Supplementary material

Exon Junction Complex (EJC) Core Genes Play Multiple Developmental Roles in *Physalis floridana*

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Supplementary material contains: Supplementary Figures S1-S13 Supplementary Tables S1-S3

PFMAGO-VIGS probe; 391 bp

(Sequence identity between PFMAGO1 and PFMAGO2 was 89.0%)

110 120 130 140 150 160 170 180 190 200 GGTTTTCCTTACCCCTGCCGTTCCAAAGATGTCGCCGTATGTTGCCGCGATAGCAGAGATGATGACAACAATGATGCCGCCGTATGATAGCAACGATGATAACAACTGCCCGCATGATAGAAGATCATGATACAACTACTACAACTGGCCTGAACCGCGATAGA

PFY14-VIGS probe; 400 bp

10 20 30 40 50 60 70 80 90 100 CRARACCTTAGGGTTCATCATCATGCCAGCTATACCTAGGCCGCCTTCTAGAAAAACCAAAAGCCGTGGTTCCC 120 110 120 130 140 150 160 170 180 190 200 GTGAAGAGCTGCTGAAGGGAAGGAATGCCCGCCTTTCTGCCCCTTTGACCCCCCGGCCCCGGCCCCGGCCCCGGACCCAAGGTGGCCCCGGACCCCAAGGTGGCCCCGGACCCATGAAGG 210 220 230 240 250 260 270 280 290 300 ATGGATTGTTTTAGTCATGGAGGTTATAGAGGAGGCTCAAGAAGATCATCTTCATATAGCATCGGCGAGATCGGAGAATCAGAAGATCATCTGAAT 380 310 320 330 340 350 360 370 380 390 400 CTGGATCGTCGTCTGGATATGCACGGTTATGCACTTTGAATATGAAGAACTATGAAGAAGCGAAGCGAATGGAATGGAATGGAAGGGAATGGAC 400 *PFeIF4A*^{*III*}-VIGS probe; 462 bp 10 20 30 40 50 60 70 80 90 100 AGGTTGTACTGATTTCTGCCACTCTTCCGAATGAAAATTTTGTGCAAACGTTGTGAAACGTGGATGAATT 200 210 220 230 240 250 260 270 280 290 300 320 330 340 350 360 370 380 390 400 AGAAGGAAAGAGATGCTATTATGGCTGAGTTCCGAGGTGGCACGACTCGTGTTCTAATCACAACAGATGTTTGGGCAAGGGAACTGGATGTTCAACAGGT 0 430 440 450 420 GTCTCTGGTGATTAATTATGACCTTCCAAACAACAGAGAGCTCTACATTCATCGCATTGGTC PFBTZ-VIGS probe; 370 bp 10 20 30 40 50 60 70 80 90 100 GGAAGCATGGGCAGTGGGCAGCAGCAGCAGCAGCAGCAGCAGCGGGGGGCATCCCTGCTGG GGAAGCATGGGCCAGCGGCGAGCAGCGGCGGGCATCCCTGCTGG

Fig. S1 Sequences used to trigger gene silencing in VIGS. From top to bottom, the trigger sequence of *PFMAGO-*, *PFY14-*, *PFeIF4AIII-* and *PFBTZ*, and each length is given.

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PIMAGO DNNWEEPDRVGRQELEIVMONEHISFTTSKIGSLVDVHSSOPPEGLRIFYYLVQDLKCFVFSLISLHEKIKPI VVMAGO DNNWEEPDRVGRQELEIVMONEHISFTTSKIGSLVDVQSSKDPEGLRIFYYLVQDLKCFVFSLISLHEKIKPI SBMAGO1 DSNWEEPDRVGRQELEIVMONEHISFTTSKIGSLVDVQSSKDPEGLRIFYYLVQDLKCFVFSLINLHEKIKPIQS SBMAGO2 DRNWEEPDRVGRQELEIVMONEHISFTTSKIGSLVDVQTSKDPEGLRIFYYLVQDLKCFVFSLINLHEKIKPIQS OSMAGO2 DNNWEEPDRVGRQELEIVMONEHISFTTSKIGSLVDVQTSKDPEGLRIFYYLVQDLKCFVFSLINLHEKIKPIQS OSMAGO2 