

Supplementary Materials

The NF-Y Transcription Factor Family in Watermelon: Re-Characterization, Assembly of CINF-Y Complexes, Hormone- and Pathogen-Inducible Expression and Putative Functions in Disease Resistance

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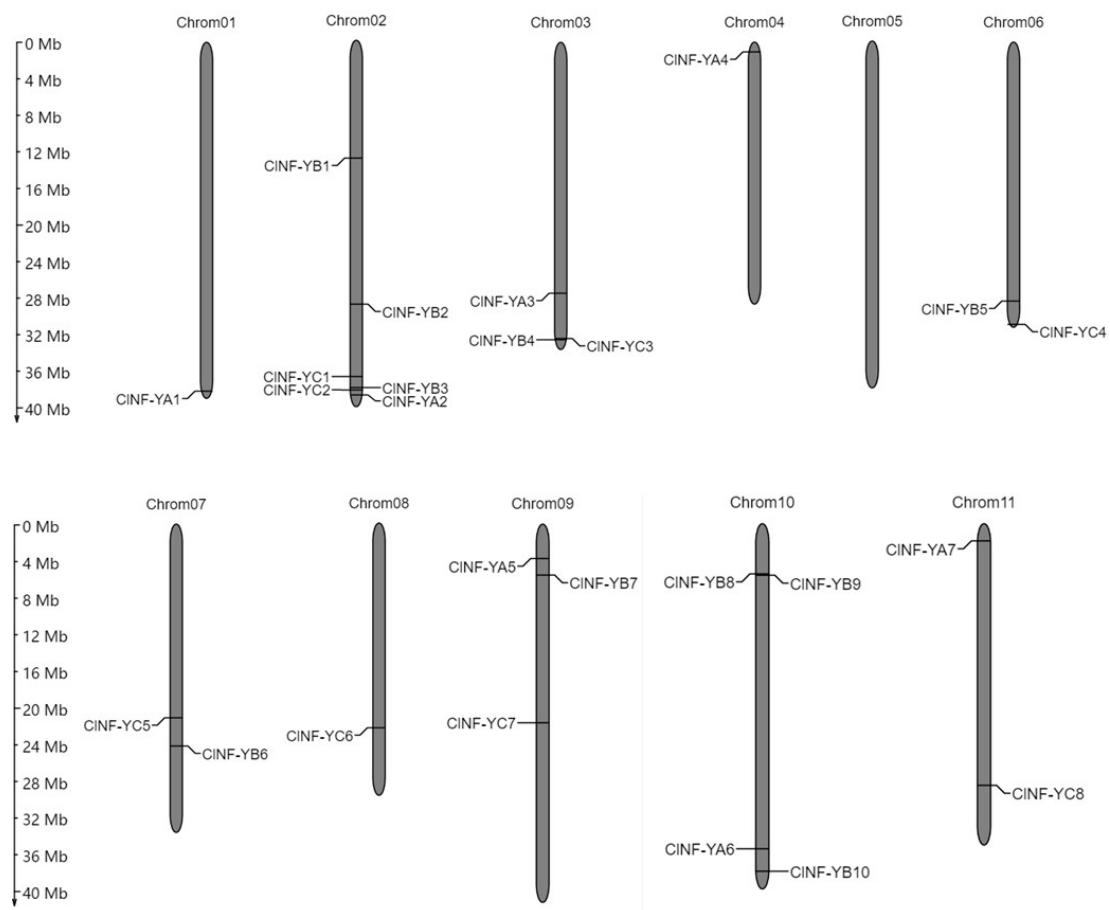


Figure S1. Distribution of *CINF-Y* genes on watermelon chromosomes.

