

Supporting Information

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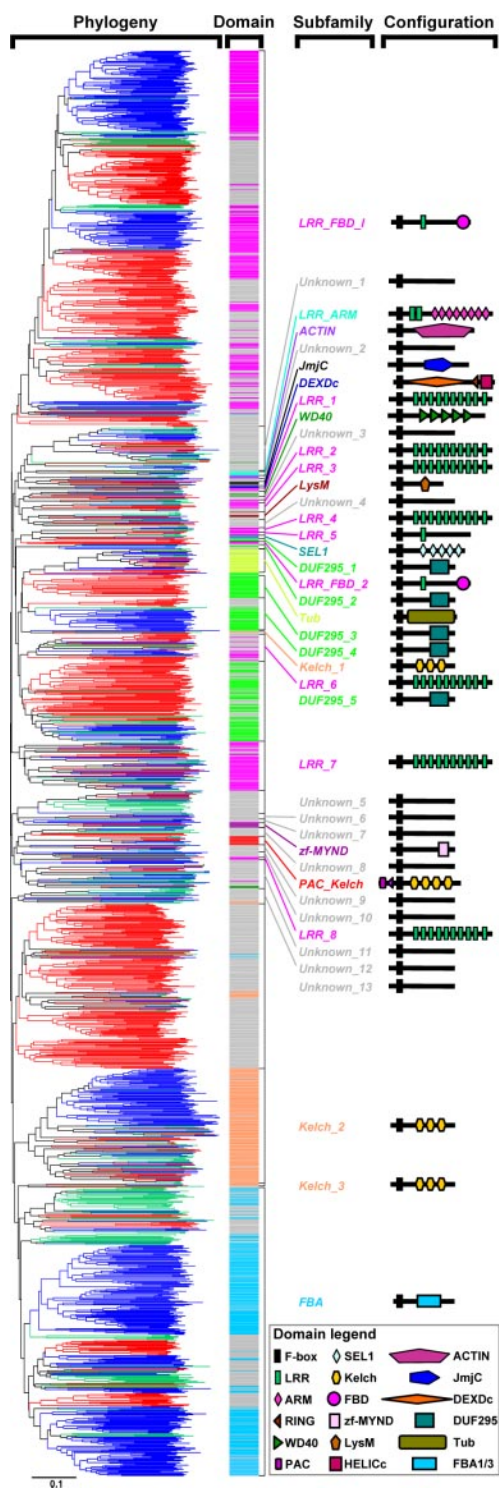


Fig. S1. Phylogenetic relationships and domain configurations of F-box proteins from Arabidopsis, poplar, and rice. The NJ tree was generated using the F-box domain only, and the sequences from Arabidopsis, poplar, and rice are color-coded blue, green, and red, respectively. The family designations are based on the presence of certain C-terminal domains.

