
Supplementary information

**Reinvention of hermaphroditism via
activation of a *RADIALIS*-like gene in
hexaploid persimmon**

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Supplementary Information for

Reinvention of hermaphroditism via activation of a *RADIALIS*-like gene in hexaploid persimmon

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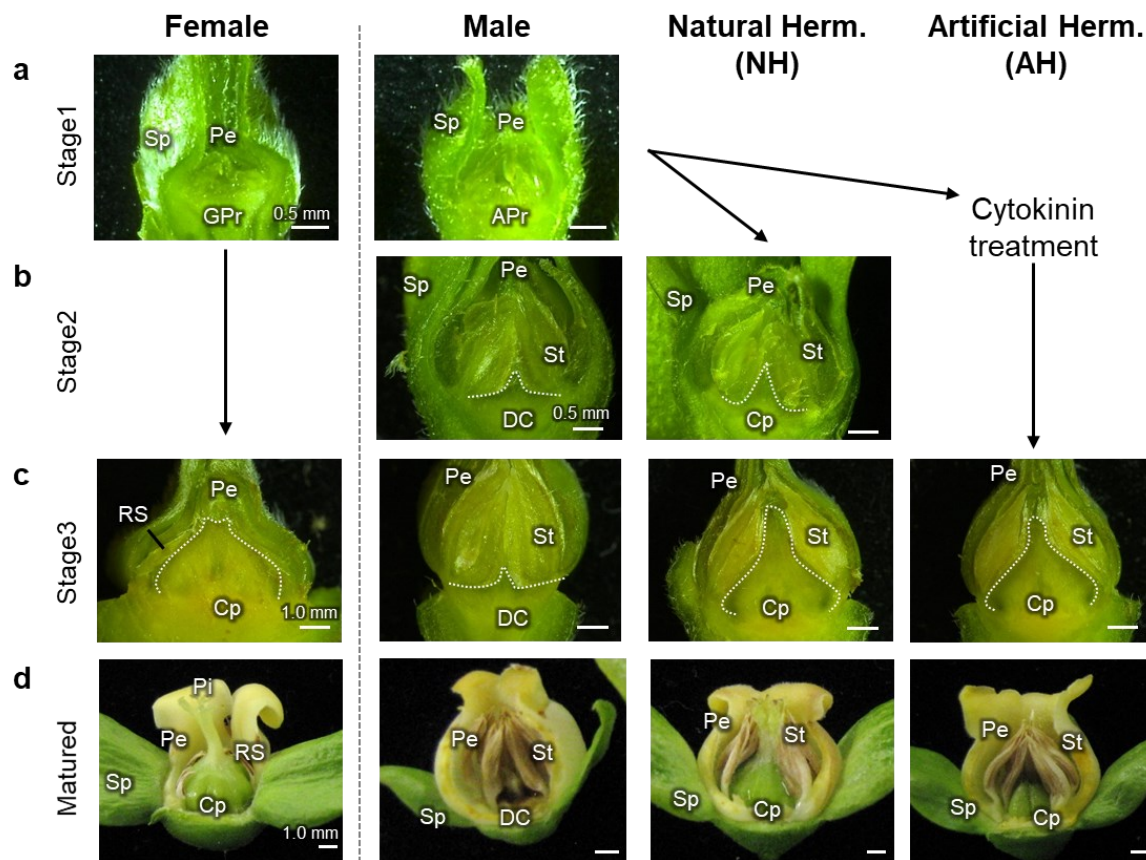
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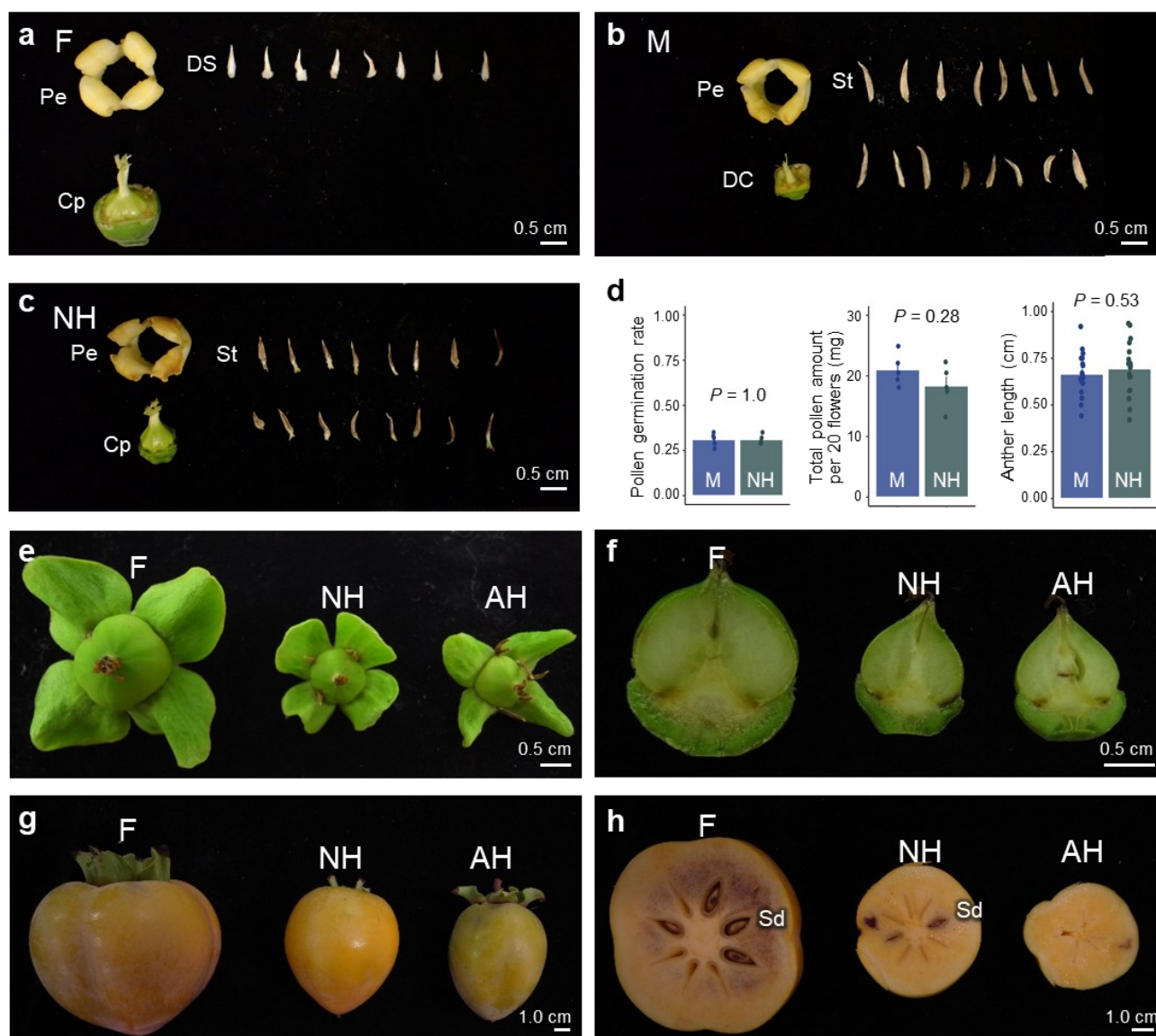
Supplementary Figure 1



