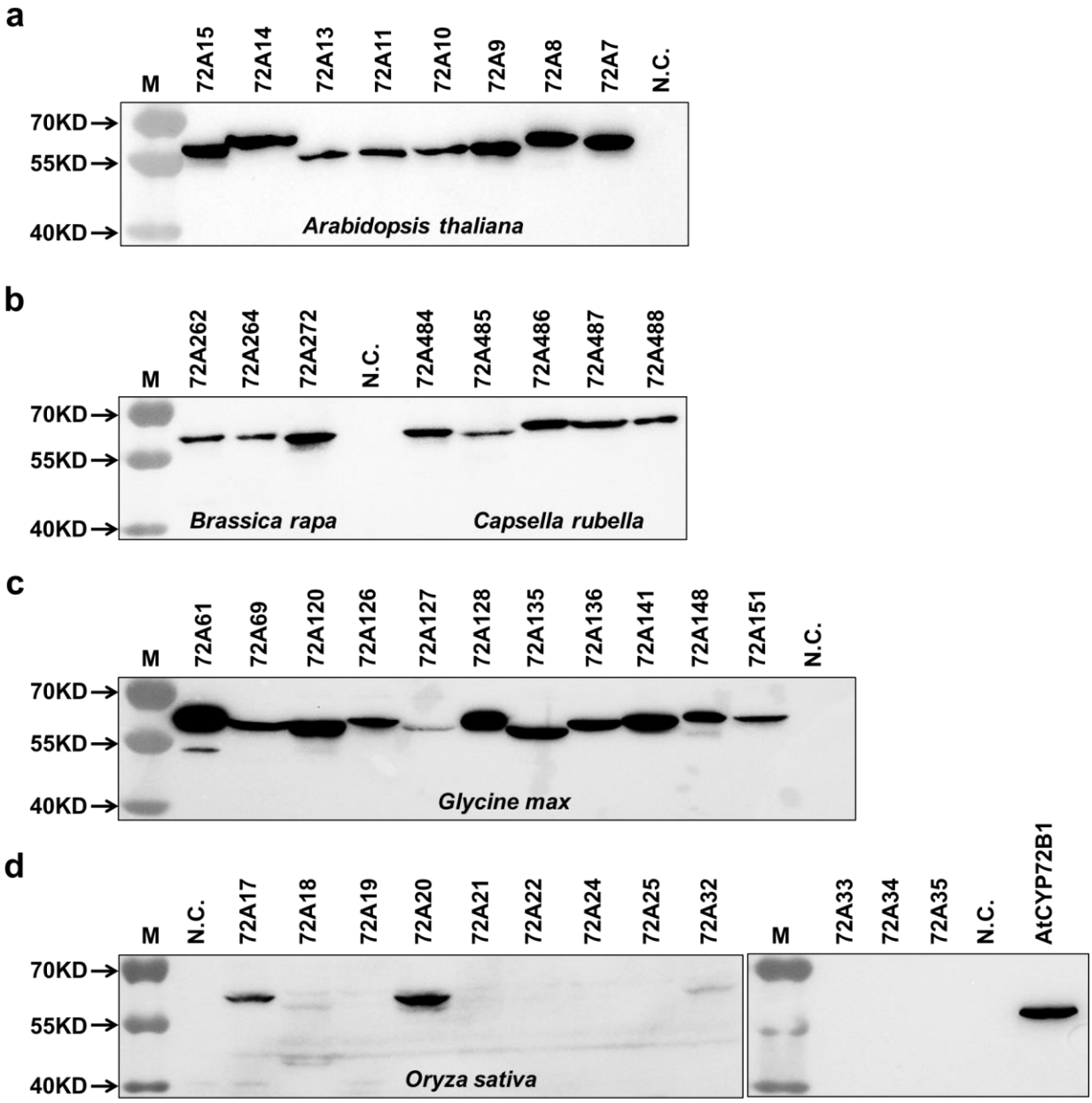
Supplementary Fig. 13 Biochemical assays of CYP72A135 from *Glycine max*. CYP72A135 converted GA_9, and GA_{12} into GA_{20} (and an unknown product) and GA_{53}, as verified by comparison to authentic standards. Chromatogram of selected ions of *m/z* 546 for GA_1, *m/z* 224 for GA_4, *m/z* 270 for GA_9, *m/z* 358 for GA_{12}, *m/z* 476 for GA_{20}, and *m/z* 239 for GA_{53}. It is noteworthy that the *y* axis scale for each reaction is arbitrary and provided for clarity. Control, yeast strain harboring pESC-Leu empty vector. The unknown product (marked by a red arrow) was the same as that shown in Supplementary Fig.12. This experiment was repeated two times with similar results.