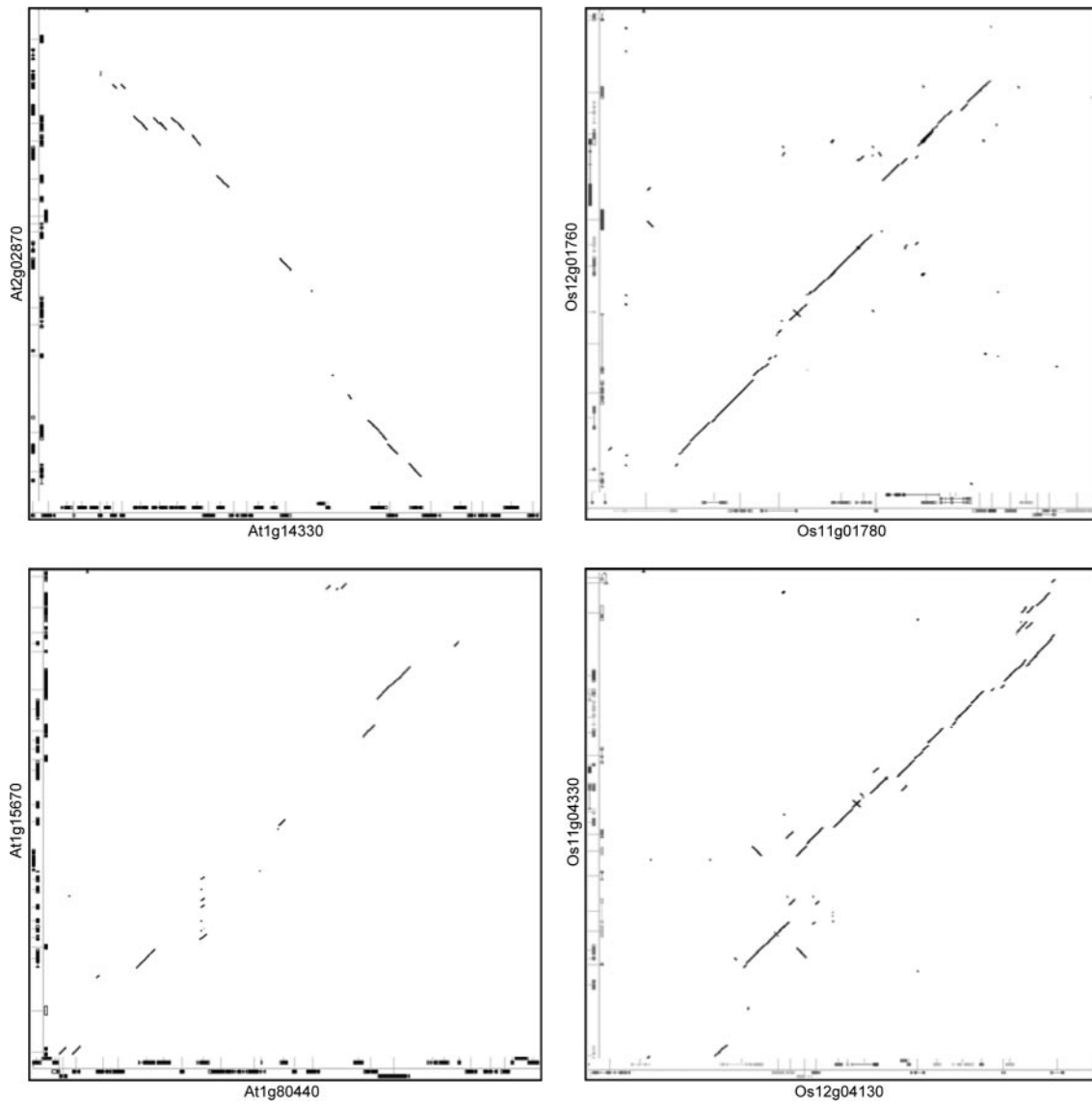


Fig. S2. Evidence for segmental gene duplication.