Supplementary Figure 1 | Developmental processes of hermaphrodite flowers (Supports Fig. 1b)

We defined four developmental stages according to Yang et al. (2019). **a**, In stage 1, androecium and gynoecium primordia are differentiated. **b**, In stage 2, the gynoecium of hermaphrodite flowers was differentiated from that of male flowers. In AH, developing flowers were artificially treated with synthetic cytokinin (CPPU) at stage 1.5. **c**, In stage 3, the gynoecium of NH and AH developing flowers exhibited enlarged carpel. **d**, At the mature stage, gynoecium and androecium from NH and AH flowers were fully matured. APr, androecium primordia; Cp, carpel; DC, deficient carpel; GPr, gynoecium primordia; Pe, petal; RS, rudimentary stamen; Sp, sepal; St, stamen. Scale bars: 0.5 mm for stages 1 and 2, and 1.0 mm for stages 3 and mature stage.

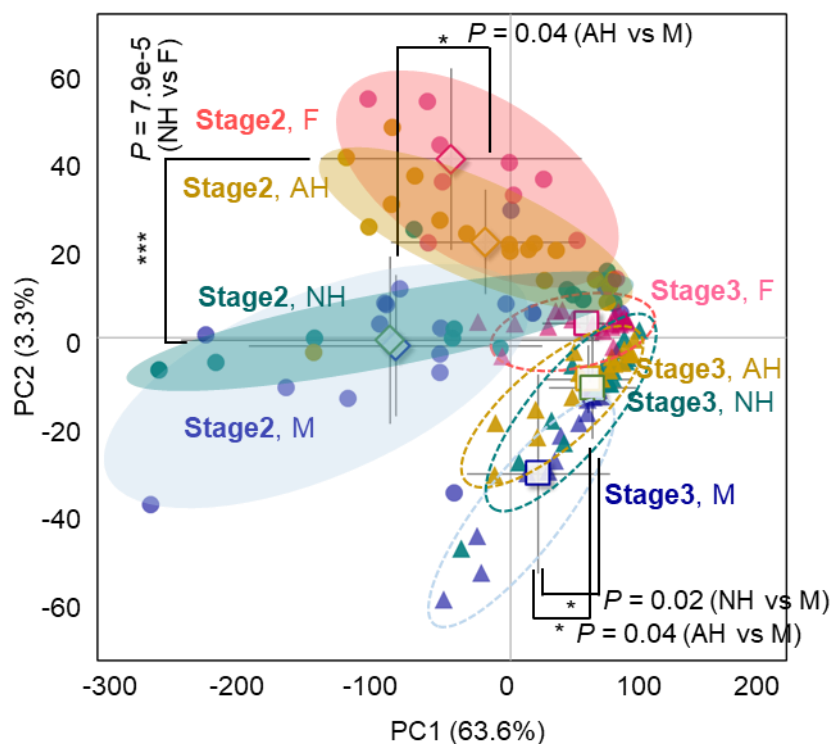
Supplementary Figure 2



Supplementary Figure 2 | Morphological observation in opened flowers and fruits

a-c, Mature organs from female (**a**), male (**b**), and NH flowers (**c**). Female flowers contained 8 stamens, while male and NH flowers contained 16, suggesting that the gynoecium of NH flowers differentiated after androecium differentiation in male flowers. **d**, Pollen germination rate, total pollen amount per 20 flowers, and anther sizes in NH flowers per exhibited no significant differences in comparison to male flowers ($n = 5, 5, 18$ for biological replicates, respectively, one-sided Student's t -test). Data were expressed as mean values $\pm$ SD. **e-h**, NH and AH flowers often produced fruits. Early (**e-f**) and late (immediately before full mature, **g-h**) fruit development stages were shown. Cp; carpel, DC, deficient carpel; DS, deficient stamen; Pe, petal; St, stamen.