DNNWEEPDRVGRQELEIVMONEHISFTTSKIGSLVDVQTSKDPEGLRIFYYLVQDLKCFVFSLINLHEKIKPIQS OSMAGO2 DNNWEEPDRVGRQELEIVMONEHISFTTSKIGSLVDVQTSKDPEGLRIFYYLVQDLKCFVFSLINLHEKIKPIQS OSMAGO2 DNNWEEPDRVGRQELEIVMONEHISFTTSKIGSLVDVQTSKDPEGLRIFYYLVQDLKCFVFSLINLHEKIKPIQS OSMAGO2 DNNWEEPDRVGRQELEIVQCGCHISFTTSKIGSLVDVQTSKDPEGLRIFYYLVQDLKCFVFSLINLHEKIKPIQS CMAGO1 DNNWEPDRVGRQELEVIQCGCHISFTTSKIGSLVDVQTSKDPEGLRIFYYLVQDIKCFVFSLINLHEKIKPIQS HMAGO2 DNNWEPDRVGRQELEVIQCGCHISFTTSKIGSLVDVQTSKDPEGLRIFYYLVQDIKCFVFSLISHEKIVPI MMMAGO1 DALWEPDRVGRQELEVICGCHISFTTSKIGSLIDVNQSKDPEGLRVFYYLVQDIKCFVFSLIGHEKIKPI MMMAGO1 DALWEPDRVGRQELEIVIGDEHISFTTSKIGSLIDVNQSKDPEGLRVFYYLVQDIKCFVFSLIGHEKIKPI MMMAGO1 DALWEPDRVGRQELEIVIGDEHISFTTSKIGSLIDVNQSKDPEGLRVFYYLVQDIKCLVFSLIGLHEKIKPI MMMAGO1 DALWEPDRVGRQELEIVIGDEHISFTTSKIGSLIDVNQSKDPEGLRVFYYLVQDLKCLVFSLIGLHEKIKPI MMMAGO1 DALWEPDRVGRQELEIVIGDEHISFTTSKIGSLIDVNQSKDPEGLRVFYYLVQDLKCLVFSLIGLHEKIKPI MMMAGO1 DALWEPDRVGRQELEIVIGDEHISFTTSKIGSLIDVNQSKDPEGLRVFYYLVQDLKCLVFSLIGLHEKIKPI MMMAGO1 DALWEPDRVGRQELEIVIGDEHISFTTSKIGSLIDVNQSKDPEGLRVFYYLVQDLKCLVFSLIGLHEKIKPI MMMAGO1 DALWEPDRVGRQELEIVIGDEHISFTTSKIGSLIDVNQSKDPEGLRVFYYLVQDLKCLVFSLIGLHEKIKPI MMMAGO1 DALWEPDRVGRQELEIVIGDEHISFTTSKIGSLIDVNQSKDPEGLRVFYYLVQDLKCLVFSLIGLHEKIKPI MMMAGO1 DALWEPDRVGRQELEIVIGDEHISFTTSKIGSLIDVNQSKDPEGLRVFYYLVQDLKCLVFSLIGLHEKIKPI MMMAGO1 DALWEPDRVGRQELEIVIGDEHISFTTSKIGSLIDVNQSKDPEGLRVFYYLVQDLKCLVFSLIGLHEKIKPI	AtMAGO		ET.ETVI.GNEHT	SFATSKIGSLVI	COSSNDPEG	LRTFYYLVO	LKCLVESLISL	HEKTKPT		
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MmMAGO2 DALWPPEDRVGRODDEIVIGDEHISFTTSKIGSLIDVNQSKDPEGLRVFYYLVQDLKCLVFSLIGLHEKIKPI DrMAGO DALWPPEDRVGROBLEIVIGDEHISFTTSKIGSLIDVNQSKDPEGLRVFYYLVQDLKCLVFSLIGLHEKIKPI XtMAGO DALWPPEDRVGROBLEIVIGDEHISFTTSKIGSLIDVNQSKDPEGLRVFYYLVQDLKCLVFSLIGLHEKIKPI	HSMAG01	DALWPPPDRVGRQ	ELEIVIGDEHI	SFTTSKIGSLI	JVNQSKDPEC	LRVFYYLVQI	JLKCLVFSLIGL	HFKIKPI	•	
DIMAGO DALWEPEDRVGROBLEIVIGDEHISFTTSKIGSLIDVNQSKOPEGLRVFYYLVQDLKCLVFSLIGLHEKIKPI Xtmago Dalwepedrvgrobleivigdehisfttskigslidvnqsk <mark>opeglrvfyylvqdlkc</mark> lvfsliglhekikpi	MmMAGO2	DALWPPPDRVGRQ	ELEIVIGDEHI	SETTSKIGŠLI	DVNQSKDPEC	LRVFYYLVQI	OLKCLVFSLIGL	HFKIKPI		
XtMAGO BALMEPEDRVEROBINITY COBHISETTSKIGSIIDVNOSKDEBGIRVFYYLVODIKCLVFSIIGIHEKIKEI	DrMAGO	DALWPPPDRV <mark>GR</mark> Q	ELEIVIGDEHI	SETTSKI GŠLI	DVNQSKDPEC	LRVFYYLVQI	OLKCLVFSLIGL	HFKIKPI		
	XtMAGO	DALMEPEDRVCRO	ELEIVIGDEHI.	SFTTSKI <mark>C</mark> SLI	VNQSKDPEC		LKCLVFSLIGL	HFKIKPI		

