

## Supplementary Information for

Interlinked regulatory loops of ABA catabolism and biosynthesis coordinate fruit growth and ripening in woodland strawberry

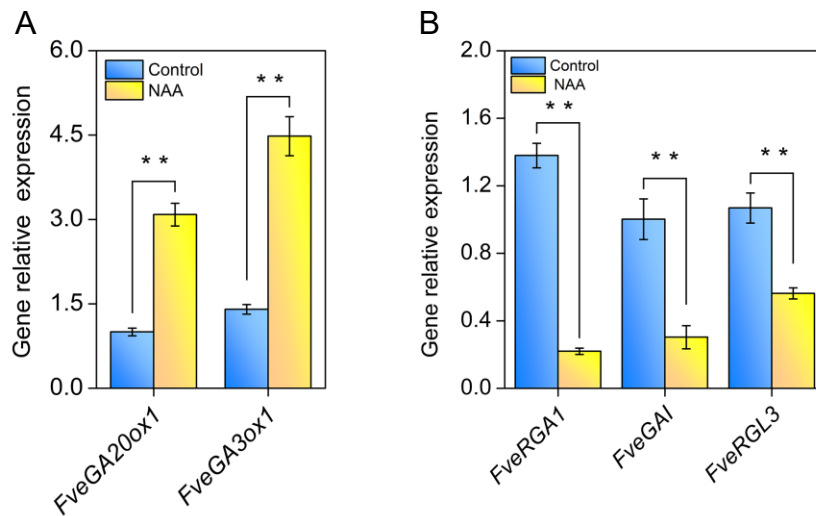
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Figs. S1 to S10

Tables S1 to S4



**Fig. S1. NAA promotes GA biosynthesis gene expression and suppress the GA negative regulator gene expression in no pollination fruit.** (A and B) Quantitative RT-PCR analysis of transcript levels for GA biosynthesis (A) and GA signaling genes (B) in NAA treated no pollination fruits (receptacle and achene). Total RNAs were isolated at 14 days after the first hormone application. *FveACTIN* was used as the internal control. Error bars represent SD of three independent replicates (20 fruits were used for each replicate). Student's *t*-test, \*\* $P < 0.01$ . *p*-value for each *t*-test was adjusted by Bonferroni procedure.

A

AtCYP707A1 ...MDISALFLTLFAGSLFLYLRLCLISQ.....RRFGSSKLPPLPGTMGWYVGETFQLYSQDPN.....VFFQSKCK 66  
 AtCYP707A2 .....MISSPEARMVLSKAHLFKPTYPFSKERMICPEALFFHGGPYHSTLKRVLQSSFMF..SALRP 0  
 AtCYP707A3 ...MDFSGFLFLTLSSAALFLCLLRFIAGV.....RRSSSTKLPPLPGTMGYFYVGETFQLYSQDPN.....VFFFAAKQR 66  
 AtCYP707A4 ...MAEIWFLVVPILILCLLLLVRVIVSK.....KKNSRGLKPPGSMGWYVGETLQLYSQDPN.....VFFTSKCK 64  
 FveCYP707A1/3 .....MFAASALIFFFSPIIKLF.....LISARHKIPLPPGSLGWYIGETFQLYSQDPN.....VFFASKIK 58  
 FveCYP707A2 MQLFSSSPFCALHSDFLVLIPIILLLLGLFLQWQYPRFYRRLPPGSMGWYVGETFQLYSQDPN.....SFFSVRCK 75  
 FveCYP707A3 .....MALFILITVALLSVFAFAFFVLRWSWSSPKSMVGI PGLGWPIVGESFSFI SEFSSPSGIYSFMHKRQ 71  
 FveCYP707A4a .....MKKSKGGGEEDPHDDH.....GHNRAAQLPPGSGFWYIGETLQLYSQDPN.....TFFSSRCK 55  
 FveCYP707A4b .....MGWPCIGETLQYMSMDPN.....IFFSTKCK 26  
 Consensus

AtCYP707A1 RYGSVFKTHVLGCPVMISSPEAAKFLVTKSHLFPKTPFASKERMICQAIFFHGGDYHAKLRKLVLRFAFMF..ESIRN 144  
 AtCYP707A2 .....MISSPEARMVLSKAHLFKPTYPFSKERMICPEALFFHGGPYHSTLKRVLQSSFMF..SALRP 62  
 AtCYP707A3 RYGSVFKTHVLGCPVMISSPEAAKFLVTKSHLFPKTPFASKERMICQAIFFHGGDYHAKLRKLVLRFAFMF..DAIRN 144  
 AtCYP707A4 RYGEIFKTRILGCPVMISSPEAAKFLVTKSHLFPKTPFASKERMICQAIFFHGGDYHAKLRKLVLRFAFMF..ETIRK 142  
 FveCYP707A1/3 RFGSIFKTHILGCPVMISSPEAAKFLVTKSHLFPKTPFASKERMICQAIFFHGGDYHAKLRKLVLRFAFMF..TALKN 136  
 FveCYP707A2 RYGSIFKSHVLGCPVMISSPEAAKFLVTKSHLFPKTPFASKERMICQAIFFHGGDYHAKLRKLVLRFAFMF..SAIKG 153  
 FveCYP707A3 RYGVVFKTFVLGRFSVMTGRERAKMLLAGRDGMVLSNLFYTGQVLPSTLQTTGEBHKLRLRLIAEPLSV..DGLKK 149  
 FveCYP707A4a RYGIIFKTHILGCPVMISSPEAAKFLVTKSHLFPKTPFASKERMICQAIFFHGGDYHAKLRKLVLRFAFMF..DAIRN 133  
 FveCYP707A4b RYGDIFKTHILGCPVMISSPEAAKFLVTKSHLFPKTPFASKERMICQAIFFHGGDYHAKLRKLVLRFAFMF..ENPNTMQK 106  
 Consensus a l g g h

AtCYP707A1 MVPIIESIAQDSLRSEWGT..MINTYQEMKTYTFNVALLSIFG.KDEVLYREDLKRCCYIILEKGYNSMNVNIPGLFHK 221  
 AtCYP707A2 TVSHIELLVQLTSSWTSQK..SINTLEYMKRYAFDVAIMSAFGDKKEEPTDIVIKLLYQRLERGYNSMPLDLIPGLFHK 141  
 AtCYP707A3 MVPIIESIAQESLNSMDGT..QLNTYQEMKTYTFNVALLSIFG.KDEVLYREDLKRCCYIILEKGYNSMNVNIPGLFHK 221  
 AtCYP707A4 LIPDIHIALSSLSQSWAMP.IVSTYQEMKFAFDVIGILAFG.HLESSYKEILKHNINIVDKGYNSFMNIPGLFHK 220  
 FveCYP707A1/3 KVGDEIAIAKDSLQSWEGR..SFNTYQEMKTYTFNVALLSIFG.KDEILYREDLKRCCYIILEKGYNSMNVNIPGLFHK 213  
 FveCYP707A2 SVSEIEQIVLKLPTWKKN..TINTLQEMKRYAFDVAIMSVLGNKRG.IEIEGIGIKHLYHCIEKGYNSMPLDLIPGLFHK 230  
 FveCYP707A3 YFQFINNLAIEIILEDMPGR..TVFVLEASFTTKVIGNIMISLEPAGEEQEKFRANFKLISSSFASLFPKIPGTAHSG 227  
 FveCYP707A4a LVPHIDATAASVTSWGTGKVINTEHEMKKFSFEVGVLVIFG.QLETRYKEELRKNMAMVNGKYNFFINIPGTYPYKA 212  
 FveCYP707A4b LVPHIEALIASLESWAAAGTVINTYHEMKKFSFEVGVLVIFG.RLDDTYREKLRKNYHMVDKGNCFINIPGTAYHKA 185  
 Consensus i w v pgt