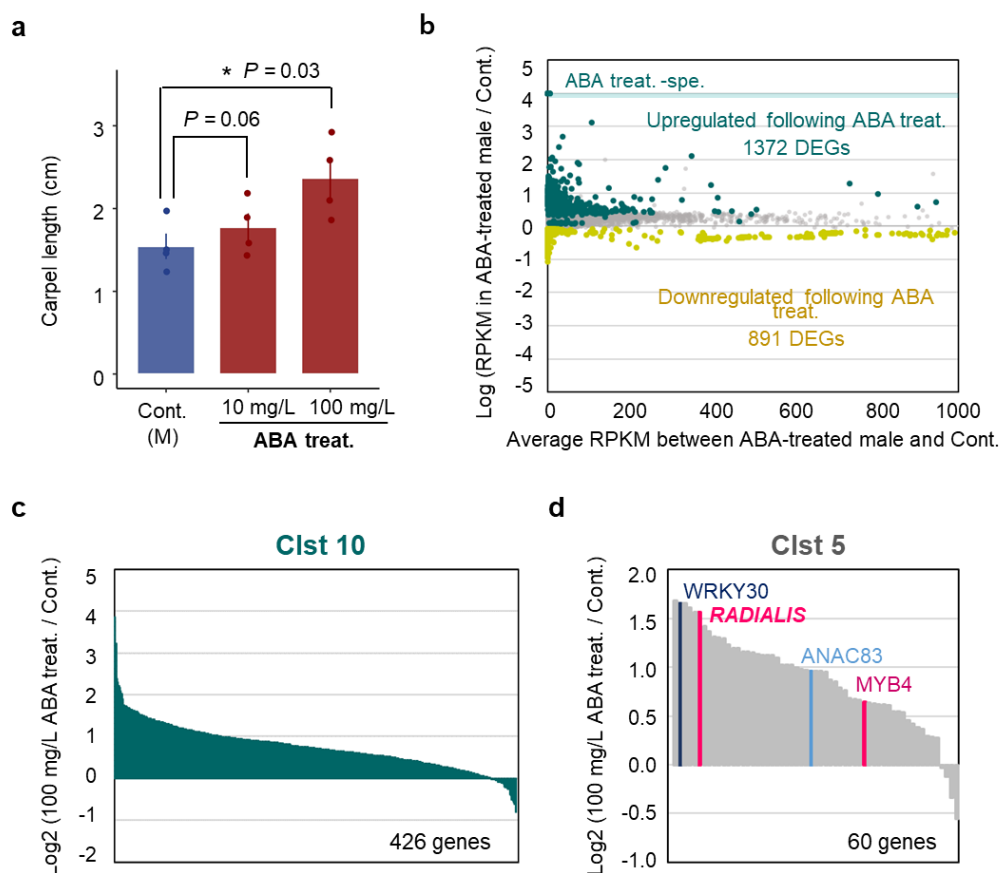
Supplementary Figure 3



Supplementary Figure 3 | Expression dynamics in the four flower types at stages 2 and 3 (Support Fig. 1c)

PCA of all transcriptomic data (15,019 genes, RPKM > 1) for the four flower types (male, female, NH, and AH flowers) at stages 2 (filled circle) and 3 (filled triangle). Male and female flowers showed distinct expression dynamics in both stages. In stage 2, expression patterns in NH and male flowers were similar, and significantly different from that of female flowers ($P = 7.9e-5$ in PC2), while AH samples were statistically apart from male samples ($P = 0.04$ in PC1), while quite similar to female samples. In stage 3, both NH and AH flowers were significantly different from male flowers in PC1 ($P = 0.02$ and 0.04 , respectively) with two-sided Student's *t*-test.

Supplementary Figure 4



Supplementary Figure 4 | Effect of ABA treatment to male flowers in hexaploid *D. kaki*

a, Restoration of gynoecium development in male flowers following ABA treatment. In comparison to male, flowers treated with higher concentration of ABA produced significantly longer carpels ($n = 4$ biological replicates). P -values were obtained by comparing mean carpel length values using paired one-sided Student's t -test. Data were expressed as mean values $\pm$ SD. **b**, Detection of differentially expressed genes (DEGs) following ABA treatment. MA plot illustrating the expression bias and average expression levels of the DEGs between ABA-treated (100 mg/L) male and control (male) flowers. The upregulated and downregulated DEGs following ABA treatment ($FDR < 0.1$, bias > 1.2 -fold) were highlighted in deep green and gold, respectively. The DEGs specific to the ABA-treated male with no expression in the control flowers were isolated to the upper green lane. **c-d**, Upregulation of almost all genes in Clst 10 and 5 following ABA treatment. Almost all genes in Clst 10 (**c**) and Clst 5 (**d**) were upregulated in male flowers treated with 100 mg/L ABA, in comparison to the control male flowers (355 of 426 genes and 56 of 60 genes, respectively, bias > 1.2 -fold). The four transcription factors identified in Clst 5 based on the presence of a TF domain were highlighted (see Fig. 1f).

Supplementary Figure 5



Supplementary Figure 5 | Treatment of diploid *D. lotus* male flowers with synthetic ABA and CK did not result in reactivation of gynoecium development (supports Fig. 2d and e)

D. lotus male flowers (cv. Kunsenshi-male and its F1 population) treated with 100 mg/L ABA (panel b) and 10 ppm CK (panel c) did not exhibit significant gynoecium restoration, in comparison to the control (panel a). DC, deficient carpel; Pe; petal, Sp; sepal, St, stamen.

Supplementary Table 1 | Plant materials used in this study.

The numbers of samples for M, NH, AH, and F at stage 2 were $n = 18, 14, 18,$ and $11,$ respectively. The numbers of samples for M, NH, AH, and F at stage 3 were $n = 15, 18, 19,$ and $20,$ respectively.