Supplementary Fig. 14 Biochemical assays of CYP72A272 from *Brassica rapa*. CYP72A272 converted GA_9, and GA_{12} into GA_{20} and GA_{53}, as verified by comparison to authentic standards. Chromatogram of selected ions of *m/z* 546 for GA_1, *m/z* 224 for GA_4, *m/z* 270 for GA_9, *m/z* 358 for GA_{12}, *m/z* 476 for GA_{20}, and *m/z* 239 for GA_{53}. It is noteworthy that the *y* axis scale for each reaction is arbitrary and provided for clarity. Control, yeast strain harboring pESC-Leu empty vector. This experiment was repeated two times with similar results.



Supplementary Fig. 15 Tissue-specificity of *CYP72A* genes in *Brassica rapa* (a) and *Capsella rubella* (b). The values are presented as the means ± SDs (n = 3 biologically independent samples).



Supplementary Fig. 16 Detection of C-terminal Myc-tagged P450 protein in the WAT11 yeast strain with anti-Myc monoclonal antibody. This experiment was repeated at least two times with similar results. a. CYP72As from *Arabidopsis thaliana*; **b.** CYP72As from *Brassica rapa* and *Capsella rubella*; **c.** CYP72As from *Glycine max*; **d.** CYP72As from *Oryza sativa*. AtCYP72B1 was included in this assay. Twenty μg of microsomal protein was loaded in each lane. The calculated molecular weight of each Myc-tagged P450 is listed below: AtCYP72A7 (59.5KD), AtCYP72A8 (59.8KD), AtCYP72A9 (59.6KD), AtCYP72A10 (59.7KD), AtCYP72A11 (59.3KD), AtCYP72A13 (59.7KD), AtCYP72A14 (59.7KD), AtCYP72A15 (59.6KD), AtCYP72B1 (60.5KD), BrCYP72A262 (59.4KD), BrCYP72A264 (59.4KD) BrCYP72A272 (59.2KD), CrCYP72A484 (59.3KD), CrCYP72A485 (59.4KD), CrCYP72A486 (59.8KD), CrCYP72A487 (59.9KD), CrCYP72A488 (59.8KD),

GmCYP72A61 (62.0KD), GmCYP72A69 (59.8KD), GmCYP72A120 (61.1KD), GmCYP72A126 (61.0KD), GmCYP72A127 (61.3KD), GmCYP72A128 (58.8KD), GmCYP72A135 (60.7KD), GmCYP72A136 (61.0KD), GmCYP72A141 (60.9KD), GmCYP72A148 (61.1KD), GmCYP72A151 (62.7KD), OsCYP72A17 (63.1KD), OsCYP72A18 (61.1KD), OsCYP72A19 (44.6KD), OsCYP72A20 (61.4KD), OsCYP72A21 (61.4KD), OsCYP72A22 (54.4KD), OsCYP72A24 (60.7KD), OsCYP72A25 (60.5KD), OsCYP72A32 (62.6KD), OsCYP72A33 (64.2KD), OsCYP72A34 (60.5KD), OsCYP72A35 (60.3KD). N.C., negative control, the microsome protein prepared from WAT11 yeast strain harboring pESC-Leu empty vector was loaded. M, protein marker.

Supplementary Table 1. Primers used in this study.