AtCYP707A1 MKARKEISQILARIISERRQN.GSSHNDLGSFMGDKEE.....LTDEQIADNIGVIFAARDTTASVMSWILKY 290  
 AtCYP707A2 MKARIELSEELRKYIEKRRENG.REEGGLLVLLGAKDQKRRG.....LSDSQIADNIGVIFAARDTTASVLTWLLKY 214  
 AtCYP707A3 MKARKELAQILANILSKRRQN.PSSHNDLGSFMEDKAG.....LTDEQIADNIGVIFAARDTTASVLTWLLKY 290  
 AtCYP707A4 LMARKQLKTIIVSEIICERRREK.RALQTDPLGHLNLFNKEKGRV.....LTDEQIADNIGVIFAARDTTASCLTWLLKY 293  
 FveCYP707A1/3 MKARKELAQILAKIISTRESKLDHNDLGSFMGDKEG.....LTDEQIADNIGVIFAARDTTASVLTWIMKY 283  
 FveCYP707A2 MKARKLLNKTRELTLQKRRSGDVQSGGLLQDLLRAKDKLKLN.....LSDSQIADNIGVIFAARDTTASVLTWLLKY 305  
 FveCYP707A3 IQARDRMAMLDLAIKRRNG.EGFQDDELESLMKHSLAGSEDNKDKLTDKQLKDNVLTLLVAGHDTTAAALTWLLKF 306  
 FveCYP707A4a LLARERLRHIIGDIHERKEK.RLPEKDLGCLLRSINEGGEV.....LSDSQIADNIGVIFAARDTTASVMTWIPKY 285  
 FveCYP707A4b LLAKRRLSILRQIISERRREK.KVLQKDLGLDNLNFQNEKQGN.....LSDSQIADNIGVIFAARDTTASVLTWLLKY 258  
 Consensus ar r l q dn a dtt w k

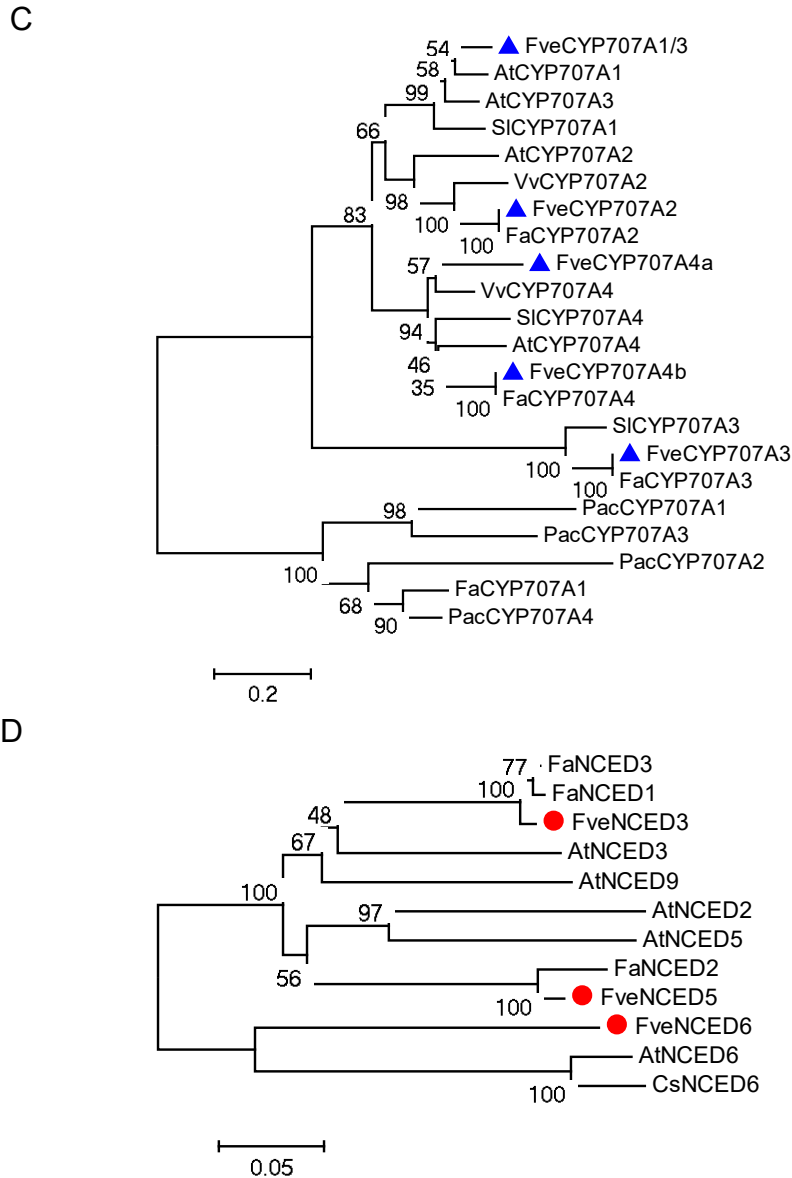
AtCYP707A1 LAENPNVLEAVTEEQEARKDKKEE.GES..LTWEDTKKMLTTRVITQETLRVASILSFTFRBAVEDVEYEGYIIPKGWKV 367  
 AtCYP707A2 LHDHFNLLQEVSRQFSRQKIKK..ENRRISMEDTRKMLTTRVITQETLRVAASVLSFTFRBAVEDVEYEGYIIPKGWKV 292  
 AtCYP707A3 LADNPTVLEAVTEEQEARKDKKEE.GES..LTWEDTKKMLTTRVITQETLRVAATILSFTFRBAVEDVEYEGYIIPKGWKV 367  
 AtCYP707A4 LHDQKLLBAVKAQKAKAYEEN.SREKPK.LTWQTRKMLTTRVITQETLRVMSIISFTFRBAVEDVEYEGYIIPKGWKV 371  
 FveCYP707A1/3 LGENPSVLEAVTEEQEARMLKEESGEEKVLNMDTKKMLTTRVITQETLRVASILSFTFRBAVEDVEYEGYIIPKGWKV 363  
 FveCYP707A2 LHDNDLLERVTRTEQEARQKMLI..EKRGFTWDDTRRMLTTRVITQETLRVASILSFTFRBAVEDVEYEGYIIPKGWKV 383  
 FveCYP707A3 LGENPVVLEQLRDEHROQANR...DGVNLTWSEVNNMFTAKVISBTLRRTILPWFESRKAQNFIEDGKIEKQWISI 382  
 FveCYP707A4a LHDEPKLLEAVKAQKAKACDAN.DGCKRS.LTWQTRKMLTTRVITQETLRVMSIISFTFRBAVEDVEYEGYIIPKGWKV 364  
 FveCYP707A4b LHDNQNLBAVKAQKAKACDAN.DGCKRS.LTWQTRKMLTTRVITQETLRVMSIISFTFRBAVEDVEYEGYIIPKGWKV 336  
 Consensus l l e i w mp v e l r a gy i gw