Fig. S2 Multiple sequence alignment of the MAGO protein family.

Shaded regions with color indicate 100% amino acid similarity. Four conserved leucine residues that constitute a potential leucine zipper in the C-terminus (Pozzoli et al. 2004; Chu et al. 2009) are labeled by black cycles.

		10	, ,	20		30)		40		50		60		70)	80
PF14	MGNG		E-E	AVDFE	P	EEDDL	MDE	D	-VEGSS	S-PRA	AIPK	LKSA	ITGG		AS	K <mark>k</mark> ir	GRGFRE
SIY14	MANP		E-E.	AVDFE	P	e <mark>ed</mark> dl	MDE	D·	-VDASS	S-PRA	APMPK	lksa	ITGGGG	G	-SSAS	K <mark>k</mark> if	(<mark>gr</mark> gfre
SpY14	MANP		E-E.	AVDFE	P	EEDDL	MDE	D	-VDASS	S-PRA	APMPK	LKSA	ITGGGG	G	SSAS	KKIF	GRGFRE
Cay14	MANV		E-E.	AVDFE AVDFE	P	EDDDL	MDE		-VEGSS -VDASS	SPRA	APIPK	LKSA	TTGGS-		-SSGS	KKTF KKTF	GRGFRE
PtY14a	MANT		EAE	AVDFE	P	EEDDL	MDE	DGAAI	DADASS	SPRA	APLPK	LKSA	ITGGSA	ASSS-	LSAP	KKTF	GRGFRE
PtY14b	MANT		EAE	AVDFE	 -P	e <mark>dd</mark> dl	MDE	dgavi	DVDASS	SPRA	APLPK	LKSA	ITGGSA	ASPS-	-LSAP	k <mark>k</mark> tľ	(<mark>gr</mark> gfre
AtY14	MANI		ESE.	AVDFE	P	EEDDL	MDE	EGTA:	IDGAD	/SPR#	AGHPR	lksa	IAGANO	SE	SA-	K <mark>K</mark> TF	(<mark>GR</mark> GFRE
VvY14	MASA	<u> </u>	DVE.	AVDFE	P	EDDDL	MDE	DGAVI	DVDNSS	S-PRA	APLPK	LKSA	ITGGAE	SSL-	-AAAP	KKTF	GRGFRD
OST14a BdY14a1	MAAVINA	4	DVE	AVDED	r		MDE	EG	-ATEPS	SPAP	APR	LRST	TAGGGG		DGP	RRTE	GRGFRE
SbY14a1	Maavtn <i>i</i>	7	DVE	VVDFD	L	DDDL	MDE	DA	GPDPA	APAPA	APASR	LRST	IAG		-DDAP	R <mark>R</mark> TF	GRGFRE
BdY14a1	MAASN		DVE	VVDFD	s	DDDL	MDD	D·	-APENN	JPAP	APR	LRST	IAAGGE	IDS	SAAAA	r <mark>k</mark> tf	(<mark>gr</mark> gfre
SbY14a2	MAAANA-		GDVD	VVDFD	s	DDDL	MDD		-ALEAY	PASE	APR	LRST	IAASGI)	SSAAA	RKTF	GRGFRE
OsY14b	MAAAA		EDVE	FVDYD. EVEVD	RDEE	DDDDC	MDE		-GGGRU	NI	- DVDU		GVM 7V7				GRLLGR
ShY14b	MVAAMGE	RAAA	EEGDVE	FVDYD	0	DDDDG	MEE	DGR	-AAR	AI	JPVPR	IVSP.	AVV			-RTF	GRFAGR
VcY14a	MA					-DD	I	DR		DI)R	MQGL	DK			– <mark>k</mark> rf	GRGHRD
CrY14b	MA					- <mark>dd</mark> em	AHD	ER·		DE	ER	MDAG	DM			– <mark>K</mark> RF	(<mark>GR</mark> GHRD
HsY14	MA		DVL	DLHEA	G	GEDFA	MDE	DG		DE	ESIHK	LKEK.	AK			-KRF	GRGFGS
MMY14	MA		DVL	DLHEA	G	GEDFA	MDE				STHK	LKEK. I KEK	AK			-KRF	GRGFGS
XtY14	MA			DLHEA	G	GEDFA	MDE				STHK	KEK.	AK				GRGFGA
								-									
		90	,	100		11	0		120		130		140		15	0	160
DE1/	.	AE <mark>r</mark> n	ARLS	 . AP	FDST	DSO	GGP	CPER	STEGWI	. VT.V1			DHLHNZ	FGE	GETKN	Т.НТ.	
SIY14	ETAEA	AERN	ARLS	AR	FDSL	DSE	GGP	GPER	SIEGWI	ILVI	IGVNEI	EAHE	DDLHNI	FGE	GEIKN	LHLN	ILDRRSG
SpY14	ETAEA	AE <mark>R</mark> N	ARLS	AR	FDSL	DSE	GGP	GPER	SIEGWI	ILVI	r <mark>gvne</mark> i	e <mark>aq</mark> e	DDLHNI	FGE	G <mark>eik</mark> n	LHL	IL <mark>DRR</mark> S <mark>G</mark>
CaY14	ETAEA	AE <mark>R</mark> N	ARLS.	AR	FDSL	MTE	GGP	GPER	SI <mark>EG</mark> WI	ILVI	r <mark>gv</mark> nei	E <mark>AQ</mark> E	DHLH <mark>D</mark> I	FGEI	GEIKN	LHLN	IL <mark>DRR</mark> S <mark>G</mark>
NtY14	EAAEA	ADRN.	ARMS.	AR	FDSL	DSD	GGP	GPER.	SIEGWI			EIQE	DDLHNE	FGE	GEIKN	VHLN	
PtY14a	EVDA EVD1		SRES	GRG	FDSL	GSD	GGP	GPOR	SVEGWI		SGVHEI		DHLOEZ	TGET	GEIKN		
AtY14	EKDS	SDRO	RRLS	SRD	FESL	GSD	GRP	GPOR	SVEGWI	ILVS	SGVHEI	ETOE	EDITNA	FGD	GEIKN	LNLN	ILDRRSG
VvY14	DTDA	ad <mark>r</mark> n	SRFA	ARD	FDS <mark>L</mark>	DSD	GGP	GPQR	SIEGWI	ILVI	r <mark>gv</mark> h <mark>e</mark> i	E <mark>A</mark> QE	ddlq <mark>n</mark> f	FGE	GEVKN	LHLN	I <mark>LDRR</mark> T <mark>G</mark>
OsY14a	DAA	AP <mark>R</mark> D	SRLAGA	GRASD	FDSL	GSD	GGP	GPVR	SI <mark>EG</mark> W]	[VLV]	r <mark>gv</mark> h <mark>e</mark> i	E <mark>AQ</mark> E	DDLH <mark>N</mark> I	FRDE	GQVKN	LHLN	IL <mark>DRR</mark> TG
BdY14a1	DPNSSAA	APRD	SRLAGV	GR-SG	FDAL	ASD	GGP	GPVR	SIEGWI				DDLHNI	FRG	GEVKN	LHL	ILDRRTG
SD114a1 BdV14a1	EPSS	SSB-	PLT	GR-AD	FDSL	GTD	DGP	GPLR	STEGWI		CVHEI		DDLQNF DDLHNZ	FREE	GOVKN	T.HT.N	
SbY14a2	EPSS	SS <mark>R</mark> -	PLA	GR-SD	FDSL	GSD	YGP	GPLR	SIEGWI	ILVI	IGIH <mark>E</mark> I	EAQE	DDLHNÆ	FREE	GQVKN	LHLN	ILDRRTG
