Table S1. Primers used for reverse transcription quantitative PCR analysis

Gene	Gene description	Locus tag	Forward primer (5′ to 3′)	Reverse primer (5′ to 3′)
PpIAA3	auxin-induced protein 22B	Prupe.6G343700	GTGATTATTGTGAGAAGGAT	CACGAAGTGATGAACATT
PpIAA5	auxin-induced protein IAA6	Prupe.3G074800	AAAGCGAAACGAAGAACCAAG	GCTCCATCCATGCTAACCTTGAC
PpIAA11	auxin-responsive protein IAA11	Prupe.8G215400	CTTCTTCGTCGTCCTCAT	AATCAGCACTTCTCTTGGT
PpIAA17	auxin-responsive protein IAA1	Prupe.3G074900	CTTCTTGACCATCCGTAA	CCATCTCTGTCCTCATAAG
PpIAA29	auxin-responsive protein IAA29	Prupe.1G481700	ATGTTGGTGAAGGTGAAG	AGCGTCTGATAAGAGTGA
PpARF5	auxin response factor 5	Prupe.1G368300	GAAGGGCTGCTAAATGACCCAAGA	ATACAGCGAACACAACCAACGA
PpARF7	auxin response factor 7	Prupe.7G194200	AATTGAGCCTGTTGTAACTCC	TGCCAAAGTCATCTCCAAGCCAA
PpARF8	auxin response factor 6	Prupe.3G182900	AGGCATCTTCTCACGACAGG	GATTTGCTCGCCGAATACCCA
PpARF16	auxin response factor 18	Prupe.2G213000	ATCAAGCATACCAGCCATCCA	GCTACAAACTGAAGGCATTGGA
PpARF18	auxin response factor 18	Prupe.2G190400	CAAAGCCAAGTAATACCCCGAT	TTTACACACTGGCTCGCTCT
PpSAUR50	auxin-responsive protein SAUR50	Prupe.6G108400	AATGTGCCAGAAGATGTG	GTGTCAAGTAACTCAATGC
PpGH3.1	probable indole-3-acetic acid-amido synthetase GH3.1	Prupe.8G137900	ATCGCTCTCCTATCTTGT	ACTCCTCCTGAATTGTTG
PpYUCCA2	indole-3-pyruvate monooxygenase YUCCA2	Prupe.7G231200	CCACTTACCCAACCAAAC	CACTCACCACTGTCATATTG
PpYUCCA6	indole-3-pyruvate monooxygenase YUCCA6	Prupe.1G453400	ATTGCTGAGGACATTGAA	GTGATGATGATGATGATAGTG
PpYUCCA10	probable indole-3-pyruvate monooxygenase YUCCA10	Prupe.8G252500	CCATTGATGTTGGAACCT	CCTCTTATGCTGCTGATT
PpSAM	S-adenosylmethionine synthase 5	Prupe.1G107000	GATGAGATTGCTGCTGAT	GTTGAGATGGAAGATGGT

PpERF4	ethylene-responsive transcription factor 4	Prupe.4G051400	TAGCGGAAACGTGAAGGAG	TCTGATCTCGGCAGCGTA
PpERF034	ethylene-responsive transcription factor ERF034	Prupe.2G123200	CAACAACAACTTCTGATTCT	CTGCCTCTTCTTCTTCTT
Ppβ-gal	beta-galactosidase 10	Prupe.4G278500	AATGTGCTGGTGATATTC	AAGATTCAAGGTCAATAGAG
PpPA	pectin acetylesterase 9	Prupe.2G296000	GAAGCAGTAGGTGATTGG	TAAGGTTATGGCAGGTAGT
PpExp2	expansin-A1	Prupe.1G276700	GTTGCTTACAGAAGGGTA	CAGGTTGAAGTAGGAGTG
PpPMEI	21 kDa protein	Prupe.2G279800	TTGATGGTGTGAAGGTAA	AATGAGGCTGTCTATGAG
PpGlu	glucan endo-1,3-beta-glucosidase 9	Prupe.6G050800	TAGTGAACAACAATAAGG	ATTATGCTGCTGATAGTA
PpPG	polygalacturonase At1g48100	Prupe.1G251200	GAATCAGCATCGGAAGTT	ACCATTCATCGTGTTGTG
PpACO1	1-aminocyclopropane-1-carboxylate oxidase 1	Prupe.4G013800	TTGATGAAGATTACAGGAAGT	CACAGCAAGTCCAGAAGT
PpTEF2	elongation factor 2	LOC18778380	GTTGCCTTGGTCGGTCTTGA	ATTGAACAGCAACACGCACAA