Cultivar name	Sampling stage	Flower sexuality ^x	Sampling year	Ploidy	Location
Amayotsumizo	2	M, NH, AH, F	2018	6x	Kyoto Univ. Japan
	3	M, NH, AH, F	2018	6x	Kyoto Univ. Japan
Cal. Fuyu	2	M, AH, F	2018	6x	Kyoto Univ. Japan
	3	AH, F	2018	6x	Kyoto Univ. Japan
Egosho	2	NH, F	2018	6x	Kyoto Univ. Japan
	3	NH, AH, F	2018	6x	Kyoto Univ. Japan
Fudegaki	2		2018	6x	Kyoto Univ. Japan
	3	NH, AH, F	2018	6x	Kyoto Univ. Japan
Hazegosho ^b	2	M, AH, F	2018	6x	Kyoto Univ. Japan
	3	M, NH	2018	6x	Kyoto Univ. Japan
Iwasedo ^a	2	M, NH, AH	2018	6x	Kyoto Univ. Japan
	3		2018	6x	Kyoto Univ. Japan
Kakiyamagaki	2	M, AH	2018	6x	Kyoto Univ. Japan
	3	M, AH, F	2018	6x	Kyoto Univ. Japan
Kanshu	2		2018	6x	Kyoto Univ. Japan
	3	M, AH, F	2018	6x	Kyoto Univ. Japan
Meotogaki	2	M, NH, AH, F	2018	6x	Kyoto Univ. Japan
	3	AH, F	2018	6x	Kyoto Univ. Japan
Muraya	2	M, AH, F	2018	6x	Kyoto Univ. Japan
	3	NH, AH, F	2018	6x	Kyoto Univ. Japan
Nishimurawase	2	M, NH	2018	6x	Kyoto Univ. Japan
	3	M, NH, AH, F	2018	6x	Kyoto Univ. Japan
Saburoza	2	NH, AH	2018	6x	Kyoto Univ. Japan
	3	M, NH, AH, F	2018	6x	Kyoto Univ. Japan
Shogatsu	2	M, NH, AH	2018	6x	Kyoto Univ. Japan
	3	M, NH, AH	2018	6x	Kyoto Univ. Japan
Sheihakuji	2	M, AH	2018	6x	Kyoto Univ. Japan
	3	AH, F	2018	6x	Kyoto Univ. Japan
Shojo	2	M, NH	2018	6x	Kyoto Univ. Japan
	3	AH, F	2018	6x	Kyoto Univ. Japan
Shirotodamashi	2	M, NH	2018	6x	Kyoto Univ. Japan
	3	M, NH, AH, F	2018	6x	Kyoto Univ. Japan
Shozaemon	2	NH, AH, F	2018	6x	Kyoto Univ. Japan
	3		2018	6x	Kyoto Univ. Japan
Taishu ^a	2	M, NH, AH, F	2018	6x	Kyoto Univ. Japan
	3	M, NH, AH, F	2018	6x	Kyoto Univ. Japan
Tohachi	2		2018	6x	Kyoto Univ. Japan
	3	M, NH	2018	6x	Kyoto Univ. Japan
Tiwanshoshi	2	M, NH, AH, F	2018	6x	Kyoto Univ. Japan
	3	M, NH, AH, F	2018	6x	Kyoto Univ. Japan
Yamgaki	2	M, AH	2018	6x	Kyoto Univ. Japan
	3	M, NH	2018	6x	Kyoto Univ. Japan
Yamatogosho	2	M, AH, F	2018	6x	Kyoto Univ. Japan
	3	NH, AH, F	2018	6x	Kyoto Univ. Japan
Zenjimar	2	M, NH, AH	2018	6x	Kyoto Univ. Japan
	3	M, F	2018	6x	Kyoto Univ. Japan
Shogatsu	2	Cont, ABA treat.	2019	6x	Kyoto Univ. Japan
Taishu	2	Cont, ABA treat.	2019	6x	Okayama Univ. Japan
Zenjimar	2	Cont, ABA treat.	2019	6x	Kyoto Univ. Japan
Kunsenshi	2	M, CK treat.	2018	2x	Kyoto Univ. Japan
	3	M, CK treat.	2018	2x	Kyoto Univ. Japan
	2	M, ABA treat.	2019	2x	Kyoto Univ. Japan

^xM; Male, NH, Natural hermaphrodite, AH; Artificial hermaphrodite, F; Female

^a two replicates of NH were collected in stage 2

^b two replicates of NH were collected in stage 3

Supplementary Table 2 | Expression pattern of the *MeGI* gene and its downstream targets (*SVP* and *KNAT/OFP/GRF*) in the four flower types, at stages 2 and 3.

Gene ID	Gene name	avr. RPKM								TAIR annotation	Description	e-value
		stage 2				stage 3						
		F	M	NH	AH	F	M	NH	AH			
Dlo_pri0799F.1_g00310.1	MeGI	17.1	2.8	2.1	1.4	4.7	0.4	0.1	0.1	AT4G36740.1	homeobox protein	2.09E-49
Dlo_pri0031F.1_g05400.1	SVP	1.3	0.7	0.7	0.6	0.2	0.2	0.2	0.3	AT2G22540.1	K-box region and MADS-box transcription factor	1.09E-109
Dlo_pri0079F.1_g02310.1	KNAT6	0.8	0.6	0.5	0.3	0.2	0.2	0.1	0.1	AT1G23380.2	KNOTTED1-like homeobox gene 6	2.11E-110
Dlo_pri0234F.1_g00670.1	KNAT1-1	1.7	1.5	1.5	0.4	0.4	0.4	0.3	0.2	AT4G08150.1	KNOTTED-like homeobox gene	9.12E-50
Dlo_pri0234F.1_g00690.1	KNAT1-2	2.7	2.1	1.9	0.8	1.2	0.4	0.3	0.3	AT4G08150.1	KNOTTED-like homeobox gene	2.08E-79
Dlo_pri0135F.1_g01240.1	STM	0.8	0.3	0.5	0.3	0.3	0.0	0.1	0.1	AT1G62360.1	KNOX/ELK homeobox transcription factor	1.65E-131
Dlo_pri0025F.1_g00500.1	OFP7	3.2	2.1	1.8	1.3	0.8	0.7	0.6	0.5	AT2G18500.1	ovatefamily protein	6.00E-28
Dlo_pri0153F.1_g01030.1	OFP4	1.9	0.2	0.3	0.7	0.2	0.1	0.0	0.1	AT1G06920.1	ovatefamily protein	2.01E-29
Dlo_pri0234F.1_g01300.1	GRF1	2.8	0.6	0.7	1.2	0.1	0.0	0.1	0.0	AT2G22840.1	growth-regulating factor 1	3.77E-100