AtCYP707A1 LPLFRNIHHSADIFSNPKKFTPSRFEVAPKPTFMFPFGNTHSCPGNELAKLEMSIMIHHLITKYSNIVGASDGIQYGP 447  
 AtCYP707A2 LPLFRNIHHSSEFFPDPEKFPDSRFEVAPKPTFMFPFGNVHSCPGSELAKLEMLLILHHLITTSFRWEVIGDEEGIQYGP 372  
 AtCYP707A3 LPLFRNIHHSADIFSDPKKFTPSRFEVAPKPTFMFPFGNTHSCPGNELAKLEISVLIHHLITKYSNIVGASDGIQYGP 447  
 AtCYP707A4 MPLFRNIHHSNPKYFSNPEVFPDSRFEVAPKPTFMFPFGNVHSCPGNELAKLEILIFLHHLVSNFRYVFHAR..... 443  
 FveCYP707A1/3 LPLFRNIHHSPELFPPEKFPDSRFEVAPKPTFMFPFGNTHSCPGNELAKLEILVLIHHLITKYSNIVGASDGIQYGP 443  
 FveCYP707A2 LPLFRNIHHCADFFPPEKFPDSRFEVAPKPTFMFPFGNVHSCPGSELAKLEMLLILHHLITTYR...GSDGEMGIAGP 459  
 FveCYP707A3 NLDVVSITHDPEVFPDPEKFPDSRFEVAPKPTFMFPFGNTHSCPGNELAKLEISVLIHHLVCKYKWKPLEKDDSVQPTL 462  
 FveCYP707A4a MPLFRNIHHSNPEFFTDDEKFPDSRFEVAPKPTFMFPFGNVHSCPGNELAKLEMLLIMIHHLVSNFRWEIEGSGQSTYGP 444  
 FveCYP707A4b MPLFRNIHHSNPEFFTDDEKFPDSRFEVAPKPTFMFPFGNVHSCPGNELAKLEMLLIMIHHLVSNFRWEIEGSGQSTYGP 416  
 Consensus ihh f p fd rf t fg g cpg lak hhl

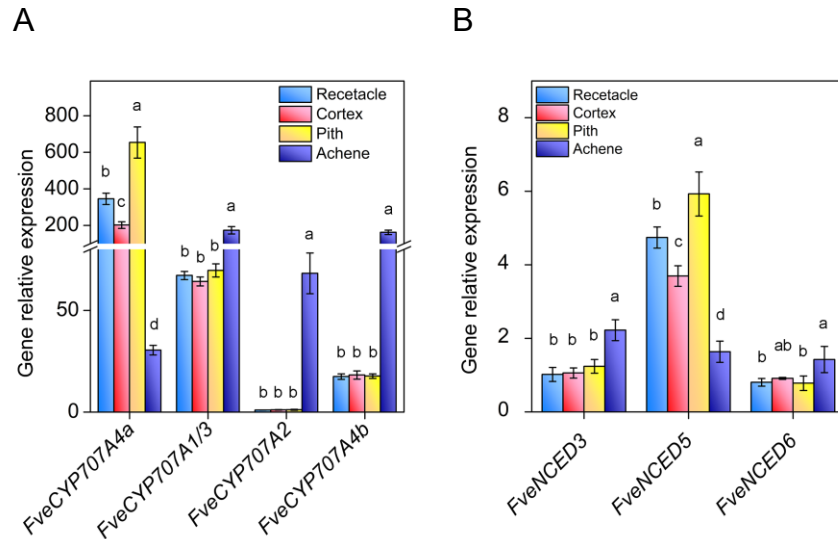
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 AtCYP707A2 FVFP...KKGLPIRVTPI..... 387  
 AtCYP707A3 FALP...QNGLPIALERK..... 462  
 AtCYP707A4 ..... 443  
 FveCYP707A1/3 FALP...QNGLPIILSSKE..... 459  
 FveCYP707A2 ELVLRWNTRLEVMVLNLL..... 478  
 FveCYP707A3 VRMP...KNKYPIVAEPL..... 477  
 FveCYP707A4a FVFP...LNGLPVKWLKLE..... 460  
 FveCYP707A4b FVFP...QHGLPARFLKEQDQGVQVLAEHDQLRPSN..... 449  
 Consensus