Table S1. Evolutionarily conserved F-box genes in Arabidopsis, poplar, and rice

Subfamily	<i>Arabidopsis thaliana</i>	<i>Oryza sativa</i>	<i>Populus trichocarpa</i>	Domain
20 evolutionarily highly conserved gene clusters, with one copy in each species				
DEXDc	At3g54460	Os01g72310	fgenes1_pg.C.LG.III001684	DEXDc+HELICc
JmjC	At5g06550	Os11g36450	eugene3.00160584	JmjC
Kelch_2	At1g30090	Os07g05880	eugene3.00061201	Kelch repeats
	At2g24540 ARF	Os06g44500	estExt_fgenes1_pm.v1.C.LG.XVIII0193	Kelch repeats
LRR_7	At3g61350	Os02g02350	eugene3.00140290	Kelch repeats
	At2g42620 ORE9	Os06g06050	fgenes1_pg.C.LG.XIV000831	LRR repeats
	At3g07550	Os11g16280	eugene3.00031484	LRR repeats
LRR_8	At3g54480 SKIP5	Os07g46560	grail3.0100009701	N (Unknown)
	At2g17020	Os03g04270	eugene3.00041397	LRR repeats
LRR_FBD	At2g39490	Os06g47100	fgenes1_pg.C.LG.VIII000419	N (Unknown)
	At4g03220	Os02g06520	fgenes1_pg.C.LG.XIII001178	LRR+FBD
LysM	At5g48170 SNE	Os03g10040	eugene3.00141133	N (Unknown)
TUB	At2g18280	Os02g47640	fgenes1_pg.C.LG.II000315	TUB
Unknown_2	At1g06110	Os11g16330	eugene3.00640134	N (Unknown)
Unknown_4	At5g45360	Os06g49530	eugene3.00860161	N (Unknown)
Unknown_10	At3g26000	Os04g40910	fgenes1_pg.C.LG.I002238	N (Unknown)
	At3g27290	Os08g33140	fgenes1_pg.C.LG.X001010	N (Unknown)
Unknown_11	At5g21040	Os04g52870	eugene3.00090125	WD40 repeats
Unknown_13	At5g03970	Os05g18660	fgenes1_pg.C.scaffold.201000011	N (Unknown)
WD40	At5g52880	Os05g45040	fgenes1_pg.C.LG.XII000097	WD40 repeats
63 evolutionarily less conserved gene clusters, with no more than three copies in each species				
JmjC	At1g78280	Os03g27250		JmjC
Kelch_3		Os01g45900	fgenes1_pg.C.scaffold.215000004	N (Unknown)
	At3g48880	Os10g35920		N (Unknown)
LRR_6	At1g10780	Os09g28120		N (Unknown)
LRR_7		Os04g42670	grail3.0023014901	LRR repeats
LRR_ARM		Os05g30920	grail3.0009050801	N (Unknown)
LRR_FBD	At1g08710	Os01g59910		N (Unknown)
LRR_FBD	At3g58910	Os01g57920		LRR
Unknown_12	At3g20270	Os09g32240		N (Unknown)
Unknown_13	At1g10890	Os07g04750		N (Unknown)
Unknown_13		Os02g33840	eugene3.00090359	N (Unknown)
Unknown_4	At5g39250	Os03g30920		N (Unknown)
Unknown_8		Os03g12940	fgenes1_pg.C.LG.I003152	N (Unknown)
ACTIN	At5g56180 ARP8	Os04g57210	fgenes1_pm.C.LG.I001101	ACTIN
			estExt_Genewise1.v1.C.LG.I6254	
FBA	At1g33010	Os12g42360 Os12g42340 Os12g42350		N (Unknown)
FBA	At5g41720	Os08g43530	eugene3.34310001	N (Unknown)
FBA		Os09g20650	eugene3.00150253	
			eugene3.00070156	FBA
			eugene3.00290314	
FBA		Os02g35560 Os07g16420 Os07g16800	fgenes1_pg.C.LG.VII000684	N (Unknown)
FBA		Os01g28150 Os01g28300	eugene3.00081534	N (Unknown)
FBA		Os02g54240	eugene3.00131008	FBA
Kelch_1	At1g23390	Os01g50840 Os09g12150	fgenes1_pg.C.scaffold.125000065	Kelch
	At1g14330 At2g02870	Os02g51350	eugene3.00100609	Kelch repeats
Kelch_2	At1g15670 At1g80440	Os02g11790 Os06g39370	fgenes1_pm.C.LG.I000404	Kelch repeats
Kelch_2	At1g22040	Os02g36520 Os10g21930	grail3.0002006301	Kelch repeats
Kelch_2	At1g55270	Os10g26990 Os03g07160	eugene3.00010072	Kelch repeats
			eugene3.00031859	
Kelch_2	At1g67480	Os02g30210 Os04g31120	eugene3.00410162	Kelch repeats
			grail3.0036011001	
			eugene3.00081637	
Kelch_2	At1g76920	Os04g59010	eugene3.00050973	Kelch repeats
Kelch_2			eugene3.00020650	
	At3g63220	Os10g24900	fgenes1_pm.C.LG.II000225	Kelch repeats
Kelch_2			eugene3.00051189	
	At4g03030	Os02g21110	estExt_Genewise1.v1.C.LG.II2588	Kelch repeats
Kelch_2	At5g26960	Os11g04330 Os12g04130	fgenes1_pg.C.LG.V001366	Kelch repeats
		Os03g30160	eugene3.00011803	Kelch repeats

