

Supplementary Table S4 Identification of *cis*-elements in the promoters of the best homologs in *P. axillaris* or *P. inflata* of each *PhWRKY* gene

Functional group	Gene	Senescence	Hormone regulation	Transcription factors	Stress responses	Others
I	OsWRKY42 (*)	ABRE (6), W-box (2), G-box (4)	AuxRR-core, CGTCA-motif, ERE	MYB (2), MYC (3)	ARE (2), DRE core, LTR (2), STRE (2)	A-box, circadian, GCN4_motif, O2-site
	Peaxi162Scf00121g00018 (PhWRKY007)	ABRE (3), G-box (3)	CARE, CGTCA-motif (4), ERE (2), P-box (2)	MYB (4), MYC (4)	ARE (3), STRE (3)	AC-II, circadian, AC-I, HD-Zip 1, O2-site, Box-4 (2)
	Peaxi162Scf00549g00222 (PhWRKY015)	ABRE (2), W-box (2), G-box (4)	CARE, CGTCA-motif, ERE (2), TATC-box, TCA-element (2)	MYB (5)	MBS (2), STRE (4), WUN-motif	CCGTCC-motif, A-box, Box-4 (2)
II	AtWRKY6 (*)	ABRE, W-box, G-box	CGTCA-motif (2), ERE, TGA-element	MYB (4), MYC (4)	ARE, MBS, WUN-motif (3)	Box-4 (4), CAT-box, I-box, MRE
	Peinf101Scf01200g03007 (PhWRKY072)	ABRE (3), W-box (1), G-box (4)	CARE, CGTCA-motif (3), ERE (4), TCA-element	MYB (3), MYC	box-S, LTR, MBS	F-box, O2-site, Box-4 (4), A-box
	Peaxi162Scf00007g00315 (PhWRKY006)	ABRE (3), W-box, G-box (3)	TCA-element(2), CGTCA-motif (5), ERE, CARE	CCAAT-box, MYC (3)	MBS(3), STRE(5), WRE3(2), TC-rich repeats, ARE	HD-Zip 1, circadian, AE-box (2), Box-4 (3)
III	AtWRKY25 (*)	W-box (2)	ERE, GARE-motif, TCA-element (3), TGACG-motif (2), TGA-element	MYB (5), MYC (2)	ARE (3), MBS	AE-box (2), Box-4
	TaWRKY7 (*)	ABRE (4), W-box (2), G-box (4)	CGTCA-motif, P-box, TCA	MYB (5), MYC (6), AT-rich element	ARE (2), MBS, STRE	A-box, CAT-box (2), O2-site (2)
	Peaxi162Scf00232g00810 (PhWRKY002)	ABRE, W-box (2)	CGTCA-motif, TCA	MYB (5), MYC (5)	ARE (4), MBS (4), STRE	CAT-box, circadian, F-box, O2-site, Box-4 (3)
	Peaxi162Scf00222g00117 (PhWRKY004)	ABRE, G-box	AuxRR-core (2), CGTCA-motif (4), ERE (3), TCA-element, TGA-element	MYC, AT-rich element	ARE, MBS (2), TC-rich repeats, WUN-motif (2)	MBSI, Box-4 (3)
	Peaxi162Scf00055g01910 (PhWRKY024)	ABRE (3), W-box, G-box (3)	CGTCA-motif (2), ERE, TATC-box, TCA (2), TGA-element	AT-rich element, MYB, MYC	ARE(2), LTR, MBS(3), STRE, TC-rich repeats, WRE3	CAT-box, GCN4_motif(2), AE-box (2), Box-4, LS7
Peaxi162Scf00744g00220 (PhWRKY033)	ABRE (2), W-box (2), G-box	CGTCA-motif (2), TCA-element, TGA-element	MYB (2), MYC (2)	ARE (2), LTR (2), STRE (5), TC-rich repeats	AC-I, CAT-box, GCN4_motif, AT1-motif (2), Box-4	
IV	AtWRKY45 (*)	ABRE (3), W-box (3), G-box (2)	GARE-motif, P-box, TCA-element	MYB (5), MYC (2)	ARE, LTR, O2-site (2), STRE (2)	Box-4, CAT-box (3)
	AtWRKY75 (*)	ABRE (5), W-box (2), G-box (6)	CGTCA-motif (6), TGA-box (3)	MYB (2), MYC (4)	ARE (3), LTR, MBS, STRE (3), WRE3	Box-4 (3), circadian (2)