OsY14b	STSVLAS	5 n <mark>r</mark> d	R		FDS <mark>L</mark>	ADAGN	PGH	GPQR	SI <mark>EG</mark> W]	LUVS	G <mark>GV</mark> K <mark>E</mark> I	D <mark>A</mark> EE	DDLY <mark>N</mark> I	FSDE	GHVKD	LHL	I <mark>LERR</mark> T <mark>G</mark>
BdY14b	SPSILSS	S S <mark>R</mark> D	R		FDSI	PGPGT	SQH	GPQR	SI <mark>EG</mark> WI	ILVS	G <mark>GV</mark> KEI	DAEE	SDLF <mark>D</mark> A	FRDE	GRVKD	LHFN	IL <mark>ERR</mark> TG
SbY14b	SPSVLTS TTEWZ	S S H Y	R		FDSI.	TNDGD	AKP	GPQR	STEGWI		GIKEI CVNEI		DDF YNA Edth <mark>e</mark> z	AFSEL	GHVKD	LHLN	
CrY14b	ATEWA	ADRY	GG	AR	FKEL	DPN	AKP	GPTA	SVEGW	VFIT	IGINE	BAOE	EDIHEA	FAE	GEVKN	IYM	ILDROTG
HsY14	EEGSF	ra <mark>r</mark> m	R	ED	YDSV	EQDG-	DEP	GPQR	SVEGWI	LFVI	r <mark>gv</mark> h <mark>e</mark> i	EATE	EDIH <mark>D</mark> F	FAE	(<mark>geik</mark> n	IHL	ILDRRTG
MmY14	EEGSF	ra <mark>r</mark> m	R	ED	YDS <mark>V</mark>	EQDG-	DEP	GPQR	SV <mark>EG</mark> W]	[LFV]	r <mark>gv</mark> h <mark>e</mark> i	E <mark>A</mark> TE	EDIH <mark>D</mark> F	(FAE)	(<mark>GEIK</mark> N	IHL	IL <mark>DRR</mark> TG
DrY14	EEGAF	RSRV	R	ED	YDTV	EQDG-	DEP	GPQR	SVEGW1	LFVI	I GVHEI	EATE	EDVH <mark>D</mark> F	FAE	GEIKN	LHLN	IL <mark>DRR</mark> TG
Xt1 14	DEGTF	KA <mark>R</mark> I	R	ED	1DSV	EQDG-	DEP	FQR	SVEGW				edin <mark>d</mark> r	CE GEL	GETUN	тнги	
		17	0	180		19	0		200	RNF	2 210		220		23	0	
DE44		· · ·				· · · ·	 			• • •		· · ·	· · · · I ·		· · · · I	 DDV	1
SIY14	FVKGYAT		ENFERA	ERAIS.		NELLT	OTT		AFSKGI	PFR	RI	RNAR	-RRSPF	SHRS	SRSP-R	RRI-	
SpY14	FVKGYAI	LIEY	ENFEEA	ERAIS	EMDG	NELLT	QTI	HVDW2	AFSKGI	PFR	RI	RNAR	-RRSPF	SHRS	SRSP-R	RRF-	
CaY14	FV <mark>KG</mark> YAI	LI <mark>E</mark> Y	enfe <mark>ea</mark> :	er <mark>a</mark> in:	em <mark>d</mark> g	NELLT	QTI	H∨ <mark>D</mark> W2	A <mark>F</mark> SKGI	PFR	RI	RNAG	-RRS	SHRS	SRSPNR	RRF-	
NtY14	FV <mark>KGYA</mark> I	LIEY	ENFEEA	QR <mark>A</mark> IN:	EK <mark>D</mark> G	AEFLT	QTI	H∨ <mark>D</mark> W2	AFSRGI	PFK	RI	RNAR	-RRSPF	GHRS	SRSP-R	RRF-	
Pt114a	FVKGYAL	TEY	EKFEQA.	ENALA.	SMNG	GTLLE	QII	Y V DW2	AFSNGE	SN-V	VASERI	KNMR	PERTN-	RS	KSP-R	RRY-	
AtY14	YVKGYAT	TEY	EKKEEA	OSATS	AMNG	AELLE	ONV	SVDW	AFSSGI	PSGGF	SYRRI	KNSR	YGRSO-	RS	SRSP-R	RRY-	
VvY14	FV <mark>KGYA</mark> I	LI <mark>E</mark> Y	ENLE <mark>EA</mark>	QA <mark>AI</mark> S.	AMNG	TELLT	QTI	SVDW	AFSNGE	PFK	RI	RNMR	-RRSPF	GHRS	SRSP-R	RRY-	
OsY14a	FV <mark>KG</mark> YAI	LI <mark>E</mark> Y	etfe <mark>ea</mark>	QA <mark>A</mark> IK.	AL <mark>D</mark> G	TELLT	QII	SV <mark>D</mark> ₩	A <mark>F</mark> SNGI	PVK	RI	RNIR	-KRSPF	RRS	SRSPPR	RRY-	
BdY14a1	FVKGYAI	LIEY	ENFE <mark>EA</mark>	QA <mark>A</mark> IK.	ASDG	TELLT	QII	SVDW	AFSNGI	PAK	RI	RNTR	-KRSPF	ANRS	BRSPPR	RRY-	
BdY14a1	FVKGYAI	TEY	ESFERA	QAALK: OAATK'	ь LDG тмрс	AELHE			AFSNCI	PAK	RI	rn'l'R rnvp	-ккзрі -в	KARS	SRSPPP	KKH- RRV-	
SbY14a2	FVKGYAT	LVEY	ESFDEA	OAATK	AMDG	TELVT	0IT		AFSSGF	PVK	RI	RNVR	-w	RS	SRSPVR	RRY-	
OsY14b	YA <mark>KGYA</mark> I	LV <mark>E</mark> Y	ESFE <mark>EA</mark>	QT <mark>AI</mark> K.	AMNG	TQLLT	RTV	Y∨ <mark>D</mark> w	AFSRGI	PIQKI	LTSTRI	PLHR		RS	RTPPR	RLAA	ALTC
BdY14b	YG <mark>KGYA</mark> I	lv <mark>e</mark> y	esfe <mark>ea</mark>	kt <mark>a</mark> ik.	AMN <mark>G</mark>	RQLLT	кт <mark>і</mark>	HV <mark>D</mark> W	A <mark>F</mark> NRGI	PIQK	JISTR	PSRP		RS	SRTPPR	RLAA	LTY
SbY14b	YAKGYAI	JIEY	ESFE <mark>E</mark> A	QA <mark>AT</mark> R.	AMNG	SQLLT	KTI	YV D W2	AFSRGI	PIQNE	FKSTRI	PSRP		RS	BRTPPR	RLAA	LRP
CrY14b	FVKGYAI	JVEY .VEY	KNHKEA V.T.ÖKEA	QAALN: OTATM	EMNG	KELT.T	OT T		AFKK						PQR	KK RR	
HsY14	YLKGYTI	LVEY	ETYKEA		GLNG	ODLMG	0PT			PR	GKRI	RGGR		-RRS	RSPDR	RRR-	
MmY14	YL <mark>KG</mark> YTI	lv <mark>e</mark> y	etyk <mark>ea</mark>	QA <mark>A</mark> ME	GLN <mark>G</mark>	QDLMG	QPI	sv <mark>d</mark> w	FVRGE	PR	GKRI	RGGR		-RRS	SRSPDR	RRR-	
DrY14	YL <mark>KGYA</mark> I	lv <mark>e</mark> y	etyk <mark>ea</mark>	QA <mark>A</mark> ME	GLN <mark>G</mark>	QELMG	QPI	sv <mark>d</mark> w(C <mark>F</mark> VRGE	PK	SKRI	RGGR		-RRS	SRSPDR	RRR-	
XtY14	FLKGYAI	VDY	ETYK <mark>da</mark>	LAAME	GL <mark>NG</mark>	ODLMG	OPT	SVDW	GEVRGI	PPK	GKRI	RSGR		-RRS	SRSPER	RRR-	
	RN	121															