Primer name	Sequence (5' to 3')
For CYP72A Gene Cloning from Brassicaceae Plants (into pENTR/D-TOPO vector)	
AtCYP72A7-F	CACCATGTCTTTTTCAGTAGTAGCAGCTTTACCG
AtCYP72A7-R	TCAGAGCTTGTGCAGAATTAGATGAGCTC
AtCYP72A8-F	CACCATGAGTGATACAAAGATATCAGCAGTAGCAG
AtCYP72A8-R	TCAGAGCATGTGGAAGATCAACGGAGCAC
AtCYP72A9-F	CACCATGGAGATAGTAATTGCATCATTGGCTTTAG
AtCYP72A9-R	TCAAAGCTTGTGCAGGATAAGATGAGCCC
AtCYP72A10-F	CACCATGGAGATATCAGTTGCATGCGTAACAGTTTC
AtCYP72A10-R	TTATAGCTTGCGCAGAATAAGATGTGCAC
AtCYP72A11-F	CACCATGGAGATATCAGTTGCATCGGTAACAG
AtCYP72A11-R	TTAGAGCTTGTGCATGATAAGAGGAGC
AtCYP72A13-F	CACCATGGAGATATCAGTTGCATCGGTAACAG
AtCYP72A13-R	TTAGAGCTTGTGCAAGATAAGAGGAGC
AtCYP72A14-F	CACCATGGAGATATCAGTTTCTTCGGTAACATTTTC
AtCYP72A14-R	TTAGAGCTTGTGCAGCATAAGATGAGC
AtCYP72A15-F	CACCATGGAGATATCGGTTGCATCGGTAAC
AtCYP72A15-R	TTAGAGCTTGTGCATGATAAGCTGAGC
BrCYP72A262-F	CACCATGGAGACATTACTTACATCATTGGC
BrCYP72A262-R	TCATAGCTTGTTTAGGATAAGATGAGCAC
BrCYP72A264-F	CACCATGGAGATATCAGTTGCGTTAGTAACAG
BrCYP72A264-R	TTATATCTTGTTAAGGATAAGATGAGCACCG
BrCYP72A272-F	CACCATGGACGTAGTTGCTTCAGTAACAATTTC
BrCYP72A272-R	TTATAGTTTGTGTAGGATAAGATGAGCAC
CrCYP72A484-F	CACCATGGAGATATCAGTTGCGTCGGTAAC
CrCYP72A484-R	TTAGAGCTTGTGCAAGATAAGAGGAGC
CrCYP72A485-F	CACCATGTATCCTGAAAATAGTCGCAGTTAC
CrCYP72A485-R	CTAGAGCTTGTGCAAGATAAGAGGAG
CrCYP72A486-F	CACCATGGAGATATCAGTAGCGTCGGTAGCAT
CrCYP72A486-R	TCATAGCTTCTTAAGGATAACAGGTGCACC
CrCYP72A487-F	CACCATGGAGATGTCTGTTTTATACTATTCAAT
CrCYP72A487-R	TTAGAGCGTGTGCAAGATAAGATGAG
CrCYP72A488-F	CACCATGAGTGATACAGAGATGTCAGCGGTAGC
CrCYP72A488-R	TCAGAGCATGTGGAAGATCAACGGAGCAC
For CYP72A Gene Cloning from Soybean	
GmCYP72A61-F	ATGCTTATGTCTGGCACAGAACAGGTG
GmCYP72A61-R	CTAGAGTTTGCGTAAAATGAGATGAGCC
GmCYP72A69-F	ATGGAAGCAGCATGGGTCAATATTCT
GmCYP72A69-R	TTATTCATATTTCTCCACCTTATGTAGAATGACTG
GmCYP72A120-F	ATGGGGTTCACTCCCACAAGTAC
GmCYP72A120-R	CTACAACTTATGTAAGATGATATGAGCACC
GmCYP72A126-F	ATGGAAGCAGCGTGGATCACAATTC
GmCYP72A126-R	TTATATTTCCACCTTTCTTAGAATGAGATGAGCAC
GmCYP72A127-F	ATGGAAGCACCATGGGCCACA
GmCYP72A127-R	TTACATTTCAACTTTACGTAAAATGACATGA
GmCYP72A128-F	ATGGAAGAAGCATCATGTGTATGCTTAGT
GmCYP72A128-R	TTATATTTCAACTTTACGTAAAATGACATGAGCACC
GmCYP72A135-F	ATGGAAGCAGCATGGGCCACA