	Peaxi162Scf00128g01541 (PhWRKY075)	ABRE (5), W-box, G-box (6)	CGTCA-motif, ERE, TCA	MYB (4), MYC	box-S (2), MBS, WRE3, WUN-motif	GCN4_motif, O2-site (3), Box-4 (4), AE-box
	Peaxi162Scf01189g00009 (PhWRKY028)	ABRE, W-box, G-box (2)	CGTCA-motif, ERE	MYB (3), MYC (3)	ARE (3), MBS (2), TC-rich repeats, WRE3 (2), WUN-motif	AE-box, Box-4 (2)
V	AtWRKY53 (*)	W-box (3)	-	MYB (5), MYC (5)	ARE (3), MBS (2), STRE (2), TC-rich repeats, WUN-motif	I-box (4), Box-4 (4)
	Peinf101Scf01632g03025 (PhWRKY030)	ABRE (3), W-box (3), G-box (2)	AuxRR-core, CGTCA-motif (2), ERE	MYB (2), MYC (3)	ARE, DRE1, STRE, WUN-motif	HD-Zip 1, RY-element, AE-box, Box-4 (2)
	Peaxi162Scf00102g01741 (PhWRKY053)	ABRE (2), G-box (3)	CGTCA-motif (2), ERE (2), SARE, TATC-box, TGA-element	MYB (4), MYC (10), AT-rich element	ARE (2), MBS, STRE, TC-rich repeats, WUN-motif (3)	ACE, Box-4
	Peinf101Scf00962g23035 (PhWRKY055)	ABRE, W-box, G-box	TCA-element, CGTCA-motif	MYB (3), MYC (3)	ARE, MBS (2), WRE3, WUN-motif	RY-element, AE-box
VI	AtWRKY70 (*)	ABRE (2), G-box (2)	CARE, CGTCA-motif (3), ERE, TGA-box	MYB (2), MYC (6)	ARE (3), box-S, LTR, MBS (3), STRE (2), WUN-motif, WRE3	A-box, Box-4 (3), O2-site
	AtWRKY54 (*)	ABRE (2), W-box, G-box (2)	ERE, CGTCA-motif (2), TATC-box, TCA-element (3)	MYB (5), MYC (3)	DRE1, MBS, O2-site (2), STRE, WUN-motif	Box 4 (5), CAT-box, circadian, F-box, GCN4_motif (2)
	Peaxi162Scf00732g00236 (PhWRKY063)	ABRE (2), W-box, G-box (2)	CGTCA-motif (2), P-box, TATC-box, TCA-element	MYB (4), MYC (4)	ARE, LTR (3), MBS, STRE, WRE3 (4)	AE-box (2), Box-4 (3)
	Peaxi162Scf00304g00719 (PhWRKY054)	-	ERE (3), TGACG-motif (3)	MYB (2), MYC (4)	ARE (2), AT-rich sequence, MBS, STRE, WRE3, WUN-motif (4), TC-rich repeats	AC-II, Box-4 (3)
Peinf101Scf00191g46015 (PhWRKY070)	ABRE (2), W-box, G-box (2)	CGTCA-motif, ERE, P-box, TATC-box	MYB	ARE (2), AT-rich sequence, MBS, STRE, WUN-motif, TC-rich repeats	AC-I (2), CAT-box (2), circadian, O2-site, AE-box (2), Box-4 (3)	
VII	Peaxi162Scf00469g00624 (PhWRKY069)	ABRE (2), G-box (4)	AuxRR-core, ERE (2), P-box, TATC-box, TCA-element (2), TGA-element	MYB (3), MYC (2)	ARE (5), MBS, STRE (2), WRE3	A-box, ACE, Box-4 (4)

Genes are showed according to their ascending functional group order. The *cis*-elements were obtained by using PlantCARE database and classified in five categories (senescence, hormone regulation, transcription factors, stress responses, and others). Promoter sequences of *WRKY* genes that encode proteins with a reported function in leaf senescence were added to the analysis and indicated with an asterisk (*). The total number of *cis*-elements of each type is indicated