Fig. S3 Multiple sequence alignment of the Y14 protein family.

Shaded regions with color indicate 100% amino acid similarity. Conserved RNA recognition motifs of RNP1 and RNP2 (Lau et al. 2003; Shi and Xu 2003; Chu et al. 2009) are labeled in the middle area.





Shaded regions with color indicate 100% amino acid similarity. N-term flanking amino acid sequence and nine conserved motifs were labeled. Q-motif, motif-I, motif-Ia and motif-Ib were required for the ATP binding region; motif-II DEAD/DESD was involved in ATP hydrolysis and coupling ATP hydrolysis to helicase activity; motif-III SAT was critical for RNA unwinding; motif-IV and motif-V were equivalent to motif-Ia and motif-Ib and responsible to RNA binding; motif-VI was involved in the ATP hydrolysis-dependent RNA binding (Andersen et al. 2006; Cordin et al. 2006; Huang et al. 2016).

	10	20		30	40	50	60	70	80	90
			· · · ·		.	.		· · · · · · · · ·	1	
PFBTZ	QQGEEEKKENEPYA	VPTAGAFY	MHDDI	RFRDNAG	GRHRRTFGG-	RKLWESR	DDRKWGHL	KFEELSVEERH	YEEGRF	GSR-GRYRG
SIBTZ1	VQGEEGKKENEPFA	VPTAGAFY	MHDDI	RFRDNAG	GRHRRTFGG-	RKLWESR	DERKWGHI) <mark>KF</mark> EELTVEERH	YDEGRF	GSR-GRYRG
SIBTZ2	PQEEE-KKENEPYA	VPKT <mark>GAF</mark> Y	M <mark>HD</mark> DI	RFGDNVG	GRQKRMSGG-	RRLWESK	DDRKWGHE) <mark>KF</mark> EELTVEQRN	YDDDRF	ISR-GRYRG
NtBTZ1	P-G-EANKPNEPYS	VPTA <mark>GAF</mark> Y	M <mark>HD</mark> DI	RFRDNAAA	APHRRTFGG-	RKLWESK	DDWK <mark>W</mark> G <mark>H</mark> I	KFEELTMEERH	YGEGRF	TSR-GRYRG
NtBTZ2	-EEEE-KKENEPFA	VPTA <mark>GAF</mark> Y	M <mark>HD</mark> DI	RFRDNAG	GRHRRTFGG-	RKLWESK	DDRK <mark>W</mark> G <mark>H</mark> I	KFEELSVEERN	YEEGRF	ASR-GRYRG
SpBTZ1	GEEGKKENEPFA	VPTA <mark>G</mark> AFY	M <mark>HD</mark> D	RFRDNAG	GRHRRTFGG-	RKLWESR	DERK <mark>W</mark> GHI) <mark>kf</mark> eeltveerh	YDEGRF	GSR-GRYRG
SpBTZ2	-QEEE-KKENEPYA	VPKT <mark>GAF</mark> Y	M <mark>HD</mark> D	RFGDNVG	GRQKRMSGG-	RRLWESK	DRK <mark>W</mark> GHI) <mark>kf</mark> eeltveqrn	YDDDRF	ISR-GRYRG
CaBTZ	GEEEE-KKENEPYA	VPTA <mark>G</mark> AFY	M <mark>hd</mark> di	RFRDNAG	GRQHRRTFGG	RKLWESR	DRK <mark>W</mark> G <mark>H</mark> I	KFEELSVEERH	YQEGRF	GSR-GRYRG
PtBTZ1	EEGEEGKKENEPFA	VPTA <mark>G</mark> AFY	M <mark>hd</mark> di	RFRDSAG	GRHRRTLGR-	RKLWESK	DNKKWGHE) <mark>KF</mark> EEMTLQERH	YEQGRF	NAK-GNFHA
VvBTZ	EEGEEGKKGNQPFA	VPTA <mark>G</mark> AFY	M <mark>hd</mark> di	RFRDSAG	GRHRRTFGG-	RNLWESK	DKKWGHL) <mark>KF</mark> EEMTSQERH	YEQGRF	TAK-GNFRA
PtBTZ2	VGGEEEKKENEPFA	VPTA <mark>G</mark> AFY	M <mark>hd</mark> di	RFRDNAG	GRHRRTLGG-	RKLWESK	DRK <mark>W</mark> G <mark>H</mark> I) <mark>KF</mark> EEMTMQERH	YEEGRF	NSK-GHYHA
AtBTZ1	EEENE-KEKLQ-AA	VPTG <mark>G</mark> AFY	M <mark>hd</mark> di	FQEMSA-	GGNRRMRGG-	RQWGSG	ERKWGHI	KFEEMNTGEKH	SDQF	MSR-GRFRG
AtBTZ2	VDGEEQKKK-EPFA	VPTA <mark>G</mark> AFY	M <mark>hd</mark> di	FQELDA-	ASNRRMRGG-	RRLWQSR	DERKWGHI	KFEEMNTQKQQ	YDRF	TSR-GRGRG
OsBTZ1	AEGEEGKKGSEPYA	VPTA <mark>G</mark> AFY	M <mark>hd</mark> di	FQEARGH	GRQRRMVGD-	RLWNAK	EDQAWVHI	<mark>RF</mark> DEMNLHDFH	NDYTRF	RPR-GRFRG
OsBTZ2	GDGEE-KKEQEPFA	VPTS <mark>GAF</mark> Y	M <mark>hd</mark> di	FQEES-R	GRRRRMFGG-	RKLWDAK	DQAWVHI	RFEEMNLHEEH	YEDKF	MSR-GRFRG
SbBTZ1	DEEEE-KKGNEPYA	VPTT <mark>G</mark> AFY	M <mark>hd</mark> di	FQEGRGRGRGR	GRQRRMV-NS	RRLWSPK	DEQAWVHI	RFDEMDLHDFH	GGNPKRKQG	GGIRGRGGG
BdBTZ1	GEEVEGKKESEPFA	VPTT <mark>GAF</mark> Y	M <mark>hd</mark> di	FQEARGR	GRGRRMLSN-	RKLW-PK	EQEWVHI	DRFDEMHPRD	YNNGNIF	NLR-GRFRG
SbBTZ2	GEGEEKEQEPFA	VPTS <mark>G</mark> AFY	M <mark>hd</mark> di	FQEENR	GRRRRMFGG-	RKLWDAK	DDQAWVHI	RFEEMNLHDDR	YEDQF	MSR-GRFRG
BdBTZ2	ADGEE-KKEQEPFA	VPTS <mark>GAF</mark> Y	M <mark>hd</mark> di	FQEDGR	GRRRRMLGG-	RKLWDAK	DQAWVHI	RFEEMNVHEER	YEDKF	MSR-GRFRG
CrBTZ	KKAKLREPFE	VPTS <mark>G</mark> AFW	IL <mark>HD</mark> D	YGAEAESAEPE	AAKPGASPTE	RKYKSDT	DGR-WQHI	KF <mark>AAIESGQEV</mark>	EDSGSE	DAFGGYSRR
VcBTZ	KKAKLREPFE	VPTS <mark>GAF</mark> W	/L <mark>HD</mark> D	FGGDEPQTE	APRPSGAV-E	RKARSDT	EGR-WL <mark>H</mark> I	KFGTLELGEAA	DDDDTE	NAFSNYRRG
HsBTZ	LDDDEDRK-N-PAY	I PRK <mark>GLF</mark> F	FEHDL	GQTQEEEVRPK	GRQ	RKLWK	DEGRWEHD	KFREDEQAPKS	RQEI	IALYGYDIR
MmBTZ	LDDDEDRK-N-PAY	I PRK <mark>GLF</mark> F	FEHDL	GQTQEEEVRPK	GRQ	RKLWK	DEGRWEHD	KFREDEQAPKS	RQEI	IALYGYDIR
DrBTZ	LDDDEDRK-N-PAY	I PRK <mark>G</mark> LFF	FE <mark>HD</mark> VI	GQATEEE-RPK	GRN	RKLWK	DEGRWEHI	KFREEEQAPKS	RDEL	IAFYGYDIR
XtBTZ	LDDDEDRK-N-PAY	I PRK <mark>G</mark> LFF	FE <mark>HD</mark> LI	RGHVNDEEVRPK	GRHP	RKLWK	DEGR <mark>W</mark> E <mark>H</mark> I	<mark>RF</mark> REDEQAPKS	REEI	ISIYGYDIR

Fig. S5 Multiple sequence alignment of the SELOR domain in the BTZ protein family. Only the SELOR domain (Degot et al. 2004), part of the whole MSA, is shown. Shaded regions with color indicate 100% amino acid similarity.