GmCYP72A135-R	TCATATTGTGACTTTACGTAGAATGATATG
GmCYP72A136-F	ATGGAAGCAGCATCGGCCA
GmCYP72A136-R	TCATATTGGCACTTTACGTAGAATGAT
GmCYP72A141-F	ATGGAGCCATTATTTTCTTCAGCAGC

GmCYP72A141-R	TCATAGTTTATGCAAAACGATGTGTGCC
GmCYP72A142-F	ATGAACGAATGGAAGATGTTAGTATCCAAAA
GmCYP72A142-R	CTATAATTTATGGAATATAATAGGCGTGCCAAATTGA
GmCYP72A148-F	ATGGGGCTACCACCCACTATTG
GmCYP72A148-R	CTACAGCTTGTGTAAAATGATATGAGCC
GmCYP72A151-F	ATGAAGTATCTTCTTCTCTCTTTGTTTCATGGTT
GmCYP72A151-R	TCATATTTCCACCTTATGTAGAATGAGATGAGCA
For CYP72As Gene Cloning from Rice	
OsCYP72A17.1-F	ATGCAGAGAGAAAAAGAAGCAATGGGCA
OsCYP72A17.1-R	TCAGAGTCGGCGCAGCCTAACCGGAACGCC
OsCYP72A17.2-F	ATGGGCATCGGCATCGGCATCGGCATC
OsCYP72A17.2-R	TCAGAGTCGGCGCAGCCTAACCGGAACGCC
OsCYP72A18-F	ATGCTGATGATGCTAGGGGCGGCCTCC
OsCYP72A18-R	TTAGATTTTCTTCAGCTTAATTTGTGCAC
OsCYP72A19-F	ATGGATCCGACCTCGGTGCCAT
OsCYP72A19-R	TCACGTTTTGAGTTTGCTCAGGCCTTCATAATC
OsCYP72A20-F	ATGGAGGAGGCCACGGGAATG
OsCYP72A20-R	TCATAGTCTTGTGAGTATAATTTGTGCACCATG
OsCYP72A21-F	ATGGTTCTTGGAGCCTGGTTGAT
OsCYP72A21-R	TCATATAGCTCTAAGCTTAATCTGCGCACC
OsCYP72A22-F	ATGGTTCTTGGAGCCGGGTT
OsCYP72A22-R	TCATATAGCTCTAAGCTTAATCTGTGCACCATG
OsCYP72A23-F	ATGCCGGATTACAAAGTTCCTGGAATTG
OsCYP72A23-R	TTAGATCATCCTAAGCTTCATCTGCGCGC
OsCYP72A24-F	ATGGGGATGGTCGTCTTCGC
OsCYP72A24-R	TCAGTTTAGCCTCGTGAGCCTGACCTG
OsCYP72A25-F	ATGGAGATTGTCGATGGCGCTTC
OsCYP72A25-R	TCAGAGTTTAGTAAGCTTAATCTGTGCC
OsCYP72A32-F	ATGGTTCTTGGAGGGTGGCTG
OsCYP72A32-R	TCATATAGCTCTAATTTTAATCTGTGCACCGTGC
OsCYP72A33-F	ATGTGGGCTCCGGCCTCATC
OsCYP72A33-R	CTAATAAAACACACTATAATCTGAAATGGTCATATAGCTC
OsCYP72A34-F	ATGCTGATCATGCTGGGGCT
OsCYP72A34-R	TCAAATTCTCTTCAGCTTAATTTGGGCACC
OsCYP72A35-F	ATGCTGGGAGAGGCCGC
OsCYP72A35-R	TAGAGCTTCTTCAATTTAATTGGAGAACC
For Enzymatic Activity Screening in WAT11 Yeast (into pESC-Leu vector)	
AtCYP72A7-ApaI-F	CGGGGGCCCATGTCTTTTTCAGTAGTAGCAGCTTTAC
AtCYP72A7-SalI-R	ACGCGTCGACGAGCTTGTGCAGAATTAGATGAG
AtCYP72A8-ApaI-F	CGGGGGCCCATGAGTGATACAAAGATATCAGCAGTAGC
AtCYP72A8-SalI-R	ACGCGTCGACGAGCATGTGGAAGATCAACGGAG
AtCYP72A9-ApaI-F	CGGGGGCCCATGGAGATAGTAATTGCATCATTGGCTTTAG
AtCYP72A9-SalI-R	ACGCGTCGACAAGCTTGTGCAGGATAAGATGAGC
AtCYP72A10-ApaI-F	CGGGGGCCCGATGGAGATATCAGTTGCATGCGTAACAG
AtCYP72A10-SalI-R	ACGCGTCGACCTTGCGCAGAATAAGATGTG