B

AtNCED2	.....MVSLLTMPMSGGKIKTPWQAQIDLGFRIKRPQKVIKCTVQIDVTELTKKRQLFTPR.....TTAT	60
AtNCED3	MASFATAAVSGRWLGGNHTQPPLSSSSQSSDLSYCSSLPMASRVTRKLNVSALHTPPALHFPKQS.....SNSPAI	72
AtNCED5	....MACSYILTPNPTKLNLSFAPSDDLADAPSSSSVSFTNTKPRRRKLSANSVSDTPNLLNFPNYPSP.....NPI	67
AtNCED6	.....MQHSLRSDDLPTKTSRSHLLPQPKNANISRRILINPFKIPTLPDLTSPVPS.....	52
FveNCED3	MPATAATATTSGTWVLLHKKRFLSSRRRDSGSSTATSLSVSSTPKNTNTITCSLQTPSFIQFPKQAPTYSQPSSSSSTTI	80
FveNCED5	MATASNSWAHTAQIPHHLSTSSSTSSSSSLLNMSFTKRSVALNRNRVTVAHSALQSPSVLNFPKQP.....YHQQV	71
FveNCED6	.....MRKTLPRETQKP.....LKPPLPIPKTKPLIEPVPE.....	31
Consensus		
AtNCED2	PPQH.....NPLR.....LNI F Q K A A A I A D A A E R A L I S . H E Q D S P L P K T A D P R V Q L A G N Y S P V P F S S W R R N	121
AtNCED3	VVKP.....KAKESNTK.....QMNLFORAAAAAADAEGFLVS.HKKLHPLPKTADPSVQLAGNFAPVNEQPVRRN	138
AtNCED5	IPEK.....DTSR.....WNPLORAAASAAIDFAETALLR.RRSRSLPKPTVDRHQLSNGYAPVPRQSVKSS	128
AtNCED6	PVK.....LKPITYP.....NLNLLQKLAATMLDKTESSIVIPMEQNRPLPKPTDPAVQLSGNFAPVNECPWNG	116
FveNCED3	LPTPKDQKPLTSSSSNSKPVVQPQQWNLFORVAAMAIDAMESALVS.KLEHPLPKTADPKVQLAGNFAPVPRQSVKSS	159
FveNCED5	ITKEATSSPSAKPKTATTTQ..QPPHWNFLORAAATAIDMLLEGALVS.RRSRSLPKTADPRVQLAGNFAPVPRQSVKSS	148
FveNCED6	IVNP.....TKPYHPS.....HLNPLQKLAASVLDKLEASVIEPLKQKLPKTIIDPAVQLSGNFAPVNECPWNG	97
Consensus	n q a d k l e a s v i e p l k q k l p k t i d p a v q l s g n f a p v n e c p w n g	
AtNCED2	L F V E G T I P D C I D G V Y I R N G A N P M F P E P T A G H H L F D G D G M V H A V K I T N . G S A S Y A C R F T E R L R V Q E K R L G R P V F P K A I G E L	200
AtNCED3	L F V V G K L P D S I K G V Y V R N G A N P L H E P V T G H H F D G D G M V H A V K F E H . G S A S Y A C R F T Q T N R F V Q R Q L G R P V F P K A I G E L	217
AtNCED5	L F V D G K I P D C I D G V Y L R N G A N P L F E P V S G H H L F D G D G M V H A V K I T N . G D A S Y S C R F T E R L R V Q E K Q L G S I F P K A I G E L	207
AtNCED6	L F V W Q I P S C L K G V Y I R N G A N P M F P L A G H H L F D G D G M H A V S I G F D N Q V S Y S C R Y T K T N R L V Q E T A L G R S V F P K P I G E L	196
FveNCED3	L F V T P K I P E C I R G V Y V R N G A N P L H E P V A G H H L F D G D G M V H A L S F N S D G S A S Y A C R F T E T H R M V Q B R A L G R P M F P K A I G E L	239
FveNCED5	L F V S G T I P E C I S G V Y V R N G A N P L H E P V A G H H L F D G D G M V H A V S I N D . G A A S Y A C R F T E Q R L V Q E R E I G R V F P K P I G E L	227
FveNCED6	L F V L Q I P S C L R G V Y V R N G A N P M F T P L G H H L F D G D G M I H A L L T L G V G N K A S Y S C R Y T R S R L K Q B A K I G R M F P K P I G E L	177
Consensus	l v g p g v y r n g a n p p g h h f d g d g m h a s y s c r t r q e g f p k igel	
AtNCED2	H G H S C I A R L M L F Y A R G L C G L I N N Q N G V G V A N A G L V Y F N R L L A M S E D D L P Y Q L K I T Q T G D L Q T V C R Y F D Q L K S A M I A H	280
AtNCED3	H G H T C I A R L M L F Y A R A A A G I V D P A H G T G V A N A G L V Y F N R L L A M S E D D L P Y Q V I T P N G D L K T V C R F T F D G Q L E S T M I A H	297
AtNCED5	H G H S C I A R L M L F Y A R G L F G L L N H K N G T G V A N A G L V Y F N R L L A M S E D D L P Y Q V R V T D N G D L E T I C R F F D G Q L S S A M I A H	287
AtNCED6	H G H S G L A R L A L F T A R A G I G L V D G T R G M G V A N A G V V F F N G R L L A M S E D D L P Y Q V K I D G Q D L E T I C R F C F D D Q I D S S V I A H	276
FveNCED3	H G H S C I A R L A L F Y L R G A C G L V D P S H G L G V A N A G L V Y F N R L L A M S E D D L P Y H V R V T K T G D L R T E C R Y F F N D Q L K S T M I A H	319
FveNCED5	H G H S G I A R L A L F Y A R G A L G L V D P S H G I G V A N A G L V Y F N R L L A M S E D D M P Y Q V R I K P S G D L E T V C R Y F F E T Q L G S T M I A H	307
FveNCED6	H G H L G L A R L G L F L A R A A I R L V D R S Q G T G V A N A G L V Y F N R L L A M S E D D L P Y N V K I R G D G L E T I R I R F F F N G G L D R P M I A H	257
Consensus	h g h g a r l l f r g v a n a g v f r l l a m s e d d p y g d l t r f i a h	
AtNCED2	P K L D P V T K E L H A L S Y D V V K K P Y L K Y F R F S P D E V K S P E L E I P L E T P T M I H D F A I T E N F V V I P D Q Q V F R L G E M I S G K S P V V	360
AtNCED3	P K V D P E S G E L F A L S Y D V V S K P Y L K Y F R F S P D E T K S P D V E I Q L D Q P T M M H D F A I T E N F V V I P D Q Q V F R L P E M I R G G S P V V	377
AtNCED5	P K I D P V T K E L F A L S Y D V V K K P Y L K Y F K F S P E G E K S P D V E I P L A S P T M M H D F A I T E N F V V I P D Q Q V F R L S D M F L G K S P V K	367
AtNCED6	P K V D A T T G D L H T L S Y N V L K P H R Y L K F N T C K K T R D V E I P L P E T M I H D F A I T E N F V V I P D Q Q V F R L S E M I R G G S P V I	356
FveNCED3	P K V D P A T G E L F A L S Y D V V Q K P Y L K Y F K F S P N E T K S P D V E I P L A Q P T M M H D F A I T E R F V V I P D Q Q V F R L P E M I R G G S P V I	399
FveNCED5	P K V D P V S S H L H T L S Y D V V K K P Y L K Y F Q F S A D G E K S P D V E I P L A A P T M M H D F A I T E N F V V I P D Q Q V F R L Q E M I T G G S P V I	387
FveNCED6	P K V D P V T G E L H A L S Y D V V N K P H L K Y Y K F D T C R K S R E V G I P L E Q P T M V H D F A I T E N Y A V I P D Q Q V F R L S E M V K G S P V I	337
Consensus	p k d l l s y v k p l y f g k i l p t m h d f a i t e v p d q q v f l m g s p v	
AtNCED2	F D G E V S R L G I M P K D A T E A S Q I I W V N S P E T F C F H L W N A W E S P E T E E . . . I V V I G S C M S P A D S I F N E R . D E S L R S V L S E I R	436
AtNCED3	Y D K N V A R F G I L D K Y A E D S S N I K W I D A P D C F C F H L W N A W E S P E T D E . . . V V V I G S C M T P P D S I F N E S . D E N L K S V L S E I R	453
AtNCED5	Y D G E I S R F G I L P R N A K D A S E M V V E S P E T F C F H L W N A W E S P E T D E . . . V V V I G S C M T P A D S I F N E C . D E Q L N S V L S E I R	443
AtNCED6	Y V K E R M A R F G V L S K Q D L T G S D I N W V D V P D C F C F H L W N A W E R T E E G D P V I V V I G S C M S P P D T I F E S . G E P T R V L S E I R	435
FveNCED3	Y D K N V A R F G I L D K N A S D A S G I R W E A P D C F C F H L W N A W E S P D T D E . . . V V V I G S C M T P P D S I F N E C . D E C L E S V L S E I R	475
FveNCED5	Y D Q N K S R F G I L A K N A T N A A D I I W V E S P D T F C F H L W N A W E S P E S D E . . . V V V I G S C M T P A D S I F N E C . D E S L K S V L S E I R	463
FveNCED6	Y D P E R M S R F G I L P K N D E E G L G I Q W I N V G C F C F H L C N A W E E T S D S G D P I I V V I G S C M N P P D S V F N D H N A B P L R V L S E I R	417
Consensus	k r g w p f c f h l n a w e v v i g s c m p d f e l s e i r	
AtNCED2	I N L R T R K T T R R S I L V N . . E D V N L E I G M V N R N R L G R K T R F A L A L A Y P W P K V S G F A K V D L C T G E M K K Y I Y G E K Y G G E P P F	514
AtNCED3	I N L K T G E S T R R P I I S N E D Q V N L E A G M V N R N R L G R K T R F A M L A L A E P W P K V S G F A K V D L T T G E V K K H I Y G D N R Y G G E P L F	533
AtNCED5	I N L K T G K S T R R T I I P G S . V Q M N L E A G M V N R N R L G R K T R Y A M L A L A E P W P K V S G F A K V D L S T G E V K N H Y G G K Y G G E P P F	522
AtNCED6	I N M R T K E S N R K V I V T G . . . V N L E A G H I N R S Y V G R K S Q F V Y I A T A D P W P K C S G I A K V D I Q N G T V S E F N Y G P S R R G G E P C F	511
FveNCED3	I N L K T G K S T R R P I C S . . . E Q M N L E A G M V N R N R L G R K T R F A M L A L A E P W P K V S G F A K V D L F T G E V K K H I Y G E Q R F G G E P L F	552
FveNCED5	I N L K T G E S K R R P I I S E A D H V N L E A G M V N R N R L G R K T R Y A M L A L A E P W P K V S G F A K V D L F T G E V K K H I Y G D R K Y G G E P P F	543
FveNCED6	M N L R S G E S S R R V I V S G . . . L N L E V G V N K Q L L G Q E T R Y L M A L A E P W P K C S G L A K V D L E T G S V T K Y M Y G C T R R G G E P F Y	493
Consensus	n r n l e g n g a a p w p k s g a k v d g y g g e p	
AtNCED2	L E G N S G N . . . . . G E N E D D G Y I F C H V H D E T K T S E L Q I I N A V N L K L E A T I K L P S R V P Y G F H G T F V D S N E L V D Q L .	583
AtNCED3	L P . . G E . . . . . G G E E D D G Y I L C F V H D E K T W K S E L Q I V N A V S L E A T V K L P S R V P Y G F H G T F I G A D D L A K Q V V	599
AtNCED5	L P . . R G L . . . . . E S D G E D D G Y I M S F V H D E S W S E L H I V N A V T L E A T V K L P S R V P Y G F H G T F V N S A D M L N O A .	589
AtNCED6	V E G . . . . . E G E E D D G Y I M G F V R D E E K D B S E F V V V D A T D M K Q V A A V R L P B R V P Y G F H G T F V S E N Q L K H Q V F	577
FveNCED3	L P . . R D P . . . . . N S E N E D D G Y I L A F V H D E K E W K S E L Q I V N A M T L K L E A S I K L P S R V P Y G F H G T F I S S K D L Q K O A .	619
FveNCED5	L P . . S S . . . . . S T G E E D D G Y I L S F V H D E K T W K S E L Q I V N A V S L K V E A T V T L P S R V P Y G F H G T F I D S K A L K N O A .	609
FveNCED6	V K L S S S G N N G V V Q E D D D E G Y L M G F V R D E R E E K S E M V I L D A S S M K Q V G S V R L P A R V P Y G F H G T F V S E Q D L K H Q A L	570
Consensus	p k l s s s g n n g v v q e d d e g y l m g f v r d e r e e k s e m v i l d a s s m k q v g s v r l p a r v p y g f h g t f v s e q d l k h q a l	