(A)

1	EEPVYVNAKQYHGILRRRQSRAKAEAENKLK
2	RKPYLHESRHLHAMRRARGSGGRFLKTKK
3	GHSIACASYPYQDPYYGGILMA
4	YSEPWWRGIGYNT
5	HARMPLPLEM
6	FGVDCNPW
7	TSPECPNGGSESNDGQSMSNDDLNEEEEDDD
8	GRYVHGGAIT
9	FGNPEF
10	NTKKMQITL

(B)

1	DAKETVQECVSEFISFVTGEASDKCQKEKRKTINGDDLLWAMATLGFEDY
2	VREQDRLPIANVSIRIMKKALPANAKISK
3	VEPLKVYLNKYRETEGEK

(C)

1	EDVRMISAEAPVLVSKACELFJLELTKRSWEITEZNKRKTL
2	VTDFKBHSLPLARIKKIMKAD
3	QKNDIAAAITRTDVDFLVDIVPRE
4	QKNDIAAAITRTDVDFLVDIVPRE
5	PYYYVPSQH
6	SKMHEAGHGISMGRGRGRGRGRGRGR
7	RPYMPFQPWPH
8	VGAPGMIMGKPLDDPNMY
9	NFDLNV
10	HQLAYQ

Figure S2. Conserved motifs in CINF-YAs (A), CINF-YBs (B), and CINF-YCs (C) identified by MEME.