AtCYP72A11-ApaI-F	CGGGGGCCCATGGAGATATCAGTTGCATCGGTAAC
AtCYP72A11-SalI-R	ACGCGTCGACGAGCTTGTGCATGATAAGAGGAGC
AtCYP72A13-ApaI-F	CGGGGGCCCGATGGAGATATCAGTTGCATCGGTAACAG
AtCYP72A13-SalI-R	ACGCGTCGACGAGCTTGTGCAAGATAAGAGGAGC
AtCYP72A14-ApaI-F	CGGGGGCCCATGGAGATATCAGTTTCTTCGGTAAC
AtCYP72A14-SalI-R	ACGCGTCGACGAGCTTGTGCAGCATAAGATGAGC
AtCYP72A15-ApaI-F	CGGGGGCCCATGGAGATATCGGTTGCATCGG
AtCYP72A15-SalI-R	ACGCGTCGACGAGCTTGTGCATGATAAGCTGAG

BrCYP72A262-ApaI-F	CGGGGGCCCATGGAGACATTACTTACATCATTG
BrCYP72A262-SalI-R	ACGCGTCGACCTTGTTTAGGATAAGATG
BrCYP72A264-ApaI-F	CGGGGGCCCATGGAGATATCAGTTGCGTTAGTAAC
BrCYP72A264-SalI-R	ACGCGTCGACTATCTTGTTAAGGATAAGATGAGC
BrCYP72A272-ApaI-F	CGGGGGCCCATGGACGTAGTTGCTTCAGTAACAAT
BrCYP72A272-SalI-R	ACGCGTCGACTTTGTGTAGGATAAGATGAG
CrCYP72A484-ApaI-F	CGGGGGCCCATGGAGATATCAGTTGCGTCGGTAAC
CrCYP72A484-ApaI-R	CGGGGGCCCCCGAGCTTGTGCAAGATAAGAGGAG
CrCYP72A485-ApaI-F	CGGGGGCCCATGTATCCTGAAAATAGTCGCAG
CrCYP72A485-SalI-R	ACGCGTCGACGAGCTTGTGCAAGATAAGAG
CrCYP72A486-ApaI-F	CGGGGGCCCATGGAGATATCAGTAGCGTCGGTAG
CrCYP72A486-SalI-R	ACGCGTCGACCTTCTTAAGGATAACAGGTGC
CrCYP72A487-ApaI-F	CGGGGGCCCATGGAGATGTCTGTTTTATACTATTC
CrCYP72A487-SalI-R	ACGCGTCGACGAGCGTGTGCAAGATAAGATGAG
CrCYP72A488-ApaI-F	CGGGGGCCCATGAGTGATACAGAGATGTCAGCGGTA
CrCYP72A488-SalI-R	ACGCGTCGACGAGCATGTGGAAGATCAACGGAG
OsCYP72A17-SalI-F	ACGCGTCGACATGCAGAGAGAAAAAGAAGCAATGGGC
OsCYP72A17-SalI-R	ACGCGTCGACGAGTCGGCGCAGCCTAACCG
OsCYP72A18-ApaI-F	CGGGGGCCCATGCTGATGATGCTAGGGGCGGCC
OsCYP72A18-ApaI-R	CGGGGGCCCCCGATTTTCTTCAGCTTAATTTGTG
OsCYP72A19-ApaI-F	CGGGGGCCCATGGATCCGACCTCGGTGCCATG
OsCYP72A19-SalI-R	ACGCGTCGACCGTTTTGAGTTTGCTCAGGCCTTCATAATC
OsCYP72A20-SalI-F	ACGCGTCGACATGGAGGAGGCCACGGGAATG
OsCYP72A20-SalI-R	ACGCGTCGACTCTTGTGAGTATAATTTGTGCACCATG
OsCYP72A21-ApaI-F	CGGGGGCCCATGGTTCTTGGAGCCTGGTTGATG
OsCYP72A21-SalI-R	ACGCGTCGACTATAGCTCTAAGCTTAATCTGCGCACC
OsCYP72A22-SalI-F	ACGCGTCGACATGGTTCTTGGAGCCGGGTTG
OsCYP72A22-SalI-R	ACGCGTCGACTATAGCTCTAAGCTTAATCTGTGCACCATG
OsCYP72A24-ApaI-F	CGGGGGCCCATGGGGATGGTCGTCTTCGCCG
OsCYP72A24-SalI-R	ACGCGTCGACGTTTAGCCTCGTGAGCCTGACCTG
OsCYP72A25-ApaI-F	CGGGGGCCCATGGAGATTGTCGATGGCGCTTC
OsCYP72A25-SalI-R	ACGCGTCGACGAGTTTAGTAAGCTTAATCTGTGCC