Supplementary Table 3 | List of enriched GO terms associated with the genes upregulated NH and AH flowers.

GO terms associated with NH-specific (a), AH-specific (b), and NH/AH-shared (c) upregulated clusters are shown. The GO terms, which are reminiscent of response to stress, photosynthesis, and cell development, are highlighted in blue, red, and yellow, respectively.

a NH-specific upregulation (Clst 10)

Ontology	Description	GO term	p-value
Biological Process	protein folding	GO:0006457	0.02
Biological Process	positive regulation of flower development	GO:0009911	0.02
Biological Process	lignan biosynthetic process	GO:0009807	0.02
Biological Process	lignan metabolic process	GO:0009806	0.02
Biological Process	photorespiration	GO:0009853	0.04
Biological Process	positive regulation of reproductive process	GO:2000243	0.04
Biological Process	photosynthesis	GO:0015979	0.05
Biological Process	xylem and phloem pattern formation	GO:0010051	0.06
Biological Process	response to wounding	GO:0009611	0.06
Biological Process	response to oxidative stress	GO:0006979	0.07
Biological Process	response to jasmonic acid	GO:0009753	0.07
Biological Process	protein targeting to vacuole	GO:0006623	0.09
Biological Process	establishment of protein localization to vacuole	GO:0072666	0.09
Biological Process	protein localization to vacuole	GO:0072665	0.09
Biological Process	positive regulation of post-embryonic development	GO:0048582	0.09
Biological Process	maintenance of meristem identity	GO:0010074	0.09
Biological Process	response to chitin	GO:0010200	0.10
Molecular Function	heat shock protein binding	GO:0031072	6.0 E-04
Molecular Function	protein kinase activator activity	GO:0030295	4.2 E-03
Molecular Function	hydrolase activity, acting on carbon-nitrogen bonds	GO:0016812	4.2 E-03
Molecular Function	kinase activator activity	GO:0019209	0.01
Molecular Function	malate dehydrogenase activity	GO:0016615	0.02
Molecular Function	manganese ion binding	GO:0030145	0.02
Molecular Function	FK506 binding	GO:0005528	0.04
Molecular Function	macrolide binding	GO:0005527	0.04
Molecular Function	peptidyl-prolyl cis-trans isomerase activity	GO:0003755	0.04
Molecular Function	drug binding	GO:0008144	0.05
Molecular Function	cis-trans isomerase activity	GO:0016859	0.05
Molecular Function	N-acetyltransferase activity	GO:0008080	0.06
Molecular Function	calcium ion binding	GO:0005509	0.06
Molecular Function	nutrient reservoir activity	GO:0045735	0.06
Molecular Function	protein tyrosine kinase activity	GO:0004713	0.06
Molecular Function	N-acyltransferase activity	GO:0016410	0.08
Molecular Function	FMN binding	GO:0010181	0.08
Molecular Function	acetyltransferase activity	GO:0016407	0.08
Molecular Function	hydrolase activity, acting on carbon-nitrogen bonds	GO:0016810	0.09
Molecular Function	oxidoreductase activity, acting on diphenols	GO:0016679	0.09
Molecular Function	unfolded protein binding	GO:0051082	0.09
Molecular Function	enzyme activator activity	GO:0008047	0.09

b AH-specific upregulation (Clst 4)

Ontology	Description	GO term	p-value
Biological Process	hemicellulose metabolic process	GO:0010410	0.01
Biological Process	cell wall polysaccharide metabolic process	GO:0010383	0.01
Biological Process	cell wall macromolecule metabolic process	GO:0044036	0.02
Biological Process	regulation of cell cycle	GO:0051726	0.02
Biological Process	cellular carbohydrate biosynthetic process	GO:0034637	0.03
Biological Process	plant-type cell wall organization or biogenesis	GO:0071669	0.04
Biological Process	unidimensional cell growth	GO:0009826	0.05
Biological Process	cell wall organization or biogenesis	GO:0071554	0.06
Biological Process	developmental growth involved in morphogenesis	GO:0060560	0.06
Biological Process	carbohydrate biosynthetic process	GO:0016051	0.07
Biological Process	cell morphogenesis	GO:0000902	0.09
Biological Process	cellular carbohydrate metabolic process	GO:0044262	0.09
Biological Process	cell growth	GO:0016049	0.10
Molecular Function	adenine phosphoribosyltransferase activity	GO:0003999	3.1 E-05
Molecular Function	cyclin-dependent protein serine/threonine kinase activity	GO:0004693	1.6 E-03
Molecular Function	cyclin-dependent protein kinase activity	GO:0097472	1.6 E-03
Molecular Function	transferase activity, transferring pentosyl groups	GO:0016763	3.3 E-03
Molecular Function	transferase activity, transferring glycosyl groups	GO:0016757	0.01
Molecular Function	protein serine/threonine kinase activity	GO:0004674	0.07
Molecular Function	transferase activity, transferring hexosyl groups	GO:0016758	0.08
Molecular Function	transferase activity	GO:0016740	0.09
Molecular Function	hydrolase activity, hydrolyzing O-glycosyl compounds	GO:0004553	0.09

c NH/AH-shared upregulation (Clst 5)