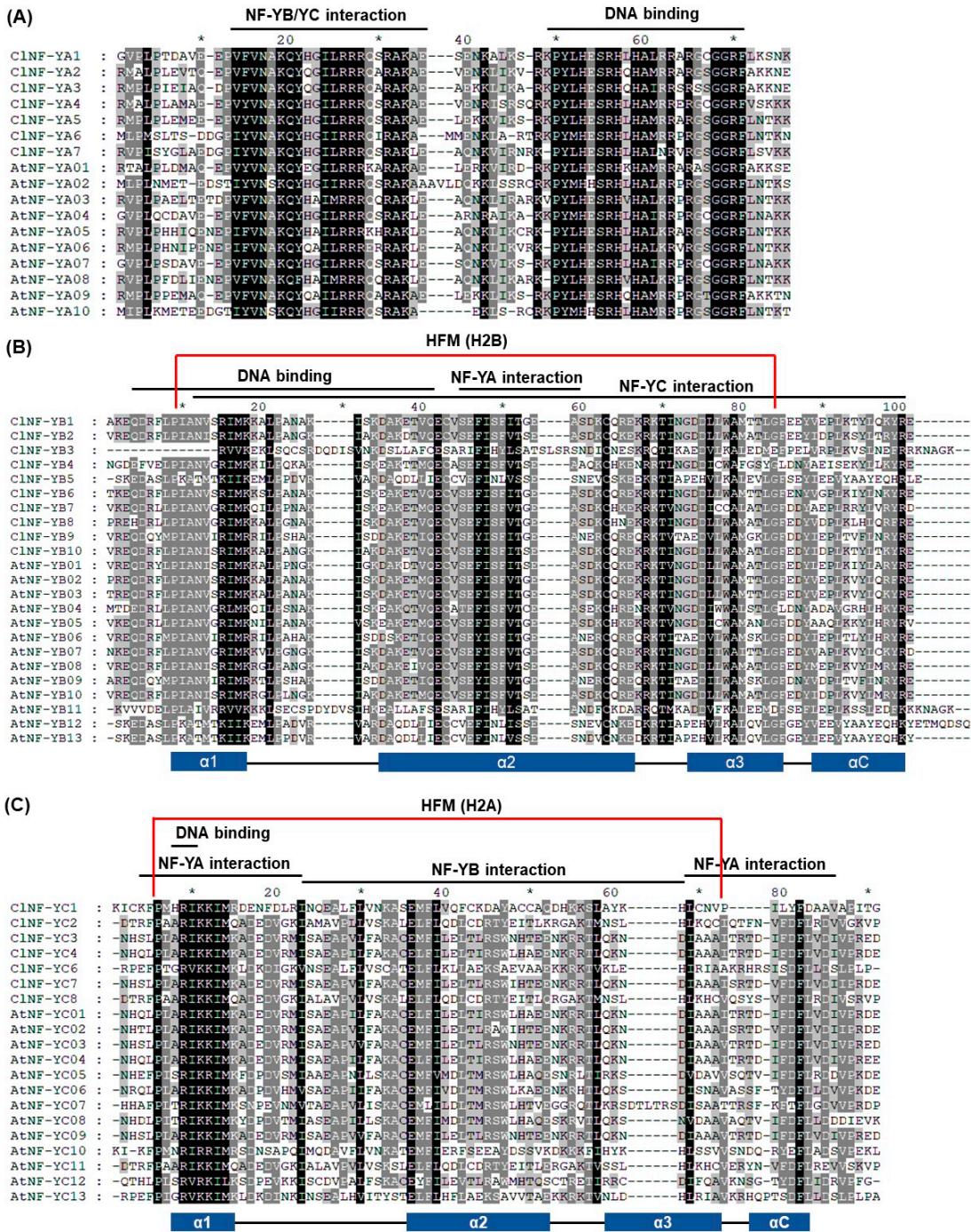


Figure S3. Sequence alignments of the conserved domains in watermelon CINF-YAs, CINF-YBs, and CINF-YCs with Arabidopsis AtNF-Ys. (A) CINF-YA subfamily; (B) CINF-YB subfamily; (C) CINF-YC subfamily. Multiple sequences alignment was constructed by DNAMAN software. The completely conserved amino acids are colored by black boxes and the relatively conserved amino acids (80%-100%) are colored by grey boxes. Regions responsible for subunit interaction and DNA binding are marked above the sequences and the structures of the conserved domains in CINF-YBs and CINF-YCs are indicated below the sequences.