Table S2. Primers used for vector construction

Name	**Forward/ Reverse primer Sequence (5′ to 3′)**	**Description**
OE-*PpIAA5* F	gagagaacacgggggactctagaATGGCCAAAGAAGGTTTAG	Primers used for inserting PpIAA5 into vector pCAMBIA3301-121
OE-*PpIAA5* R	ataagggactgaccacccgggTTATTTAGGATCATCTTTCATAGTT	
OE-*PpARF8* F	gagagaacacgggggactctagaATGAGACTTTCGTCTTCATCATC	Primers used for inserting PpARF8 into vector pCAMBIA3301-121
OE-*PpARF8* R	ataagggactgaccacccgggGTAGTCCAGTGAGCCCAACGA	
pTRV2-*PpARF8* F	aaggttaccgaattctctagaCTTCATCATCGGCTTCGGGTTTTAA	Primers used for inserting PpARF8 into vector pTRV2
pTRV2-*PpARF8* R	ggtaccggatccccatggaggCCCAACTCCGCAGGCAGTAGGTATA	
GFP-*PpIAA5* F	gagaacacgggggactctagaATGGCCAAAGAAGGTTTAG	Primers used for inserting PpIAA5 into vector pBI121-GFP
GFP-*PpIAA5* R	ggactgaccacccgggTTATTTAGGATCATCTTTCATAGTT	
GFP-*PpARF8* F	gagaacacgggggactctagaATGAGACTTTCGTCTTCATCATC	Primers used for inserting PpARF8 into vector pBI121-GFP
GFP-*PpARF8* R	ggactgaccacccgggGTAGTCCAGTGAGCCCAACGA	
CE-*PpIAA5* F	CGggatccATGGCCAAAGAAGGTTTAGGG	Primers used for inserting PpIAA5 into pSPYCE (M)
CE-*PpIAA5* R	GGggtaccTTTAGGATCATCTTTCATAGTTGCC	
NE-*PpARF8* F	ggagagaacacgggggactctagaATGAGACTTTCGTCTTCATCATC	Primers used for inserting PpARF8 into pSPYNE173
NE-*PpARF8* R	ttgctccatcccgggagcggtaccGTAGTCCAGTGAGCCCAACGA	

Table S3. Primers for yeast-two hybrid vector construction

GENE	Forward primer (5′ to 3′)	Reverse primer (5′ to 3′)	Amplicon Size (bp)
PpARF2	ATGACGTCATCGGAGGTTTCG	AGGAAGTAGCTGAGACTTCCCCTC	2517
PpARF3	ATGGGGGGTCTAATCGATC	TCCTTGTAAACAGCTTTCCATC	2166
PpARF4	ATGGAAATTGATCTGAACCATGCAG	GACCCTGATTACTGTTGGGGAAGAA	2409
PpARF6	ATGAGGCTCTCATCTGCT	ATACTCGAGTGACCCCAC	2661
PpARF7	ATGAAGGCTCCTTCAAATGGG	TTTTTGATTGCGATTAAATGAGG	3504
PpARF8	ATGAGACTTTCGTCTTCATCATC	GTAGTCCAGTGAGCCCAACGA	2757
PpARF19	ATGAAGCCGCCCGCGAA	GGCATTCCCACCATCTGAGC	3417
PpIAA5	ATGGCCAAAGAAGGTTTAG	TTATTTAGGATCATCTTTCATAGTT	573

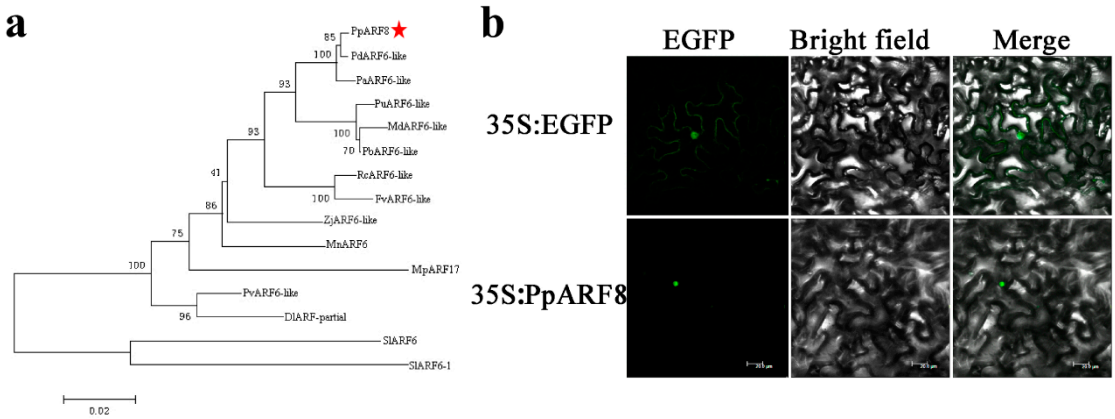

Figure S1. Analysis of PpARF8 characteristics. (**a**) Homology of PpARF8 homologues among different species. (Note: Phylogenetic tree derived from amino acid sequences of ARFs in peach and other species. PpARF8 was highlighted with the red pentagram. The phylogenetic tree was constructed using the maximum-likelihood method by MEGA 5.0. Numbers indicate bootstrap test result with 1000 replicate analyses. The scale bar represents 0.02 substitutions per site.); (**b**) The results of subcellular localization showed that PpARF8 was localized in the nucleus, Scale bar = 20 μm.