Α		PFMAGO1	PFMAGO2	PFY14	PFelF4AⅢ	PFBTZ
	Residue range	9-151	9-151	77-170	5-391	144-217
	Tertiary structural modeling	Nt-β1-β2-β3- β4-α1-β5-β6- α2-α3-Ct	I-β2-β3- Νt-β1-β2-β3- Νt-β I-β5-β6- β4-α1-β5-β6- β3-α ·α3-Ct α2-α3-Ct		Νt-α1-α2-β1-α3-β2-α4- β3-α5-β4-β5-α6-α7-β6- α8-β7-β8-α9-β9-α10- β10-α11-β11-α12-β13- α13-β13-α14-α15-Ct	No α-helix nor β-sheet
	Template (PDB ID)		X-	Ray, 2.30 Å, PDE	3 ID: 3EX7	
	Identity (%)	82.52	81.25	54.29	78.97	27.63
	GMQE	0.89	0.88	0.43	0.92	0.03
	QMEAN4	-1.05	-0.95	-0.22	-0.46	-5.24
	Organism			Homo sapie	ens	



Fig. S6 Tetrameric structure modeling of EJC core components in *P. floridana*.

a Quality factors of *Physalis* EJC protein structure modeling. Nt, protein N-terminal; Ct, protein C-terminal; α , α -helix; β , β -sheet. **b** The tetrameric structure reconstruction of the *Physalis* EJC core based on human EJC (PDB ID: 3EX7). Conserved protein domains of EJC core components were predicted using the Pfam program and are presented in the pink box. The position of each conserved region or motif is given. Bar, 100 amino acids (AA).







Fig. S8 PPIs among *Physalis* EJC core proteins revealed by yeast two-hybrid analysis.

Yeast cell growth on a high-stringency selective plate (SD/-Leu-Trp-His-Ade) (Left panel) and nonlethal β -galactosidase tests were used to confirm the interactions (right panel). The empty pGADT7 and pGBKT7 constructs were used as the negative controls.

A	Gene/VIGS	Infected seedling number	Mutated seedling number	Gene express mutants at 14 compared to	ion of 4 DAI 9 NC	Surv num (rati	ival ber o)	Pollen viability	Fruit setting rate by self / cross- pollination	
-	WT	-	-	1.00±0.05 (<i>PF</i> A 1.06±0.16 (<i>PF</i> A 0.99±0.21 (<i>PF</i> A 0.95±0.11 (<i>PF</i> A 1.03±0.18 (<i>PF</i> A	/AGO1) /AGO2) /14) hIF4A]]]) 3TZ)	30 (10	0%)	96.1%	95.5%/94.3%	
	TRV2 (NC)	30	-	1.0 (for each g	gene)	30 (10	0%)	95.8%	95.3%/94.6%	
	PFMAGO	120	115	$0.26 {\pm} 0.13$ (PFM $0.32 {\pm} 0.12$ (PFM	ЛАGO1) ЛАGO2)	25 (21	.7%)	45.2%	35.3%/89.5%	
	PFY14	120	112	0.22±0.1	5	0 (0))	35.3%	0/0	
	PFeIF4AIII	120	113	0.35±0.2	.1	44 (38	.9%)	90.9%	95.2%/94.1%	
_	PFBTZ	120	115	0.33±0.1	8	115 (1	00%)	50.1%	67.5%/92.3%	
в	WT		TRV2	PFMAGO-VIGS	PFY14-	VIGS	PFelF 4	A <u>∭</u> -VIGS	PFBTZ-VIGS	
70	JAI									
140)AI									weller
210	IAC									
28E	IAC						P			

Fig. S9 Overall analysis of EJC core gene-VIGS in *P. floridana*.

a Evaluated parameters are as indicated. **b** Phenotypic variation of VIGS plants at vegetative stages compared to WT and NC. 7DAI, 14DAI, 21DAI and 24DAI indicated 7-, 14-, 21- and 24-d after infection, respectively.



Fig. S10 PFY14-VIGS analysis in P. floridana.

a, **b** Plant growth of NC and *PFY14*-VIGS plants at 28DAI stage. **c**, **d** Shoot apex of NC and *PFY14*-VIGS plants. **e**, **f** Flower morphology of NC and *PFY14*-VIGS plants. **g**, **h** Pollen viability of NC and *PFY14*-VIGS plants, which was evaluated by I_2 -KI staining. **i** The *PFY14* expression in flowers of plants as indicated. WT, wild type; NC, negative control; VIGS, *PFY14*-VIGS flowers showing severe pollen abortion. The flower number (n) investigated in each case was indicated. Bars, 10 cm in **a**, **b**, 1 cm in **c**-**f**, 100 µm in **g**, **h**. Significance relative to NC was evaluated by a two-tailed Student's *t* test, and ** indicates significance at *P* < 0.01.



Fig. S11 PFBTZ-VIGS analysis in P. floridana.

a, **b** Phenotype of NC and *PFBTZ*-VIGS plants at the fruiting stage. **c**, **d** Flower morphology of NC and *PFBTZ*-VIGS plants. **e**, **f** Fruit morphology of NC and *PFBTZ*-VIGS plants. **g**, **h** Pollen viability of NC and *PFBTZ*-VIGS flowers, which was evaluated by I₂-KI staining. **i** The *PFBTZ* expression in flowers of plants as indicated. WT, wild type; NC, negative control; VIGS-I, *PFBTZ*-VIGS flowers showing pollen abortion; VIGS-II, *PFBTZ*-VIGS flowers having WT-like pollen development. The flower number (n) investigated in each case was indicated. Bars, 10 cm in **a**, **b**, 1 cm in **c-f**, 100 µm in **g**, **h**. Significance relative to NC was evaluated by a two-tailed Student's *t* test, and ** indicates significance at P < 0.01.