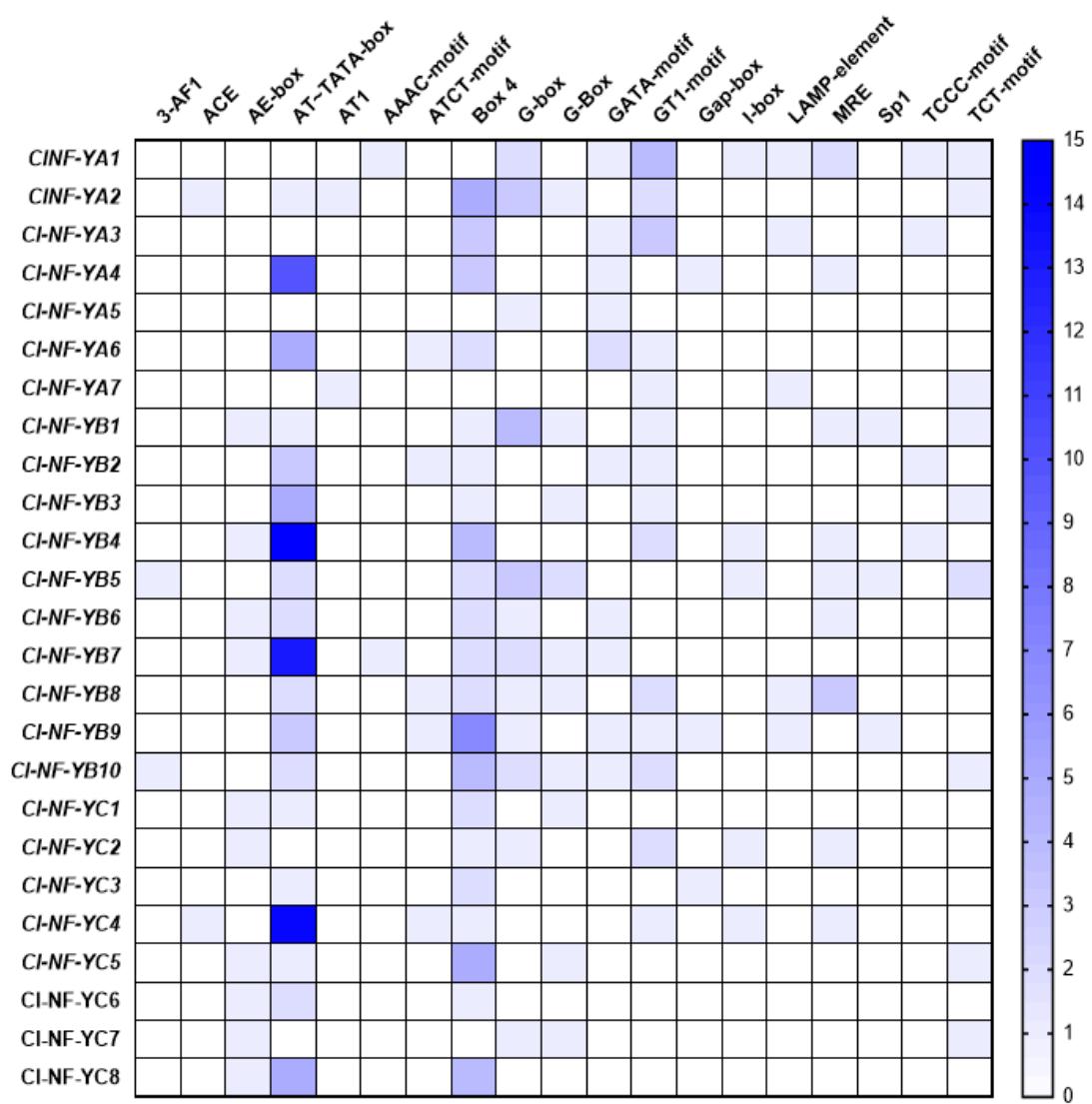


Figure S4. Light-responsive *cis*-elements present in promoters of the watermelon *CINF-Y* genes.

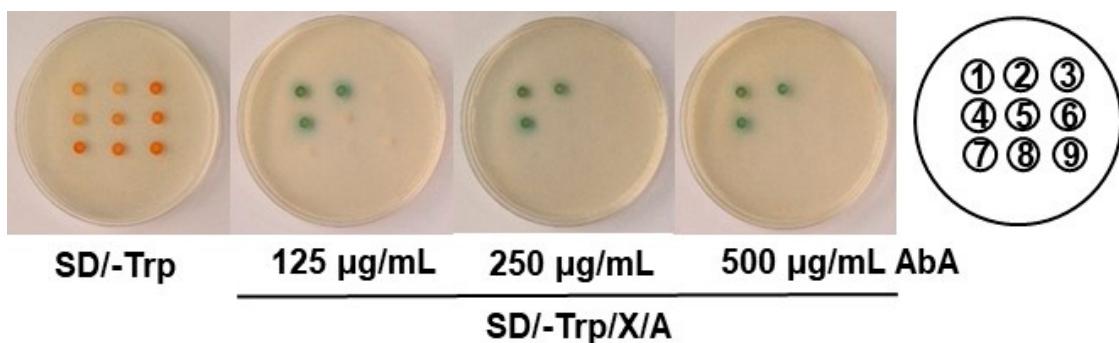
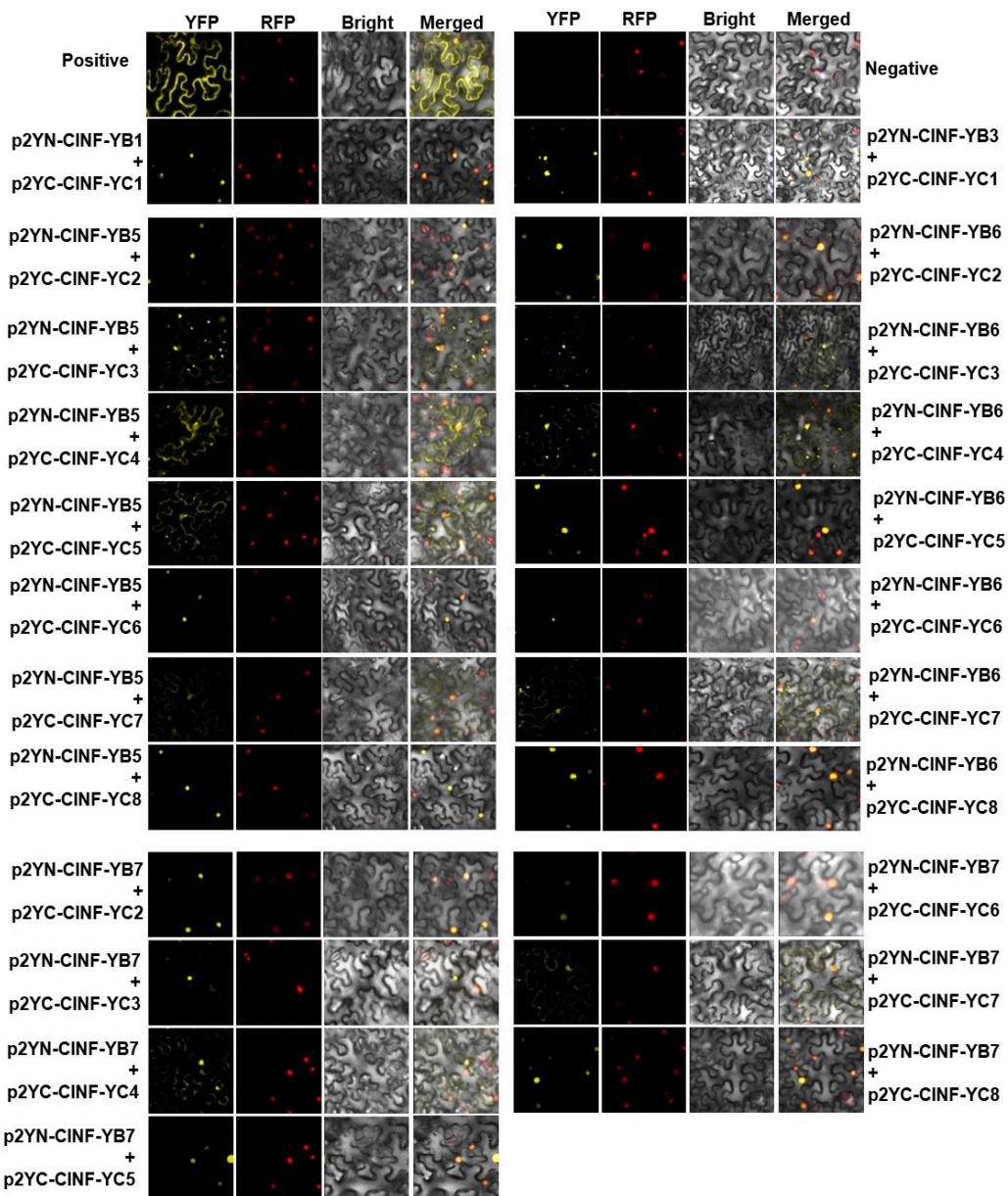