OsCYP72A32-ApaI-F	CGGGGGCCCATGGTTCTTGGAGGGTGGCTGT
OsCYP72A32-SalI-R	ACGCGTCGACTATAGCTCTAATTTTAATCTGTGCACCGTGC
OsCYP72A33-ApaI-F	CGGGGGCCCATGTGGGCTCCGGCCTCATC
OsCYP72A33-SalI-R	ACGCGTCGACATAAAACACACTATAATCTGAAATGGTCATAT
OsCYP72A34-ApaI-F	CGGGGGCCCATGCTGATCATGCTGGGGCTGG
OsCYP72A34-SalI-R	ACGCGTCGACAATTCTCTTCAGCTTAATTTGGGCACCG
OsCYP72A35-SalI-F	ACGCGTCGACATGCTGGGAGAGGCCGCC
OsCYP72A35-SalI-R	ACGCGTCGACGAGCTTCTTCAATTTAATTGGAGAACCG
GmCYP72A61-ApaI-F	CGGGGGCCCATGCTTATGTCTGGCACAGAACAGGTG
GmCYP72A61-SalI-R	ACGCGTCGACCTAGAGTTTGCGTAAAATGAGATGAGCC
GmCYP72A69-SalI-F	ACGCGTCGACATGGAAGCAGCATGGGTCAATATTCT
GmCYP72A69-SalI-R	ACGCGTCGACTTCATATTTCTCCACCTTATGTAGAATGACTG
GmCYP72A120-ApaI-F	CGGGGGCCCATGGGGTTCACTCCCACAAGTAC
GmCYP72A120-SalI-R	ACGCGTCGACCTACAACTTATGTAAGATGATATGAGCACC
GmCYP72A126-ApaI-F	CGGGGGCCCATGGAAGCAGCGTGGATCACAATTC
GmCYP72A126-SalI-R	ACGCGTCGACTATTTCCACCTTTCTTAGAATGAGATGAG
GmCYP72A127-ApaI-F	CGGGGGCCCATGGAAGCACCATGGGCCACA
GmCYP72A127-SalI-R	ACGCGTCGACCATTTCAACTTTACGTAAAATGACATGA
GmCYP72A128-ApaI-F	CGGGGGCCCATGGAAGAAGCATCATGTGTATGCTTAGT
GmCYP72A128-SalI-R	ACGCGTCGACTATTTCAACTTTACGTAAAATGACATGAG
GmCYP72A135-ApaI-F	CGGGGGCCCATGGAAGCAGCATGGGCCACA

GmCYP72A135-SalI-R	ACGCGTCGACTCATATTGTGACTTTACGTAGAATGATATG
GmCYP72A136-ApaI-F	CGGGGGCCCATGGAAGCAGCATCGGCCA
GmCYP72A136-SalI-R	ACGCGTCGACTCATATTGGCACTTTACGTAGAATGAT
GmCYP72A141-ApaI-F	CGGGGGCCCATGGAGCCATTATTTTCTTCAGCAGC
GmCYP72A141-SalI-R	ACGCGTCGACTCATAGTTTATGCAAAACGATGTGTGCC
GmCYP72A148-ApaI-F	CGGGGGCCCATGGGGCTACCACCCACTATTG
GmCYP72A148-SalI-R	ACGCGTCGACCTACAGCTTGTGTAAAATGATATGAGCC
GmCYP72A151-ApaI-F	CGGGGGCCCATGAAGTATCTTCTTCTCTCTTTGTTTCATGGT
GmCYP72A151-SalI-R	ACGCGTCGACTCATATTTCCACCTTATGTAGAATGAGATGAG
AtCYP72B1-ApaI-F	CGGGGGCCCATGGAGGAAGAAAGTAGCAGCTGGTTC
AtCYP72B1-SalI-R	ACGCGTCGACATCCTCATGATTGGTCAATCTCCGGA
For Subcellular Localization (pJIT163-hGFP vector)	
CYP72A9-SalI-F	GCGTCGACATGGAGATAGTAATTGCATCATTG
CYP72A9-BamHI-R	CGGGATCCAAGCTTGTGCAGGATAAGATGAGCC
For Promoter::GUS (pMD162 vector)	
At3g14630-promoter-F	CACCTGCATGTGTTTCTCTTAGAATAAGATGGATTTC
At3g14630-promoter -R	TTGCTGATGTTTTTGGTCTCTTAAAATTTTTGAG
For qRT-PCR Analysis	
Actin2-RT-F	AGTCTTGTTCCAGCCCTCGTTTGTG
Actin2-RT-R	TCCTGGACCTGCCTCATCATACTCG