Subfamily	<i>Arabidopsis thaliana</i>	<i>Oryza sativa</i>	<i>Populus trichocarpa</i>	Domain
Kelch_2	At5g60570	Os04g52830	fgenes1_pg.C.LG.XIII000754 fgenes1_pm.C.LG.XIX000107	Kelch repeats
LRR_1	At4g33210	Os10g25680	fgenes1_pg.C.LG.VI001526 fgenes1_pg.C.LG.XVIII000231	LRR repeats
LRR_2	At5g67140	Os06g07000	fgenes1_pm.C.LG.VII000276 grail3.0027007101	LRR repeats
LRR_3	At1g21760 AtFBP7	Os04g35190	estExt_fgenes1_pg.v1.C.LG.II1921 eugene3.00050859	N (Unknown)
LRR_3	At3g54650	Os03g43390 Os12g40860	eugene3.00051255 fgenes1_pg.C.LG.II000408	LRR repeats
LRR_4	At1g21410 At1g77000	Os01g65920 Os05g35110	estExt_fgenes1_pg.v1.C.LG.V1038 estExt_fgenes1_pm.v1.C.LG.II0833	LRR repeats
LRR_5	At1g67190	Os01g64030	fgenes1_pg.C.LG.IX000059 grail3.0066013301	LRR repeats
LRR_6	At4g08980	Os02g52130 Os06g11630	estExt_fgenes1_pg.v1.C.LG.II1760	LRR repeats
LRR_7	At2g39940 COI1	Os05g37690 Os01g63420		LRR repeats
LRR_7	At3g50080 VFB2 At5g67250 SKIP2/VFB4	Os09g02530	grail3.0019001201 grail3.0027009201	LRR repeats
LRR_7	At3g62980 TIR1 At3g26810 AFB2	Os04g32460	fgenes1_pg.C.LG.XIV001459 fgenes1_pg.C.LG.XIV000748	LRR repeats
LRR_7	At4g24390 At5g49980	Os02g52230		LRR repeats
LRR_7	At5g01720	Os12g01760 Os11g01780	eugene3.00060921 eugene3.00161229	LRR repeats
PAC_Kelch	At1g68050 FKF1	Os11g34460	estExt_fgenes1_pm.v1.C.LG.X0330 fgenes1_pm.C.LG.VIII000539	PAC+Kelch repeats
PAC_Kelch	At2g18915 LKP2 At5g57360 ZTL	Os02g05700 Os06g47890	fgenes1_pm.C.LG.XVIII000262 estExt_fgenes1_pm.v1.C.1210015	PAC+Kelch repeats
SEL1	At1g70590	Os04g40030	grail3.0036022401 fgenes1_pg.C.LG.VIII001698	SEL1
TUB	At1g25280 At1g76900	Os11g06420 Os12g06630		TUB
TUB	At1g61940 At2g47900	Os03g22800 Os07g47110	estExt_fgenes1_pg.v1.C.LG.X0225 fgenes1_pg.C.LG.VIII001778	TUB
TUB		Os01g64700 Os05g36190	eugene3.00020634 fgenes1_pm.C.LG.V000374	TUB
Unknown_1	At3g53000	Os02g45320 Os04g48270	fgenes1_pm.C.scaffold.28000105	N (Unknown)
Unknown_11	At4g10925	Os01g36940	eugene3.00031139 fgenes1_pg.C.LG.I000760	N (Unknown)
Unknown_13	At1g27340	Os01g69940	estExt_Genewise1.v1.C.LG.I7714 fgenes1_pm.C.LG.III000563	N (Unknown)
Unknown_13	At1g30950 UFO	Os06g45460	fgenes1_pg.C.LG.III000528 grail3.0029002001	N (Unknown)
Unknown_13	At3g61590 HWS	Os02g15950	eugene3.00140382 fgenes1_pm.C.LG.II000715	Kelch
Unknown_13	At4g33160	Os03g28130 Os07g42590	fgenes1_pg.C.LG.VI001490	N (Unknown)
Unknown_13	At5g15710	Os04g57290	eugene3.01550050 eugene3.01650022	N (Unknown)
Unknown_13	At5g42350 At5g42360	Os09g38300	eugene3.00051584	Kelch repeats
Unknown_13		Os02g41910 Os02g41930	eugene3.00410164	N (Unknown)
Unknown_3	At4g00755	Os03g64360	grail3.0035010801 grail3.0039000401	N (Unknown)
Unknown_4		Os07g07520	fgenes1_pg.C.LG.VIII001571 estExt_fgenes1_pg.v1.C.LG.X0453	N (Unknown)
Unknown_5	At5g46170 At4g18380	Os01g56390 Os05g43490	eugene3.00100423 eugene3.00040307 eugene3.00110432	N (Unknown)
WD40	At3g52030	Os09g19720 Os11g07970	eugene3.00091084	WD40
zf-MYND	At5g50450 At1g67340	Os01g69270 Os04g31610	eugene3.00120908 fgenes1_pg.C.LG.XV000697	zf-MYND

Paired genes (BOLD) are those that were generated through segmental duplications.