Figure S5. Autoactivation activity of CINF-YCs in Y2H assays. Yeast cells were transformed with pGBT7-CINF-YCs and grown on SD/-Trp medium. Autoactivation activity was visualized by the appearance of blue color of the yeast cells after adding 40 µg/mL X- α -gal. Different concentrations of AbA were supplemented into SD/-Trp medium to inhibit putative autoactivation activity. Experiments were repeated three times with similar results.



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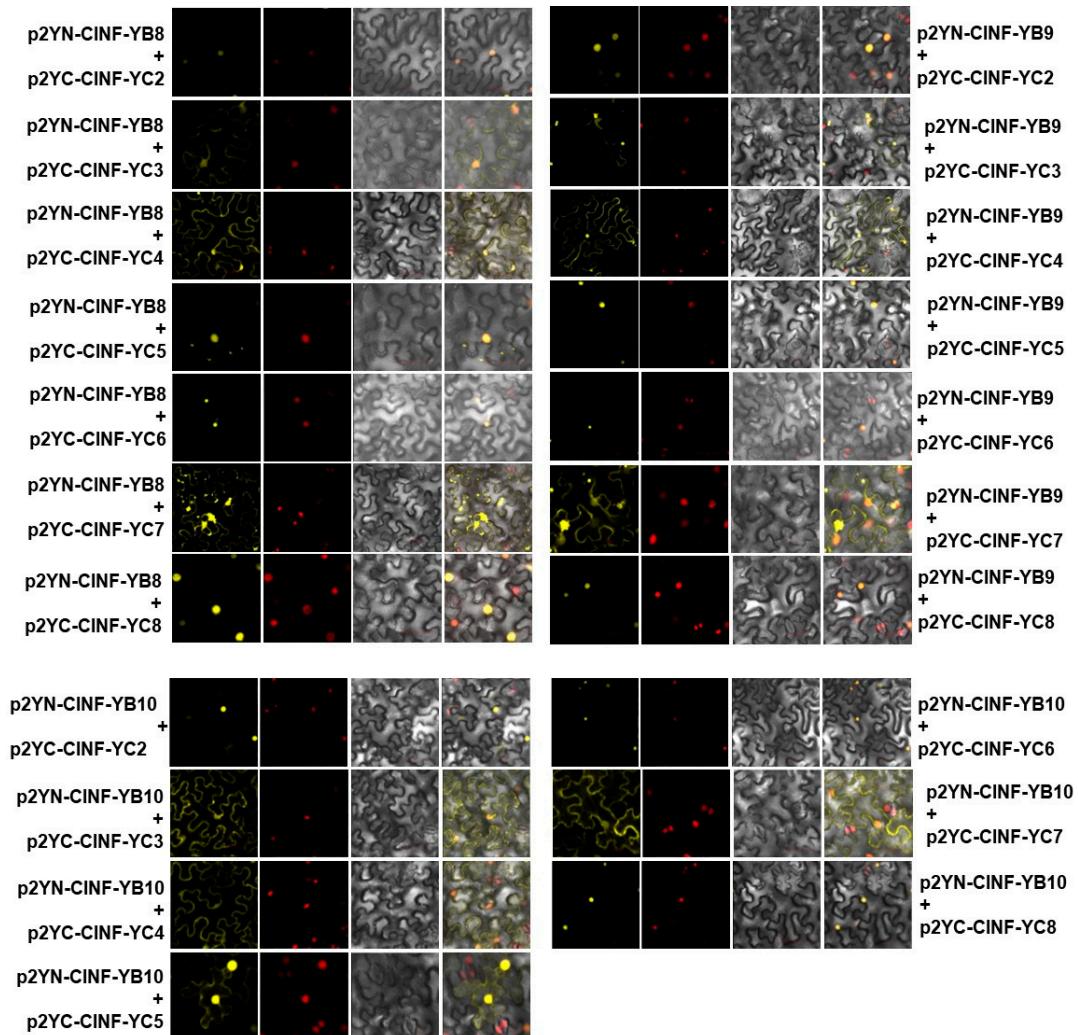