AtCYP72A7-RT-F	TCCCTGCGTTCTACCATTGT
AtCYP72A7-RT-R	AAACGGGAGAAAGCGAGAGA
AtCYP72A8-RT-F	ACGGTATGGATATGGAAAGGTCTG
AtCYP72A8-RT-R	CTTTGATGTGTTCTGGTTTCGTCA
AtCYP72A9-RT-F	AACAATAATGAATCCACAGCTG
AtCYP72A9-RT-R	ACGACCCTTTATCTGAAACTAA
AtCYP72A10-RT-F	GAGCTAATCAAAGAAGTGTTCAACAAAG
AtCYP72A10-RT-R	TTGTAAGATGAGATGTACTAGTTCTGCT
AtCYP72A11-RT-F	ACGATTTACTGGGAATACTTCTTGAATC
AtCYP72A11-RT-R	GGACTAGAAGGATAGGTAGATTGATCAG
AtCYP72A13-RT-F	TCTTGTCGGTGATTTGAAGAGAAAT
AtCYP72A13-RT-R	GTTGAACACTTCTTTGATTTGCTCA
AtCYP72A14-RT-F	CAAAAGGGAAAGGGCAAGAGAA
AtCYP72A14-RT-R	TGGACTACAGGAGGATAAAGCC
AtCYP72A15-RT-F	CAGAGCTGTAGGGAAGTTGTTG
AtCYP72A15-RT-R	AAGTATTCCCAGCAAATCGTCG
BrCYP72A262-RT-F	ATGCTACAAGGATAAAGACAATAGT
BrCYP72A262-RT-R	CTTGCAATCTTCAATAATTTCTTCG
BrCYP72A264-RT-F	GTACTTCTGGTCTGGATAATGATTA
BrCYP72A264-RT-R	CCTCATAAAGAATCATCGTCATAAC
BrCYP72A272-RT-F	AGGAATTTTAGTATGATGATGGAGG
BrCYP72A272-RT-R	ATCCATTATAGTGATTGTTGGTGTA
Br_Actin-RT-F	CTCACTCTCAAGTATCCGATCGAG
Br_Actin-RT -R	GACGAAGGATAGCATGAGGAAGAG
Cr_Actin -RT-F	CTCACCCTGAAGTATCCAATCGAG
Cr_Actin-RT-R	GATAGCATGAGGAAGAGCATACCC
CrCYP72A484-RT-F	CTTGAGAGTTATTTGAGAAGACAAG
CrCYP72A484-RT-R	CATTATAGTGATGGTTGGTATAGGT
CrCYP72A485-RT-F	CTACAAAGAAGGACAGAGGATATTT
CrCYP72A485-RT-R	TTTTGTTAATGATCCCTCTCAGTAT
CrCYP72A486-RT-F	AACTTTGAATTGGGTTTGGT
CrCYP72A486-RT-R	AAAAAGTCCTTCCGTGAGTC
CrCYP72A487-RT-F	ACTGTGAGAAGATAAAGAATATGGT

CrCYP72A487-RT-R	TGAAATATCCTCTTCCCTTGTTTAT
CrCYP72A488-RT-F	TAGTAGCTACGAGGAAGGTAACAGA
CrCYP72A488-RT-R	ACATCTTCAATACTCATACCGTGAT
GA2ox1-F	TGAGGACGAGAGGTTGTACGA
GA2ox1-R	TCCTTTCGAATTGTTGAAGCC
GA2ox2-F	CCGGTTCTCACTTCCCATT
GA2ox2-R	GCTTCCGGATCGGCTAG
GA2ox3-F	AGGAGAAGCTGAGCCGTTT
GA2ox3-R	TTCTCCGGGTAATGGTTCAT
GA2ox4-F	GGCTCCAAGTGTCCAATTCA
GA2ox4-R	TCCTACATTGACGCAGAAAGC
GA2ox6-F	GGGACAGAAGTCTAGCGAAGTG
GA2ox6-R	TCGCTACGAACGTCTCTGATC
GA2ox7-F	AGTAATGGAGTGTACCAAAGCG
GA2ox7-R	GAAAGCTATTGACATCCTCTCG
GA2ox8-F	GTGTGAGAAATACATGTTATCTAAG
GA2ox8-R	TACACCTCCGATGGTTTGG
GA20ox1-F	GATCCATCCTCCACTTTAGA
GA20ox1-R	GTGTATTCATGAGCGTCTGA
GA20ox2-F	ACCGAGACTATTTCCGAGGATT
GA20ox2-R	TGTTTGGCATGGAGGATAATG
GA20ox3-F	AAAGCTCCTTAATCAGCACTCG
GA20ox3-R	TGAGTGGGACTTGGAGAGGTT
GA20ox4-F	GTCTTGGTATCAAAAGGGAGCAT