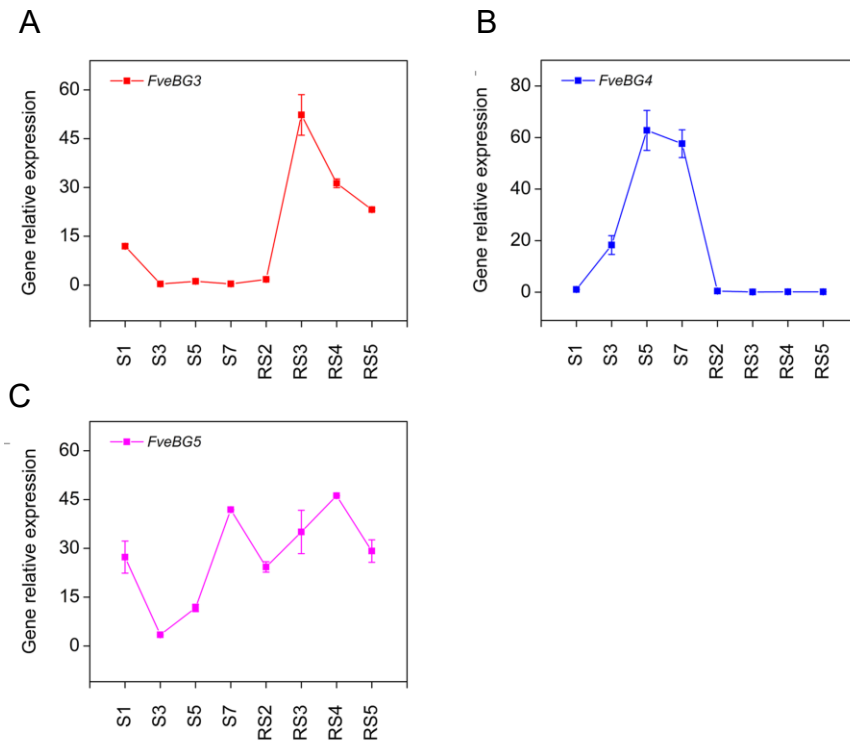


**Fig. S2. CYP707As and NCEDs family members in *Fragaria vesca*.** (A and B) The alignments of the deduced amino acid sequences of FveCYP707As and AtCYP707As (A), and FveNCEDs and AtNCEDs (B). Identical and conserved amino acids were indicated by black and pink, respectively. (C and D) Phylogenetic analysis of CYP707As (C) and NCEDs (D) family members from different plant species including *Fragaria vesca* and *Arabidopsis thaliana*. The phylogenetic tree was constructed using the neighbor-joining method with 1000 bootstrap replications. Bootstrap percentages are shown at dendrogram branch points.