			10 .			20		.	3() 	. .		40 			50 . .			6	°	. .		70 			80 . .			90) 	. .	:	100 			110			120 .
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playti	M	C 1	K E	Т	I	I	Т	D	A	I	т	Y	I	R	Е	L	Q	М	N	V	D	N	L	S	Е	Q	L	L	Е	М	Е	A	Т	Q	G	Е	Q	L	Е
PFDYT1	 ATTAZ		130 . A TGA	 AGA	 GAT	140 AAT	GA	.∣ ГАСТ	15 GCA	0 GAG	. . GAG	i ATG	160 GGT	 AAA		170 . .	ATA	 GAG	18 	••••	• •	1 	90 	•••		200		···	21 ••	0 	. .		220	· ·		230			240 •
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	Ił	ς .	N E	: E	I	1 260	D	т	A 27	E	Е	м	G	к	W	G 290	I	Е	V 30	G	N	F	Y 10	V	Ť	N 320	Q	S	Y 33	N	L	Ť	Y 340	S	Ť	V 350	к	к	G 360
PFDYT1								.	•••	· · ·	. . 	 				• •				 CCI	. . GAA	GTG	CAG	 G <mark>T</mark> G	GCT	. . CAC	ATT	 GGT		ACT	. . 'AAG	СТТ	TGG	 ATZ		.	TC1	rg <mark>cc</mark>	. AG
pfdyt1	AATTI N B	rtC	TAAT L I	CTA Y	CTA Y	TTAC	T	AGTA V	AAA K	CAA Q	CTT L	TTI F	F	GTT V	S	L	L	K K	Q Q	P P	GAA E	GTG V	CAG Q	G <mark>T</mark> G V	GCT A	CAC. H	ATT I	GGT G	P P	ACT T	AAG K	L	TGG W	ATZ I	K K	GTAC	v V	rgcc C	AG Q
			370 .			380		.	39 	0	. .		100 			410			42	20	. .	4	30 			440			45 	0	. .		460 			470			480 .
pfdyt1	K F AAGAA		GAGG	TGG	ATT ATT	TAC:	K K	L ACTG	M ATG	EGAG	A GCA	M ATG	N AAT N	U GTT V	CTT	GGA	F	D	L ICTT	N AAT N	D GAC	T ACT.	S AGT	V GTC	T ACT	A GCC	S TCC	K K AAA K	GGA GGA	A GCT		CTI	U GTT V	T ACI	S TCA	S TCT	V TGG TGG	E GAGG	TA V
	IX I	х.,	490		-	500	K	ц	51	0	л	11	520	v	1	530	Ľ	D	54	10	D	± 5	50	v	1	560	5	K	57	0	1		580	1	5	590	v	5	600
PFDYT1					· ·			.	•••		· ·			•••		• •					• •		• • 	•••		• •		• • 	· ·		• •			· ·		• • •	•••		•
pfdyt1	AGAG	AAA	CATA	TGG	TAA	AAA	AAA	GCAA	GCT	TTT	TAG	CAG	CAA	TAA	AAA	GCI	ATT	GCC	TGT	AAT	AGT	ACA.	AAA	AGG	AGA	TCT	TGC	TAA	GCA	ССТ	TGT	ACI	GGG	TGI	GCT	GCA	TAT	TAAG	AA
PFDYT1			610 • • •		• • 	620 •• •		.	63 	0	. . 	GTG V	540 GTT V	। САС Н	 GGT G	650 . . GGA G	L	 AC1 T	66 IGAA E	GCI A	. . 'AAT N	6 CAA	70 ATC I	 AGA R	GAC D	680 . . ATC I	 TTG L	I CTG L	69 GAG E	0 ATC I	. . ATC I	 САС Н	700 AGA R	 ATC I	 CTAC Y	710 . . TAG *			
pfdyt1	CATAA H H	AAC.	AATI Q F	TGT	AAA N	P	F	F	GTA V	F	CAG Q	GTG V	U V	H	GGT	GGA G	L	T	E E	A	N N	Q	ATC. I	AGA R	GAC D	ATC I	TTG L	CTG L	GAG E	ATC I	I	H	R	ATC I	Y Y	TAG			

Fig. S12 Sequence comparison of different PFDYT1 transcripts.

The normal cDNA of *PFDYT1* was 429 bp long, and putatively encoded a peptide of 142 amino acids (aa). Aberrant transcript (pfdyt1) was 711 bp, and maximally encoded a putative 65-aa peptide. Stop codon (*) was highlighted by black arrows. The - indicates the nucleotide acid gap.





a Full-length transcripts of the indicated genes in flower organs. WT, NC, MV, YV, eV and BV respectively represent wild type, negative control (*TRV2*), and *PFMAGO-*, *PFY14-*, *PFeIF4AIII-* and *PFBTZ-*VIGS *P*. *floridana* plants. The cycle number is given in the bracket. **b** The gene expression in 7DBF floral buds of the indicated plants. **c** Full-length transcripts of *PFWRKY* family genes in shoot apex or root collar. WT, NC, MV, YV, eV and BV respectively represent wild type, negative control (*TRV2*), and *PFMAGO-*, *PFY14-*, *PfeIF4AIII-* and *PFBTZ-*VIGS *P. floridana* plants. The sample between the two dashed lines is root collar, and others are the shoot apex. The cycle number is given in the bracket. **d** The gene expression of *PFWRKY* family in the shoot apex or root collar of the indicated plants. Significance relative to WT was evaluated by two-tailed Student's *t* test, and ** indicates significance at P < 0.01.