GA20ox4-R	GCCCCGTACCTAGTACAAGATCT
GA20ox5-F	GCTCACGGTACTTTTCTAGTGG
GA20ox5-R	ACTCGATATCTCAAGCGCC
GA3ox1-F	CCATTCACCTCCCACACTCT
GA3ox1-R	GCCAGTGATGGTGAAACCTT
GA3ox2-F	TGGTCCGAAGGTTTCAC
GA3ox2-R	GGGTCGAGTCTGTATGG
GA3ox3-F	TCCTACCCGGTTTGCC
GA3ox3-R	ACGGTGCATTGTACTTC
GA3ox4-F	GCCGATGACTCCTACC
GA3ox4-R	ACACTTGTAGCCCTCC
GMAT-1-F	TGTTGTTTATGCTGATGGGTGGTC
GMAT-1-R	CGCAATCTCTTCGGTGGTTCTAA
GMAT-2-F	CGTCCTTCAGGCTCAAGTAGTC
GMAT-2-R	CCCTATCTTGAAACCACCACAACGGTC
CYP714A1-F	TCCGCCGTCGCTATTTCGT
CYP714A1-R	TGTTGTTGTGAGTGATGGCC
CYP714A2-F	GTCGGAATCTTCAGCGTAGGTT
CYP714A2-R	GGCGTTTGGTGATGTGAGTGA
GID1a-F	GATGTCTTGATTGATCGCAGGAT
GID1a-R	AGGAGGTTGCTCTTGATCTGCA
GID1c-F	CTGTGAATTATCGTCGTGC
GID1c-R	GGCTACACGCTGGATG
RGA-F	AGAAGCAATCCAGCAGA
RGA-R	GTGTACTCTCTTCTTACCTTC
For Transgenic Plants Analysis	
35S-PROM	TCCTTCGCAAGACCCTTC
35S-TER	GAGAGAGACTGGTGATTTTTGCG
GUS-R	CCACCAACGCTGATCAATTCCAC

GFP-R	CCTTGAAGTCGATGCCCTTCAGC
GFP-F	GACCACATGAAGCAGCACGACT
For Cas9-edited Mutant Analysis	
At3g14630-target-F	ATTGAGAATTACATTCCTGCATAC
At3g14630-target-R	ACCCGTATGCAGGAATGTAATTCT
At3g14630-check-F	GCATCGAGGTCATGTGTGAATGGGAG
At3g14630-check-R	CATGTTCAGTCCATTTCCTTTACTTTGC
For T-DNA Insertion Mutant Analysis	
SALK_130811C-F	GGATGAAAACAATAGTCAAAGAAATCCAAG
SALK_130811C-R	AGAAGAAGCAGACCTGGTTCTTTGTTGCGC
LBb1.3	ATTTTGCCGATTTCGGAAC

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Supplementary Table 2. MRM parameters for GA profiling in Arabidopsis plants.

Compound	MRM transitions (*m/z*)	CE (V)
GA_{12}	331.2 > 313.2	-38
	331.2 > 269.2	-44
GA_{15}	329.1 > 257.1	-34
	329.1 > 131.0	-40
GA_{24}	345.2 > 257.2	-36
	345.2 > 213.2	-41
GA_{9}	315.1 > 271.1	-28
	315.1 > 253.1	-35
GA_{4}	331.1 > 257.1	-30
	331.1 > 213.1	-42
GA_{53}	347.2 > 303.2	-37
	347.2 > 189.1	-48
GA_{44}	345.2 > 301.2	-35
	345.2 > 273.2	-35
GA_{19}	361.2 > 273.2	-37
	361.2 > 229.1	-42
GA_{20}	331.1 > 287.1	-30
	331.1 > 243.1	-26
GA_{1}	347.1 > 273.1	-32
	347.1 > 229.1	-42
GA_{7}	329.1 > 223.1	-27
	329.1 > 211.1	-37
GA_{3}	345.1 > 143.1	-40
	345.1 > 239.1	-20
GA_{8}	363.1 > 275.1	-24
	363.1 > 257.1	-24
GA_{29}	347.1 > 259.1	-24
	347.1 > 241.1	-32
GA_{51}	331.1 > 287.1	-24
	331.1 > 243.1	-23