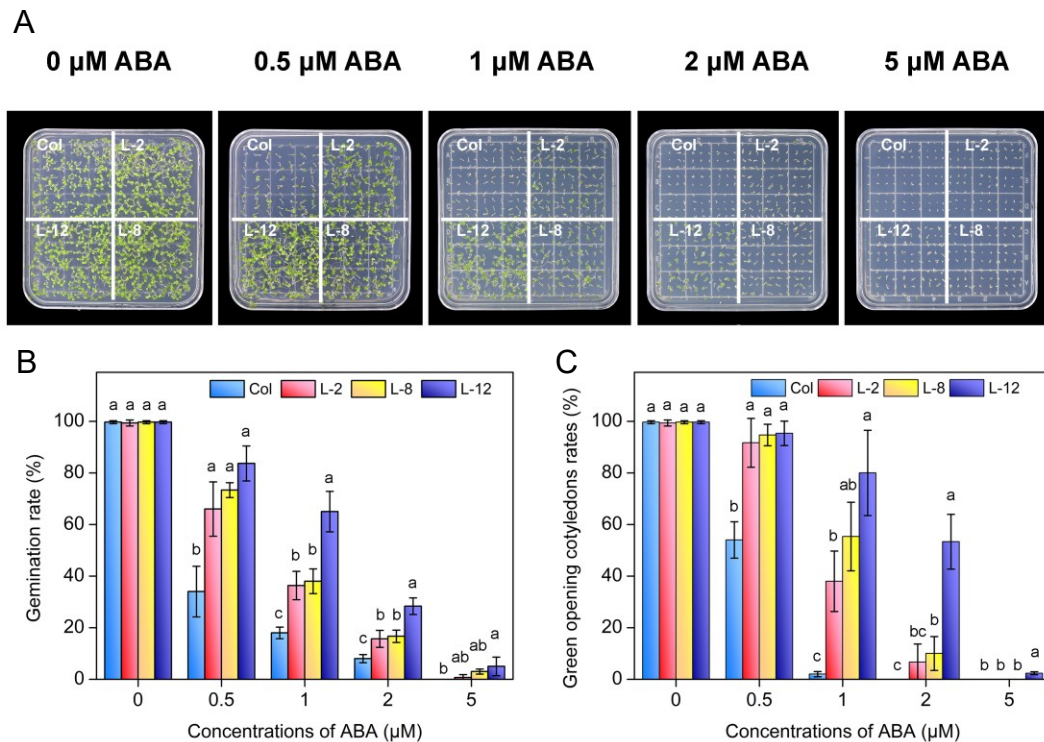


**Fig. S3. ABA levels in receptacle are mainly controlled by *FveCYP707A4a* and *FveNCED5*.**

(A and B) Quantitative RT-PCR analysis of transcript levels for *FveCYP707As* and *FveNCEDs* genes in strawberry fruit at S5. (A) *Fve707A4a* is highly expressed in receptacle, but other *FveCYP707A* members are mainly expressed in achenes. (B) *FveNCED5* was mainly expressed in receptacle. *FveACTIN* was used as the internal control. Error bars represent SD of three independent replicates (10-15 fruits were used for each replicate). Letter in figure indicate significant differences between groups ( $P < 0.05$ , one-way ANOVA, Tukey's HSD post hoc test).

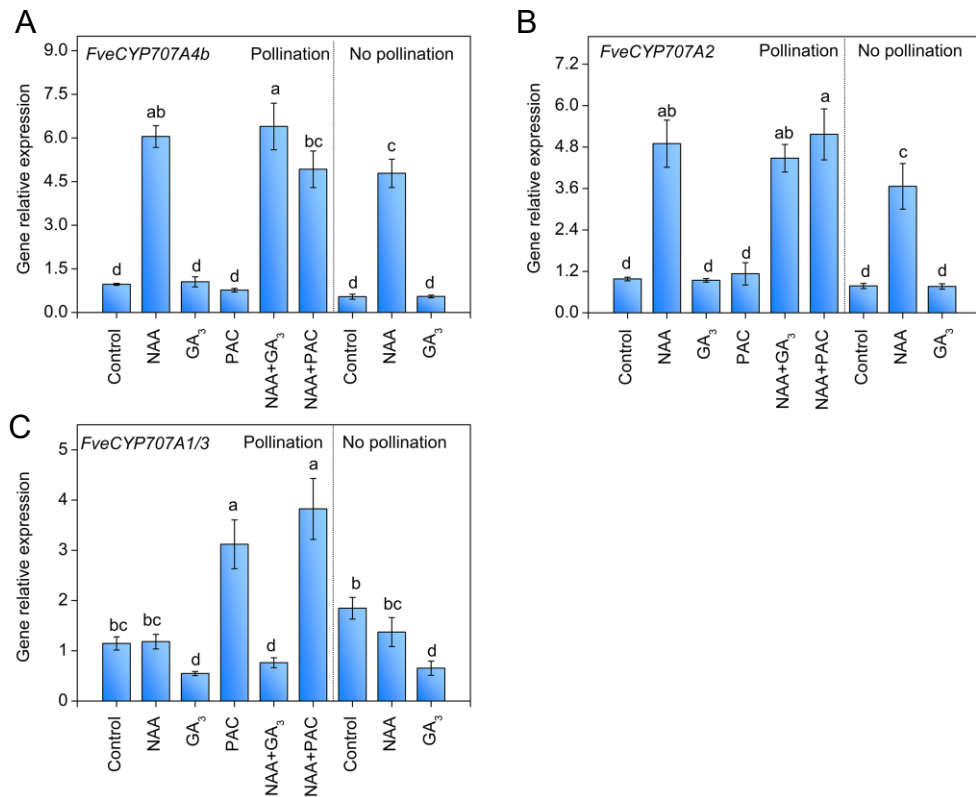


**Fig. S4. BG genes expression during fruit development.** (A to C) Quantitative RT-PCR analysis of transcript levels in pollinated fruit (receptacle and achene). The expression level of *FveBG3* (A) *FveBG4* (B) and *FveBG5* (C) in fruits of different developmental stages. *FveACTIN* was used as the internal control. Error bars represent SD of three independent replicates (10-15 fruits were used for each replicate).

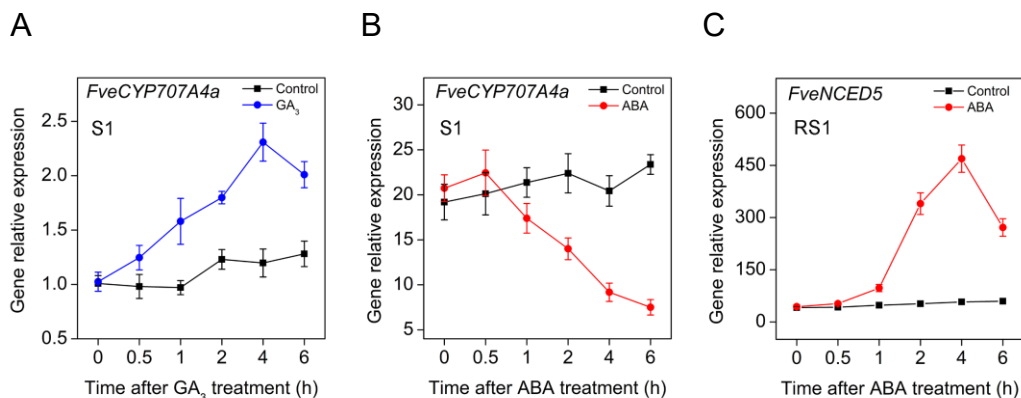


**Fig. S5. Overexpression of *FveCYP707A4a* in Arabidopsis caused hypo-sensitivity to ABA during seed germination and seedling growth. (A to C)** Seeds of three independent transgenic lines of *35S::FveCYP707A4a* (L2, L8, L12) and Col were germinated and grown on ABA (0  $\mu\text{M}$ , 0.5  $\mu\text{M}$ , 1  $\mu\text{M}$ , 2  $\mu\text{M}$ , and 5  $\mu\text{M}$ ) containing medium. 7 days old seedlings of *35S::FveCYP707A4a* transgenic lines and Col (A) the germination rate of 3 days old seedling (B) green opening cotyledons rates of 7days old seedling (C). Error bars represent SD of three independent replicates (100 seeds were used for each replicate). Letter in figure indicate significant differences between groups ( $P < 0.05$ , one-way ANOVA, Tukey's HSD post hoc test).