Ontology	Description	GO term	p-value
Biological Process	translation	GO:0006412	3.6 E-04
Biological Process	peptide biosynthetic process	GO:0043043	3.8 E-04
Biological Process	amide biosynthetic process	GO:0043604	4.3 E-04
Biological Process	peptide metabolic process	GO:0006518	4.4 E-04
Biological Process	cellular amide metabolic process	GO:0043603	5.2 E-04
Biological Process	organonitrogen compound biosynthetic process	GO:1901566	1.2 E-03
Biological Process	organonitrogen compound metabolic process	GO:1901564	2.0 E-03
Biological Process	ribosome biogenesis	GO:0042254	3.7 E-03
Biological Process	ribonucleoprotein complex biogenesis	GO:0022613	0.01
Biological Process	response to auxin	GO:0009733	0.01
Biological Process	response to temperature stimulus	GO:0009266	0.02
Biological Process	cellular macromolecule biosynthetic process	GO:0034645	0.03
Biological Process	DNA replication	GO:0006260	0.03
Biological Process	macromolecule biosynthetic process	GO:0009059	0.03
Biological Process	seed germination	GO:0009845	0.04
Biological Process	cellular protein metabolic process	GO:0044267	0.04
Biological Process	seedling development	GO:0090351	0.04
Biological Process	cell growth	GO:0016049	0.04
Biological Process	nitrogen compound metabolic process	GO:0006807	0.05
Biological Process	response to heat	GO:0009408	0.05
Biological Process	cellular nitrogen compound biosynthetic process	GO:0044271	0.05
Biological Process	single-organism developmental process	GO:0044767	0.06
Biological Process	anatomical structure development	GO:0048856	0.06
Biological Process	developmental process	GO:0032502	0.07
Biological Process	cellular component organization or biogenesis	GO:0071840	0.07
Biological Process	root morphogenesis	GO:0010015	0.08
Biological Process	gene expression	GO:0010467	0.08
Biological Process	protein metabolic process	GO:0019538	0.09
Biological Process	embryo development	GO:0009790	0.09
Biological Process	anatomical structure morphogenesis	GO:0009653	0.09
Biological Process	cellular nitrogen compound metabolic process	GO:0034641	0.10
Molecular Function	structural constituent of ribosome	GO:0003735	2.6 E-09
Molecular Function	structural molecule activity	GO:0005198	3.7 E-09
Molecular Function	phosphoprotein phosphatase activity	GO:0004721	0.05
Molecular Function	nucleic acid binding transcription factor activity	GO:0001071	0.10
Molecular Function	transcription factor activity, sequence-specific DNA binding	GO:0003700	0.10

Supplementary Table 4 | Functional annotation of DEGs in the NH-specific, AH-specific, and NH/AH-shared upregulated clusters (support Figure 1f).

Please see Supplementary Tables.

Supplementary Table 5 | List of enriched GO term in the DEGs between the ABA-treated and the control male flowers in hexaploid *D. kaki*.

GO terms enriched in the upregulated **(a)** and downregulated **(b)** DEGs are shown. The GO terms which are associated with response to stress, photosynthesis, cell development, and carpel development are highlighted in blue, red, yellow, and green, respectively.

a	GO term	Ontology	Description	Number in input list	p-value
	GO:0009108	Biological Process	coenzyme biosynthetic process	14	0.0011
	GO:0072525	Biological Process	pyridine-containing compound biosynthetic process	5	0.0026
	GO:0051188	Biological Process	cofactor biosynthetic process	18	0.0044
	GO:0085029	Biological Process	extracellular matrix assembly	6	0.005
	GO:0010927	Biological Process	cellular component assembly involved in morphogenesis	6	0.005
	GO:0010208	Biological Process	pollen wall assembly	6	0.005
	GO:0043062	Biological Process	extracellular structure organization	7	0.0079
	GO:0030198	Biological Process	extracellular matrix organization	7	0.0079
	GO:0006732	Biological Process	coenzyme metabolic process	19	0.0083
	GO:0009611	Biological Process	response to wounding	16	0.012
	GO:0009615	Biological Process	response to virus	8	0.018
	GO:0008219	Biological Process	cell death	14	0.021
	GO:0009266	Biological Process	response to temperature stimulus	31	0.028
	GO:0051186	Biological Process	cofactor metabolic process	23	0.03
	GO:0010243	Biological Process	response to organonitrogen compound	12	0.031
	GO:0009404	Biological Process	toxin metabolic process	6	0.033
	GO:0010200	Biological Process	response to chitin	10	0.039
	GO:0002252	Biological Process	immune effector process	6	0.05
	GO:0006468	Biological Process	protein phosphorylation	46	0.051
	GO:1901698	Biological Process	response to nitrogen compound	16	0.052
	GO:0072524	Biological Process	pyridine-containing compound metabolic process	9	0.057
	GO:0006457	Biological Process	protein folding	15	0.058
	GO:0048646	Biological Process	anatomical structure formation involved in morphogenesis	12	0.064
	GO:0006733	Biological Process	oxidoreduction coenzyme metabolic process	9	0.069
	GO:0048440	Biological Process	carpel development	6	0.075
	GO:0042430	Biological Process	indole-containing compound metabolic process	6	0.083
	GO:0019362	Biological Process	pyridine nucleotide metabolic process	8	0.087
	GO:0009408	Biological Process	response to heat	12	0.087
	GO:0000910	Biological Process	cytokinesis	7	0.093
	GO:0010090	Biological Process	trichome morphogenesis	5	0.098
b	GO term	Ontology	Description	Number in input list	p-value
	GO:0019684	Biological Process	photosynthesis, light reaction	6	0.0043
	GO:0015979	Biological Process	photosynthesis	8	0.0078
	GO:0007167	Biological Process	enzyme linked receptor protein signaling pathway	5	0.016
	GO:0007169	Biological Process	transmembrane receptor protein tyrosine kinase signaling	5	0.016
	GO:0006468	Biological Process	protein phosphorylation	17	0.031
	GO:0006820	Biological Process	anion transport	6	0.042
	GO:0006869	Biological Process	lipid transport	5	0.046
	GO:0006811	Biological Process	ion transport	12	0.055
	GO:0043623	Biological Process	cellular protein complex assembly	5	0.069
	GO:0010876	Biological Process	lipid localization	5	0.071
	GO:1901698	Biological Process	response to nitrogen compound	6	0.074
	GO:0000271	Biological Process	polysaccharide biosynthetic process	5	0.075
	GO:0009793	Biological Process	embryo development ending in seed dormancy	9	0.084
	GO:0016051	Biological Process	carbohydrate biosynthetic process	7	0.086