Table S2. Evolutionary change of the number of F-box proteins in extant and ancestral plants

Family	Number of Genes in Species and Nodes					Number of genes gained/lost along branch			
	Ath	Ptr	Osa	N1	N2	N1 to N2	N1 to Osa	N2 to Ath	N2 to Ptr
LRR_FBD.1	171	44	265	32	27	9/14	241/8	152/8	26/9
Unknown.1	21	18	16	13	14	4/3	10/7	12/5	9/5
LRR_ARM	2	4	1	2	4	2/0	0/1	0/2	1/1
ACTIN	1	2	1	2	2	0/0	0/1	0/1	1/1
Unknown.2	1	1	2	2	1	0/1	0/0	0/0	0/0
JmjC	2	1	2	2	2	0/0	0/0	0/0	0/1
DEXDc	1	1	1	1	1	0/0	0/0	0/0	0/0
LRR_1	1	2	1	1	1	0/0	0/0	0/0	1/0
WD40	2	2	3	4	3	0/1	1/2	0/1	0/1
Unknown.3	1	2	1	1	1	0/0	0/0	0/0	1/0
LRR_2	1	2	1	1	1	0/0	0/0	0/0	1/0
LRR_3	2	4	5	3	2	0/1	2/0	0/0	2/0
LysM	2	6	2	3	2	0/1	0/1	0/0	4/0
Unknown.4	2	4	4	4	3	0/1	0/0	0/1	2/1
LRR_4	2	2	2	1	1	0/0	1/0	1/0	1/0
LRR_5	1	2	1	1	1	0/0	0/0	0/0	1/0
SEL1	1	2	1	1	1	0/0	0/0	0/0	1/0
DUF295.1	0	0	4	1	0	0/1	3/0	0/0	0/0
LRR_FBD.2	0	0	3	1	0	0/1	2/0	0/0	0/0
DUF295.2	4	2	0	1	2	1/0	0/1	2/0	1/1
TUB	10	7	13	12	11	0/1	7/6	3/4	4/8
DUF295.3	0	0	28	1	0	0/1	27/0	0/0	0/0
DUF294.4	26	4	11	1	1	0/0	10/0	25/0	3/0
Kelch.1	1	1	2	1	1	0/0	1/0	0/0	0/0
LRR_6	10	4	21	10	8	1/3	15/4	4/2	0/4
DUF295.5	16	12	73	12	11	5/6	63/2	10/5	4/3
LRR_7	23	19	20	21	23	4/2	5/6	5/5	7/11
Unknown.5	6	18	5	7	8	2/1	3/5	1/3	13/3
Unknown.6	3	3	1	2	4	2/0	0/1	0/1	1/2
Unknown.7	5	0	0	1	1	0/0	0/1	4/0	0/1
zf_MYND	2	2	2	1	2	1/0	1/0	0/0	1/1
Unknown.8	3	4	4	3	3	1/1	2/1	1/1	1/0
PAC_Kelch	3	5	3	2	3	1/0	1/0	0/0	3/1
Unknown.9	4	3	2	3	3	1/1	0/1	1/0	2/2
Unknown.10	3	2	2	5	5	0/0	0/3	0/2	0/3
LRR_8	1	1	1	1	1	0/0	0/0	0/0	0/0
Unknown.11	17	13	6	9	13	5/1	2/5	7/3	3/3
Unknown.12	6	12	1	3	7	4/0	0/2	0/1	6/1
Unknown.13	9	13	186	17	10	0/7	169/0	1/2	4/1
Kelch.2	93	29	23	30	32	6/4	7/14	67/6	9/12
Kelch.3	1	2	1	1	1	0/0	0/0	0/0	1/0
FBA	230	81	54	20	33	16/3	43/9	209/12	57/9

Ath, Arabidopsis; Ptr, poplar; Osa, rice; Node N1, MRCA of all three species; Node N2, MRCA of Arabidopsis and poplar.