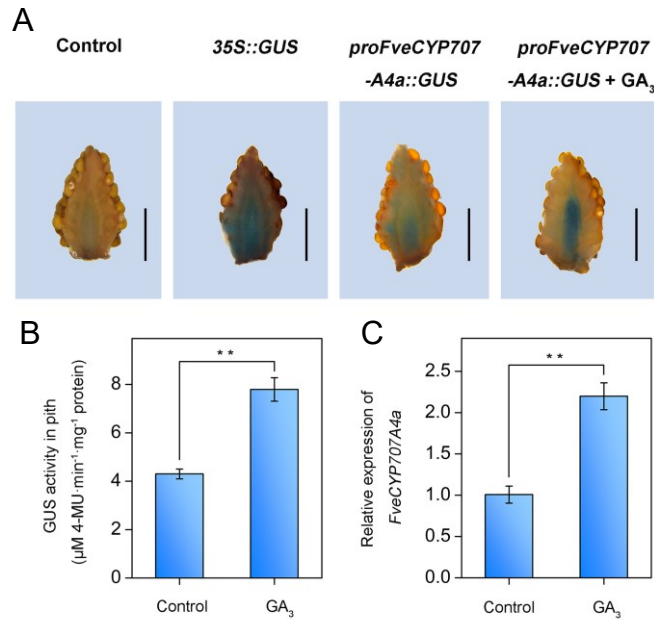




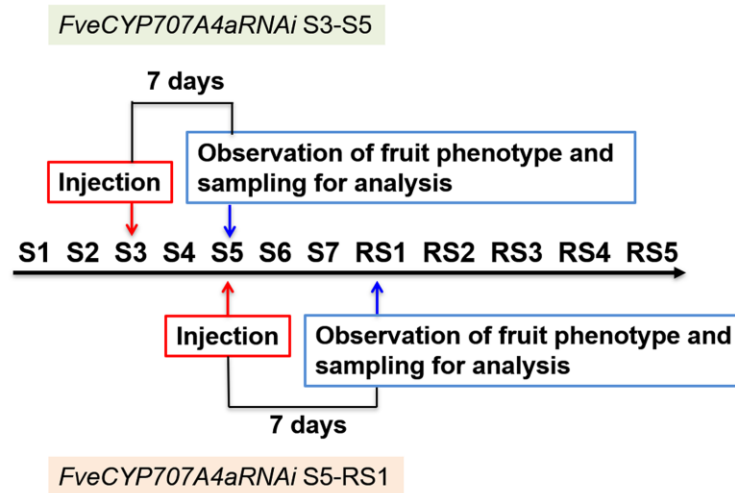
**Fig. S6. The effect of auxin and GA on the expression of *FveCYP707As*.** (A to C) Quantitative RT-PCR analysis of *FveCYP707A4b* (A), *FveCYP707A2* (B), and *FveCYP707A1/3* (C) in pollination and no pollination fruits. RNA was isolated 14 days after first hormone application. GA treatment did not cause major changes in *FveCYP707A4b* and *FveCYP707A2* expression, while PAC (GA biosynthesis inhibitor) significantly up-regulated *FveCYP707A1/3* expression, suggesting different GA effect on the regulation of expression among family members. The conditions for the experiments was the same as that of Fig. 3C. Letter in figure indicate significant differences between groups ( $P < 0.05$ , one-way ANOVA, Tukey's HSD post hoc test). Error bars represent SD of three independent replicates (15 to 20 fruits were used for each replicate).



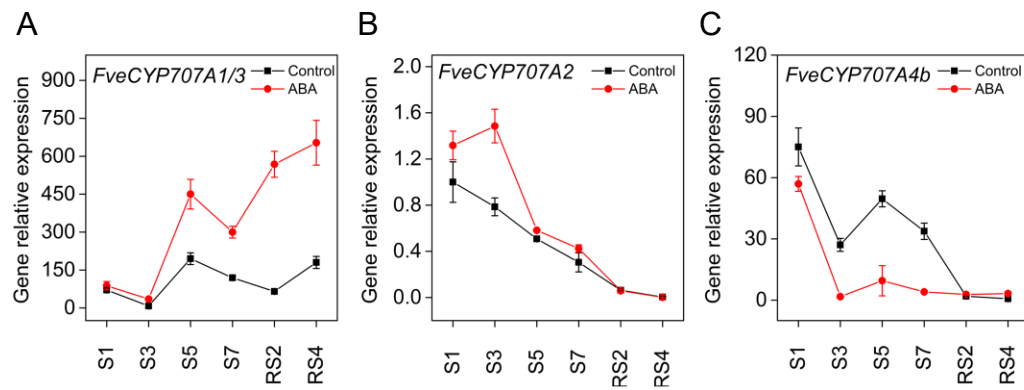
**Fig. S7. The effect of plant hormones on the expression of *FveCYP707A4a* and *FveNCED5* after short-term treatment.** (A to C) Quantitative RT-PCR analysis of transcript levels in pollinated fruit (receptacle and achene). The expression level of *FveCYP707A4a* (A and B) and *FveNCED5* (C) in after short-term hormone treatment. S1 and RS1 in figure indicate the stage of the fruit. *FveACTIN* was used as the internal control. Error bars represent SD of three independent replicates (20 fruits were used for each replicate).



**Fig. S8. GA promotes *proFveCYP707A4a::GUS* expression.** (A to C) Promoter region (1823 bp fragment upstream of the ATG start codon) of *FveCYP707A4a* was fused to GUS genes (*proFveCYP707A4a::GUS*). Transient expression was performed by agrobacterium infiltration in fruits at S5. GUS staining (A) and GUS activity assay (B) and quantitative RT-PCR analysis of transcript levels for *FveCYP707A4a* as control (C) for fruit expressing *proFveCYP707A4a::GUS* were performed after GA<sub>3</sub> (100  $\mu\text{M}$ ) treatment for 3 h. 10 Fruits for each experiment. *FveACTIN* was used as the internal control. Error bars represent SD of three independent replicates (20 fruits were used for each replicate). p-value for each t-test was adjusted by Bonferroni procedure. Bar=5mm. Transient expression of *35S::GUS* was performed as positive control.



**Fig. S9. Experimental schedule of *FveCYP707A4aRNAi*.** Time course of the experimental schedule for *FveCYP707A4aRNAi* S3-S5 and *FveCYP707A4aRNAi* S5-RS1. The interval between “agrobacterium injection” and “observation and sampling for analysis” were 7 days.



**Fig. S10. The effect of ABA on the expression of *FveCYP707As* in fruits of different developmental stages.** (A to C) Quantitative RT-PCR showed different ABA effect on the expression among family members. Error bars represent SD of three independent replicates (10-15 fruits were used for each replicate). The experimental condition were the same as that of Fig. 3D.

**Table S1. Effect of different hormone treatments on the length and width of receptacle at 14 DAP**

Treatments		Vertical diameter (cm)	Horizontal diameter (cm)
Pollination	Control	0.91 ± 0.03c	0.52 ± 0.02bc
	NAA	1.03 ± 0.01b	0.72 ± 0.05a
	GA <sub>3</sub>	1.11 ± 0.02a	0.56 ± 0.07b
	PAC	0.4 ± 0.01g	0.33 ± 0.01ef
	ABA	0.68 ± 0.02e	0.47 ± 0.01d
	NAA+PAC	0.71 ± 0.03e	0.7 ± 0.07a
	ABA+PAC	0.36 ± 0.01gh	0.29 ± 0.02f
No pollination	Control	0.51 ± 0.07f	0.33 ± 0.03ef
	NAA	0.83 ± 0.04d	0.67 ± 0.05a
	GA <sub>3</sub>	1.01 ± 0.02b	0.37 ± 0.03e
	ABA	0.32 ± 0.03h	0.26 ± 0.01f

Letters indicate significant differences between groups ( $P < 0.05$ , one-way ANOVA, Tukey's HSD post hoc test), n = 20.