Supplementary Table 6 | Expression pattern of the Clst 5 genes in hexaploid *D. kaki* and diploid *D. lotus*.

Please see Supplementary Tables.

Supplementary Table 7 | List of the genes expressed specifically in hexaploid but not diploid persimmon.

Among the genes differentially expressed NH/AH and male flowers of hexaploid *D. kaki*, the genes with little or no expression in diploid *D. lotus* (RPKM<1) were listed.

Please see Supplementary Tables.

Supplementary Table 8 | Characterization of the *A. thaliana* transgenic lines over-expressing *DkRAD*.

T1 Line ID	Elongation of carpel	Length of carpel (mm)	Stamen deficiency	Failure of self-fertilization (<i>n</i> = biological replicates)
At-pFAST-DkRAD-1	—	2.90±0.03	—	NA
At-pFAST-DkRAD-2	+	3.05±0.01	—	— (4)
At-pFAST-DkRAD-3	—	2.78±0.07	—	— (4)
At-pFAST-DkRAD-4	+	3.07±0.15	—	— (5)
At-pFAST-DkRAD-5	—	NA	—	NA
At-pFAST-DkRAD-6	—	2.49±0.13	—	++ (9)
At-pFAST-DkRAD-7	—	NA	—	— (5)
At-pFAST-DkRAD-8	—	2.66.0±0.07	—	+ (8)
At-pFAST-DkRAD-9	—	2.94±0.09	—	— (5)
At-pFAST-DkRAD-10	++	3.45±0.10	—	+ (9)
At-pFAST-DkRAD-11	—	2.87±0.22	—	— (5)
At-pFAST-DkRAD-12	++	3.23±0.12	—	++ (3)
Control 1	—	2.91±0.05	—	— (6)
Control 2	—	2.94±0.06	—	— (5)
Control 3	—	NA	—	NA
Control 4	—	NA	—	NA
Control 5	—	NA	—	NA
Control 6	—	NA	—	NA
Control 7	—	NA	—	NA
++	Severely long carpel with ability for fertilization			
+	Long carpel with ability for fertilization			
—	No phenotype			

Supplementary Table 9 | Characterization of the *N. tabacum* transgenic lines over-expressing *DkRAD* and its paralog gene.

T1 Line ID	Introduced construct	Elongation of carpel	Stamen deficiency	Narrow leaf	Elongation of lateral bud	Plant height
35S-DkRAD-1	pPLV26-DkRAD (Dlo_pri016F.1_g05470.1)	++	—	+	—	7 cm
35S-DkRAD-paralog-1		—	—	+	—	30 cm
35S-DkRAD-paralog-2		++	—	+	+	32.5 cm
35S-DkRAD-paralog-3	pPLV26-DkRAD2	+	—	+	—	30 cm
35S-DkRAD-paralog-4	(Dlo_pri0120F.1_g01930.1)	++	—	+	+	25 cm
35S-DkRAD-paralog-5		++	—	+	+	25 cm
35S-DkRAD-paralog-6		++	—	+	—	15 cm
Control 1		—	—	—	—	63 cm
Control 2	NA	—	—	—	—	58 cm
Control 3		—	—	—	—	55 cm

++ Severely long carpel with ability for fertilization
 + Long carpel with ability for fertilization
 — No phenotype

Supplementary Table 10 | List of DEGs in the *DkRAD* ox. and control lines of *A. thaliana*.

Please see Supplementary Tables.

Supplementary Table 11 | List of enriched GO term in the DEGs between the *DkRAD* ox. and control lines of *A. thaliana*.