Usage	Primer name	Forward sequence	Reverse sequence
	PFMAG01	AGAATTCGAGTTTCGTCCCGAC	TGACAATCTCAAGCTCTTGCCTC
	PFMAG02	AGTTTTACCTGAGATATTACGTG	AAGGGGTGAGGAAGACTTCCTTG
	PFY14	AATCAAAGGCCGTGGTTTCCG	AGCCTCCTCATTAACTCCAGTG
	PFelF4A///	TATTATGGCTGAGTTCCGAGGTG	CGACCAATGCGATGAATGTAG
	PFBTZ	GTGGTGGCATTCCTGCTGTTG	TTCTGACGCTGGCCTAAGTCG
	PFDYT1 (E1F-E3R)		CTAGTAGATTCCGTGGATGATCTC
	PFDYT1 (E1F-I1R)	ATGACAAAAGAAACCATAATCACTG	GTTGTTTTACTGTCTAATAG
	PFDYT1 (I1F-E2R)	AATCTTTGATATTCTTGAGTC	TCCAAGAACATTCATTGCCTC
	PFDYT1 (I2F-E3R)	GCTAAGCACCTTGTACTGGG	
qRT-PCR	PFDYT1 (E3F-E3R)	CCTGAAGTGCAGGTGGCTCAC	CTAGTAGATTCCGTGGATGATCTC
	PFTDF1	ACTAGCTGGGAGCAACTAGCTGGG	CTTTGTTTGACCCATCTTGAGCACC
	PFAMS	GGATTGCTCGAGTTGTTCAGTACG	TCCCGAATTTGATCTTCCGTTATC
	PFbHLH	TACCCAAGTTTAGGTCTGCAGAAG	GAGGTATGGAGCTTCAGGCATTGG
	PFAspP	GCTACCCTAGGAGTTGGACAACC	GCAAACACTGAGTCACTAGGTCCG
	PFCvsP	GTTGTGGAAGCTGTTGGGCGTTCTC	GCCACTTATTGTAACTGCATGCTG
	PEWRKY31	GTCAGATGATGGATACAATTGGAG	GATATCGATATCGCTTGTAGTTTG
	PEWRKY75	TCTTGGGGCTAATGGCAAGCATGG	GGAAGCATAGATTTGCATCTGACTC
	PFWRKY81	TAATTCGTGGTCGGGAGTTTACC	GTCTTGAATTIGTTGCACTIGTTTG
	PEACTIN		CONTATCOTOCONATTOCTO
	PEDVT1		
	PETDE1		
	DEAMS		
	DELULU		
	PE4opB		
RT-PCR	PFAspP		
	PECYSP		
	PFWRK131		
	PFWRKY75		
	PFWRK181		
	PFACTIN		
	PFMAGO1	GCCCATGGGGGAATTGGAAGAGAATG	AIGGATCCGGGTTTGATCTTGATATGGAG
	PFMAG02	GGCCATGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ATGGATCCGGGTTTGATCTTGAAATGGAG
Y2H	PFY14	ATCCATGGGGAACGGGGGGGGGGGGGGGGGGGGGGGG	ATGGATCCTTAGTATCTCCCCCTGGGACTTC
	PFelF4A///	IGCCATGGAAGAAGACCGGTTAGTTTCG	AAGGATCCTATCAATTCAGCCACGTTCATTGG
	PFBTZ	TGACATATGGCGAGTGCTTGGAGAAGCAG	AAGGATCCTCACTGATCAAACTTCATCTCCG
	PFMAG01	CACGGGGGACTCTAGAATGGGGGGAATTGGAAGAGAATG	CGATGGATCCACTAGTAATGGGTTTGATCTTGAAATG
	PFMAG02	CACGGGGGACTCTAGAATGGGGGGAGATGGCAGAGAAC	CGATGGATCCACTAGTAATGGGTTTGATCTTGAAATG
BiFC	PFY14	CACGGGGGACTCTAGAATGGGGAACGGGGAGGAGGGC	CGATGGATCCACTAGTGTATCTCCTCCTGGGACTTC
	PFelF4A///	CACGGGGGACTCTAGAATGGAAGAAGACCGGTTAGTTTTC	CGATGGATCCACTAGTTATCAATTCAGCCACGTTCATTGG
	PFBTZ	CACGGGGGACTCTAGAATGGCGAGTGCTGGAGAAGCAG	CGATGGATCCACTAGTCTGATCAAACTTCATCTCCGT
	PFMAG01	AACCATGGGGGAATTGGAAGAGAATG	ATACTAGTAATGGGTTTGATCTTGAAATGG
Subcellular	PFMAG02	ATUCATGGGGGAGATGGCAGAGAAC	ATACTAGTAATGGGTTTGATCTTGAAATGG
localization	PFY14-1302	AACCATGGGGAACGGGGGGGGGGGGGGGGG	CCACTAGTGTATCTGGTCCTGGGACTTC
	PFelF4A///	CACCATGGAAGAAGACCGGTTAGTTTTC	CCACTAGTTATCAATTCAGCCACGTTCATTGG
	PFBTZ-1300	AATCTAGATGGCGAGTGCTGGAGAAGCAG	AAGGTACCCTGATCAAACTTCATCTCCGTATATC
	PFMAGO	ACGGATCCAGTTCGGGCACGAGTTCT	TGCTCGAGATGGGTTTGATCTTGAA
VIGS	PFY14	ACGGATCCGACGAAGACGTTGAGGG	TGCTCGAGGCTCATTCCCATCCATT
	PFelF4A]]]	ACGGATCCAGGTTGTACTGATTT	TGCTCGAGCGACCAATGCGATGAA
	PFBTZ	ACGGATCCGGAAGCATGGGCAGT	TGCTCGAGGGCCTAAGTCGTCATTTG

Table S1 Primers used in the present study.

Gene	Accession number	ORF length (bp)	Protein length (Amino acid)	Grand average of hydropathicity
PFMAG01	EF205415	456	151	-0.523
PFMAG02	EF205416	456	151	-0.508
PFY14	KF051015	567	188	-0.973
PFeIF4AIII	MH319840	1176	391	-0.171
PFBTZ	MH319841	2067	688	-1.024

Table S2 Molecular information of the isolated *Physalis* EJC core genes.

Creation	Abbrevietien	Accession number									
Species	Appreviation	MAGO	Y14	elF4A3	BTZ						
Physalis floridana	PF	EF205415 EF205416	KF051015	MH319840	MH319841						
Solamun lycopersicum	SI	NM_001291909	NM_00129108	XM_004250609	XP_010318560 XP_004252328						
Solamun pennellii	Sp	XP_015067364	XP_01508009	XP_015058616	XP_015070832 XP_015060990						
Nicotiana tomentosiformis	Nt	XP_009593407	XP_009586749	XP_009616974	XP_009586607 XP_009595299						
Capsicum annuum	Са	XP_016558805.1	XP_016574886	XP_016554349	PHT88780						
Populus trichocarpa	Pt	XM_006375098	XM_002299753 XM_002314049	XM_002306354 XM_002310627	XM_006369105 XM_002303242						
Arabidopsis thaliana	At	NM_100094	NM_104029	NM_112866	NM_202458 NM_101397						
Vitis vinifera	Vv	XP_002281294	XP_002281228	XP_002275011	XP_010654695						
	0	KF051011	KF051016	NM_001050208	XP_015650091						
Oryza sativa	Us	KF051008	KF051017	NM_001057041	XP_015640548						
sorghum bicolor	Sb	02g027660 07g027660	XP_002439249 XP_002457845 XP_002466233	04g038330	XP_002455883 XP-021303601						
Brachypodium distachyon	Bd	XP_003573269	XP_003568971 XP_003567720 XP_003559268	XP_003570724	XP_003569296 XP_003565997						
Volvox carteri nagariensis	Vc	XM_001770356	XP_002953417	XP_002958883	XP_002951521						
Chlamydomonas reinhardtii	Cr	XM_001763749	XP_001696992	XP_001699375	XP_001698374						
Homo sapiens	Hs	NM_002370 NM_018048	NM_005105	NM_014740	XM_005257163						
Mus musculus	Mm	NM_001282737 NM_025564	NM_001102407	NM_138669	NM_138660						
Danio rerio	Dr	NP_001017700	NP_001013363	NP_957372	NM_205716						
Xenopus tropicalis	Xt	XP_002931471	NP_001039147	NP_001084200 NP_001107349	NM_001012652						

 Table S3 Sequences used in the present study.