**Table S2. Primers used for qRT-PCR**

<b>Gene</b>	<b>Forward primers (5'-3')</b>	<b>Reverse primers (5'-3')</b>
<i>ACTIN</i>	GCCAGAAAGATGCTTATGTCGGTG	TGGGGCAACACGAAGTCAT
<i>FveBG3</i>	TTGACTACCACTCCGCCA	TGATGCCAAACCGAACAGT
<i>FveBG4</i>	CCTTCGTGACTTTGCTCCA	CATTCATTGTGACCCAGTGC
<i>FveBG5</i>	GATGGCACAGAAATAGCAGTTG	TGGTTCCGTCAGGCAATAG
<i>FveCYP707A1/3</i>	CGACCTTCTTGCTCTTTCA	GCTTCTTGCTCTTCGGTGAC
<i>FveCYP707A2</i>	CCCTGTGTGATGATAACGAGC	GCCTGAACCACCTTCTTTAGC
<i>FveCYP707A3</i>	CAGGAAGAGACGGAATGGTAAG	AACCGATAGAGGCTCAGCAA
<i>FveCYP707A4a</i>	CCCCTACAAAGAAGAACTGA	TGTCACCGATAATGTGCCCTC
<i>FveCYP707A4b</i>	CACAAAGCAGAAGAGGTATGGAG	GTGAAAGAACAAAAGCAGAAGGG
<i>FveGA20ox1</i>	CCAGACCAGACTTTAGGCACA	CCATTCTTCGTCCACAAAACAC
<i>FveGA20ox2</i>	CAGGTTCCTCCAAACTTCC	TCTGCGAAATCTTACCCCA
<i>FveGA20ox3</i>	GGATTCTTCCTCATTGTGAACC	CAACTGTCTCCAACCTTCCTCT
<i>FveGA20ox4</i>	CAGAGAAAGTCGTGGTGGATTT	GCCAAACTCGTCATTGCTTC
<i>FveGA20ox5</i>	GGGAGGTTGAAGAGTGTAGTGC	TTGTGGCAGAATCAGAGGG
<i>FveGA3ox1</i>	AAGGTGGCTTTGAAGACGC	GGTGGATGATTGTGAGGAGG
<i>FveGA3ox2</i>	TCATCGTGTGGTGGTGAAC	CTCCTTAGCAGTAACAGAGCGA
<i>FveGA3ox3</i>	CACAGACACCTCCATTGTAACC	CCAGTTCACCAGAATCCA
<i>FveGA3ox4</i>	AAACCAGCGGTCTCCAAGT	CCACACGATGAAGAACACTGA
<i>FveGA3ox5</i>	CATTATCCAGGCGTGTGAGA	GAGCAAACAACCTATGAGTCTGAG
<i>FveGA3ox6</i>	CAGACTCATAGGTTGTTGCTCTC	TTCTTGCCACAGTTTACGG
<i>FveGAI</i>	GCCGTGACTCGCTAAGAGAA	ACCGCTTCCTTTGGACTCA
<i>FveNCED3</i>	CGTTGTCCAGAAGCCTTACC	GGGATTACGACGAACCGTT
<i>FveNCED5</i>	CTGTCCGTCATTCACTCCCT	CACCGTCATTGATGCTAACG
<i>FveNCED6</i>	CTGTTTGACGGAGACGGAAT	CTCACCAATCGGCTTAGGAA
<i>FveRGA1</i>	CCTAATCCAAACCCATCCG	CTTCACCTTGTAACCCAACACA
<i>FveRGL1</i>	CCCTACATCAAGTTCGCTCA	TCTTTCACCGCCTCTATGC
<i>FveRGL2</i>	GCCTTTGAGGGAGAGAGTTTC	GCCAACACCAGTTATCCGA
<i>FveRGL3</i>	GGAAGAAGGAAGTGGAGATGG	GGAATGATGTCCCAAAGACCT

**Table S3. Primers used for construction**

<b>Primers</b>	<b>Sequences (5'-3')</b>	<b>Vector</b>
FveCYP707A4a-OE F	ACGCGTATGAAGAAGAGCAAGGGAGG	pCAMBIA1305
FveCYP707A4a-OE R	GTCGACCTATTCTAATTCCAAAGTTTGACC	
FveCYP707A4a-RNAi F	GAATTCTTGGTCCCTCCGCATTATT	TRV2
FveCYP707A4a-RNAi R	GGATCCTTTGTATGGCGTCCAGGA	
proFveCYP707A4a F	ACCATGATTACGCCAAGCTTTCAAAGAGGACCAGGAAAAT	PBI121
proFveCYP707A4a R	CCACCCGGGGATCCTCTAGAGAAAATGTACAAGAAGATAAGGGTTA	



**Table S4. Accession numbers**

Gene	Accession number	Gene	Accession number	Gene	Accession number
<i>AtNCED2</i>	AT4G18350	<i>AtNCED3</i>	AT3G14440	<i>AtNCED5</i>	AT1G30100
<i>AtNCED6</i>	AT3G24220	<i>AtNCED9</i>	AT1G78390	<i>FaNCED1</i>	HQ290318
<i>FaNCED2</i>	JX013945	<i>FaNCED3</i>	JX013946	<i>CsNCED6</i>	XP_010488479.1
<i>FveBG3</i>	FvH4_3g43520.1	<i>FveBG4</i>	FvH4_7g00230.1	<i>FveBG5</i>	FvH4_6g53030.1
<i>FveCYP707A1/3</i>	FvH4_5g25150.1	<i>FveCYP707A2</i>	FvH4_3g36810.1	<i>FveCYP707A3</i>	FvH4_2g14100.1
<i>FveCYP707A4a</i>	FvH4_2g34420.1	<i>FveCYP707A4b</i>	FvH4_2g06010.1	<i>FveGA20ox1</i>	FvH4_7g28670.1
<i>FveGA20ox2</i>	FvH4_7g12600.1	<i>FveGA20ox3</i>	FvH4_7g12610.1	<i>FveGA20ox4</i>	FvH4_2g35050.1
<i>FveGA20ox5</i>	FvH4_5g19970.1	<i>FveGA2ox7</i>	FvH4_4g36520.1	<i>FveGA3ox1</i>	FvH4_6g30780.1
<i>FveGA3ox2</i>	FvH4_2g30040.1	<i>FveGA3ox3</i>	FvH4_2g30020.1	<i>FveGA3ox4</i>	FvH4_2g30020.1
<i>FveGA3ox5</i>	FvH4_2g30010.1	<i>FveGA3ox6</i>	FvH4_2g27140.1	<i>FveGAI</i>	FvH4_1g04080.1
<i>FveNCED3</i>	FvH4_3g16730.1	<i>FveNCED5</i>	FvH4_3g05440.1	<i>FveNCED6</i>	FvH4_4g05900.1
<i>FveRGA1</i>	FvH4_4g34110.1	<i>FveRGL1</i>	FvH4_6g53920.1	<i>FveRGL2</i>	FvH4_5g07610.1
<i>FveRGL3</i>	FvH4_4g24820.1	<i>PacCYP7071</i>	GU559987	<i>PacCYP7072</i>	GU559988
<i>PacCYP7073</i>	GU559990	<i>PacCYP7074</i>	GU559989	<i>SICYP707A1</i>	EU183406
<i>SICYP707A3</i>	AI484420	<i>SICYP707A4</i>	XM_004245970	<i>VvCYP707A2</i>	XP_010651002.1
<i>VvCYP707A4</i>	XP_002282788.1				