GO term	description	pvalue
GO:0010200	response to chitin	4.40E-08
GO:0010243	response to organonitrogen compound	1.10E-07
GO:0009611	response to wounding	6.50E-07
GO:0009753	response to jasmonic acid	1.00E-06
GO:0009813	flavonoid biosynthetic process	1.10E-05
GO:0009699	phenylpropanoid biosynthetic process	1.70E-05
GO:0010584	pollen exine formation	2.10E-05
GO:1901698	response to nitrogen compound	2.90E-05
GO:0009812	flavonoid metabolic process	3.80E-05
GO:0009698	phenylpropanoid metabolic process	5.30E-05
GO:0009266	response to temperature stimulus	7.60E-05
GO:0085029	extracellular matrix assembly	9.70E-05
GO:0010927	cellular component assembly involved in morphogenesis	9.70E-05
GO:0010208	pollen wall assembly	9.70E-05
GO:0009739	response to gibberellin	0.00012
GO:1901700	response to oxygen-containing compound	0.00012
GO:0009628	response to abiotic stimulus	0.00027
GO:0009411	response to UV	0.00028
GO:0010224	response to UV-B	0.0004
GO:0009409	response to cold	0.00059
GO:0043062	extracellular structure organization	0.00065
GO:0030198	extracellular matrix organization	0.00065
GO:0001101	response to acid chemical	0.001
GO:0009414	response to water deprivation	0.0015
GO:0009415	response to water	0.0019
GO:0042545	cell wall modification	0.0022
GO:0006970	response to osmotic stress	0.0023
GO:0044550	secondary metabolite biosynthetic process	0.004
GO:0009719	response to endogenous stimulus	0.0054
GO:0010035	response to inorganic substance	0.0075
GO:0044711	single-organism biosynthetic process	0.0088
GO:0007623	circadian rhythm	0.011
GO:0009751	response to salicylic acid	0.013
GO:0009416	response to light stimulus	0.013
GO:0009651	response to salt stress	0.014
GO:0072330	monocarboxylic acid biosynthetic process	0.015
GO:0048511	rhythmic process	0.016
GO:0046148	pigment biosynthetic process	0.017
GO:0009867	jasmonic acid mediated signaling pathway	0.018
GO:0009314	response to radiation	0.019
GO:0048646	anatomical structure formation involved in morphogenesis	0.02
GO:0071395	cellular response to jasmonic acid stimulus	0.021
GO:0010033	response to organic substance	0.028
GO:0019748	secondary metabolic process	0.029
GO:0033993	response to lipid	0.032
GO:0006950	response to stress	0.035
GO:0045229	external encapsulating structure organization	0.035
GO:0042440	pigment metabolic process	0.043
GO:0009642	response to light intensity	0.044
GO:0046394	carboxylic acid biosynthetic process	0.047
GO:0009737	response to abscisic acid	0.05
GO:0097305	response to alcohol	0.053
GO:0050896	response to stimulus	0.054
GO:0014070	response to organic cyclic compound	0.056
GO:0009725	response to hormone	0.062
GO:0006633	fatty acid biosynthetic process	0.063
GO:0009408	response to heat	0.064
GO:0006790	sulfur compound metabolic process	0.067
GO:0044283	small molecule biosynthetic process	0.069
GO:0042221	response to chemical	0.072
GO:0046686	response to cadmium ion	0.082
GO:0032989	cellular component morphogenesis	0.084
GO:0016053	organic acid biosynthetic process	0.086
GO:0009723	response to ethylene	0.093
GO:0009733	response to auxin	0.1
GO:0044262	cellular carbohydrate metabolic process	0.1

Supplementary Table 12 | List of DEGs among the transient overexpression of *DkRAD* and NH and AH persimmon flowers, respectively.

Please see Supplementary Tables.

Supplementary Table 13 | List of enriched GO term in the DEGs among the transient overexpression of *DkRAD*, NH persimmon flowers, and AH persimmon flowers.

GO term	Description	p-value
GO:0050896	response to stimulus	5.00E-07
GO:0042221	response to chemical stimulus	3.60E-06
GO:0009987	cellular process	2.10E-05
GO:0006950	response to stress	5.80E-05
GO:0009628	response to abiotic stimulus	0.00022
GO:0010035	response to inorganic substance	0.00026
GO:0006979	response to oxidative stress	0.00035
GO:0010033	response to organic substance	0.00039
GO:0006325	chromatin organization	0.00045
GO:0051276	chromosome organization	0.00048
GO:0000302	response to reactive oxygen species	0.00086
GO:0009644	response to high light intensity	0.00094
GO:0009266	response to temperature stimulus	0.0013
GO:0022622	root system development	0.0016
GO:0048364	root development	0.0016
GO:0044237	cellular metabolic process	0.0017
GO:0009733	response to auxin stimulus	0.0022
GO:0006730	one-carbon metabolic process	0.0031
GO:0051179	localization	0.0033
GO:0009791	post-embryonic development	0.0036
GO:0006333	chromatin assembly or disassembly	0.0042
GO:0043414	macromolecule methylation	0.0044
GO:0009411	response to UV	0.0044
GO:0009408	response to heat	0.0046
GO:0015979	photosynthesis	0.0048
GO:0009314	response to radiation	0.0048
GO:0006810	transport	0.0051
GO:0051234	establishment of localization	0.0053
GO:0065003	macromolecular complex assembly	0.0054
GO:0065007	biological regulation	0.0054
GO:0008152	metabolic process	0.0056
GO:0009642	response to light intensity	0.0061
GO:0032259	methylation	0.0061
GO:0009725	response to hormone stimulus	0.0061
GO:0009719	response to endogenous stimulus	0.008
GO:0009416	response to light stimulus	0.0084
GO:0065008	regulation of biological quality	0.0098
GO:0009814	defense response, incompatible interaction	0.0099

Supplementary Table 14 | Primer Table.

Primer name	Sequence (5'-3')	targeted
For construction		
pPLV26-RAD2-F3	CGAGCTAGTTGGAATAGGTTATGGCATCAATGTCCTCCCG	DkRAD1 full length (Dlo_pri0016F.1_g05470.1)
pPLV26-RAD2-R	TGCAGTATGGAGTTGGGTTCTAGTTTCCTTGGCCACTCC	
pPLV26RAD1-F	CGAGCTAGTTGGAATAGGTTATGGCCTCAATGTCCTCTCG	DkRAD2 full length (Dlo_pri0120F.1_g01930.1)
pPLV26RAD1-R	TGCAGTATGGAGTTGGGTTCTTACCTTTGCTCCTCCTCGC	