Table S4. Characteristics of functionally studied F-box genes

Name	Full name	Family	Locus number	Putative Ortholog	Clade ratio	Functions	Ref.
ARP8		ACTIN	At5g56180	Os04g57210	1:1	nucleolar functions	1
CEG	CEGenduo	FBA	At3g22650	None	113:0	negative regulator of auxin-mediated lateral root formation	2
SON1	Suppressor Of Nim1-1	FBA	At2g17310	None	113:0	defense responses	3
ARF	Attenuated Far-red Response	Kelch_2	At2g24540	Os06g4450	1:1	positive regulator of phytochrome A-mediated light signaling	4
AtFBP7		LRR_3	At1g21760	Os04g35190	1:1	translation during temperature stress	5
AtSKP2;1		LRR_4	At1g21410	Os01g65920, Os05g35110	2:2	photomorphogenesis	6
AtSKP2;2		LRR_4	At1g77000	Os01g65920, Os05g35110	2:2	photomorphogenesis	6
AFB1	Auxin signaling F-Box protein 1	LRR_7	At4g03190	Os04g32460	2:1	auxin receptor; plant growth and development	7
AFB2	Auxin signaling F-Box protein 2	LRR_7	At3g26810	Os04g32460	3:1	auxin receptor; plant growth and development; glucose repression	7
AFB3	Auxin signaling F-Box protein 3	LRR_7	At1g12820	Os11g31620, Os02g52230	1:0	auxin receptor; plant growth and development	7
AFB5	Auxin signaling F-Box protein 5	LRR_7	At5g49980	Os02g52230	2:1	auxin receptor; plant growth and development	8
COI1	Coronatine Insensitive 1	LRR_7	At2g39940	Os01g63420, Os05g37690	1:2	jasmonate-regulated defense responses; pollen fertility	9–14
EBF1	EIN3-Binding F-box protein 1	LRR_7	At2g25490	Os02g10700, Os06g40360	2:2	negative regulator of ethylene signaling; plant growth	15, 18
EBF2	EIN3-Binding F-box protein 2	LRR_7	At5g25350	Os02g10700, Os06g40360	2:2	negative regulator of ethylene signaling; plant growth	15, 18
ORE9/ MAX2	Oresara 9/More Axillary 2	LRR_7	At2g42620	Os06g06050	1:1	regulation of leaf senescence; selective repression of axillary shoots	19, 22
SKIP2/ VFB4		LRR_7	At5g67250	Os09g02530	2:1	plant growth and lateral root formation	23
TIR1	Transport Inhibitor Response 1	LRR_7	At3g62980	Os04g32460	2:1	auxin receptor	24, 30
VFB1		LRR_7	At1g47056	None	2:0	plant growth and lateral root formation	23
VFB2		LRR_7	At3g50080	Os09g02530	2:1	plant growth and lateral root formation	23
VFB3		LRR_7	At4g07400	None	2:0	plant growth and lateral root formation	23
ARABIDILLO-1		LRR_ARM	At2g44900	None	2:0	lateral root development	31
ARABIDILLO-2		LRR_ARM	At3g60350	None	2:0	lateral root development	31
SNE	SNEezy	LysM	At5g48170	Os03g10040 (GID2)	1:1	positive regulator of Gillerellic acid signaling	32, 34
FKF1	Flavin-binding Kelch-repeat F-box 1	PAC_Kelch	At1g68050	Os11g34460	1:1	circadian clock; photoperiodic-specific light signalling	35, 39
LKP2		PAC_Kelch	At2g18915	Os02g05700, Os06g47890	2:2	circadian oscillator	36, 40
ZTL/ LKP1	Zeitlupe	PAC_Kelch	At5g57360	Os02g05700, Os06g47890	2:2	circadian clock; photomorphogenesis and flowering time	40, 45
SLY1	SLepY 1	Unknown_11	At4g24210	None	1:0	positive regulator of Gillerellic acid signaling	34, 46–48
EID1	Empfindlicher Im Dunkelrotenlicht 1	Unknown_12	At4g02440	None	1:0	negative regulator of phytochrome A-specific light signaling	46, 49–51
HWS		Unknown_13	At3g61590	Os02g15950	1:1	organ fusion and growth	

Name	Full name	Family	Locus number	Putative Ortholog	Clade ratio	Functions	Ref.
UFO	Unusual Floral Organs	Unknown_13	At1g30950	Os06g45460 (APO1)	1:1	patterning and growth in the floral meristem; floral organ identity	

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Other Supporting Information Files

[Dataset S1 \(TXT\)](#)