Figure S6. Interactions between CINF-YBs and CINF-YCs in BiFC assays. Experiments were performed three times with similar results.

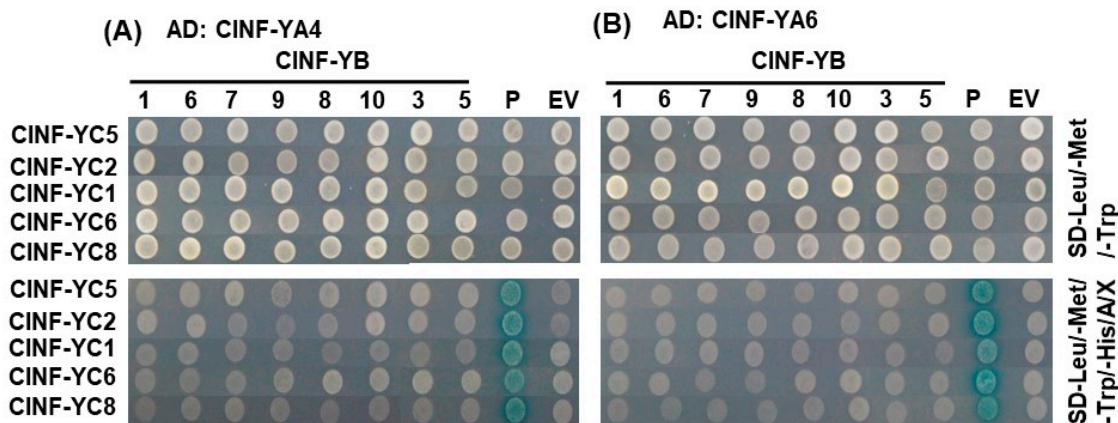


Figure S7. CINF-YA4 and -YA6 did not assemble into CINF-Y complexes with any of the CINF-YB/-YC heterodimers in Y3H assays. CINF-YA4 and CINF-YA6 were cloned into pGADT7 to fuse with the GAL4 activation domain, while paired combinations of CINF-YBs and CINF-YCs were cloned into pBridge to fuse with the GAL4 DNA binding domain. Growth of yeasts co-transformed with pGADT7 and pBridge vectors were grown on SD-Leu/-Met/-Trp noninteraction selective medium or on SD-Leu/-Met/-Trp/-His/A/X interaction selective medium. Experiments were performed three times with similar results.

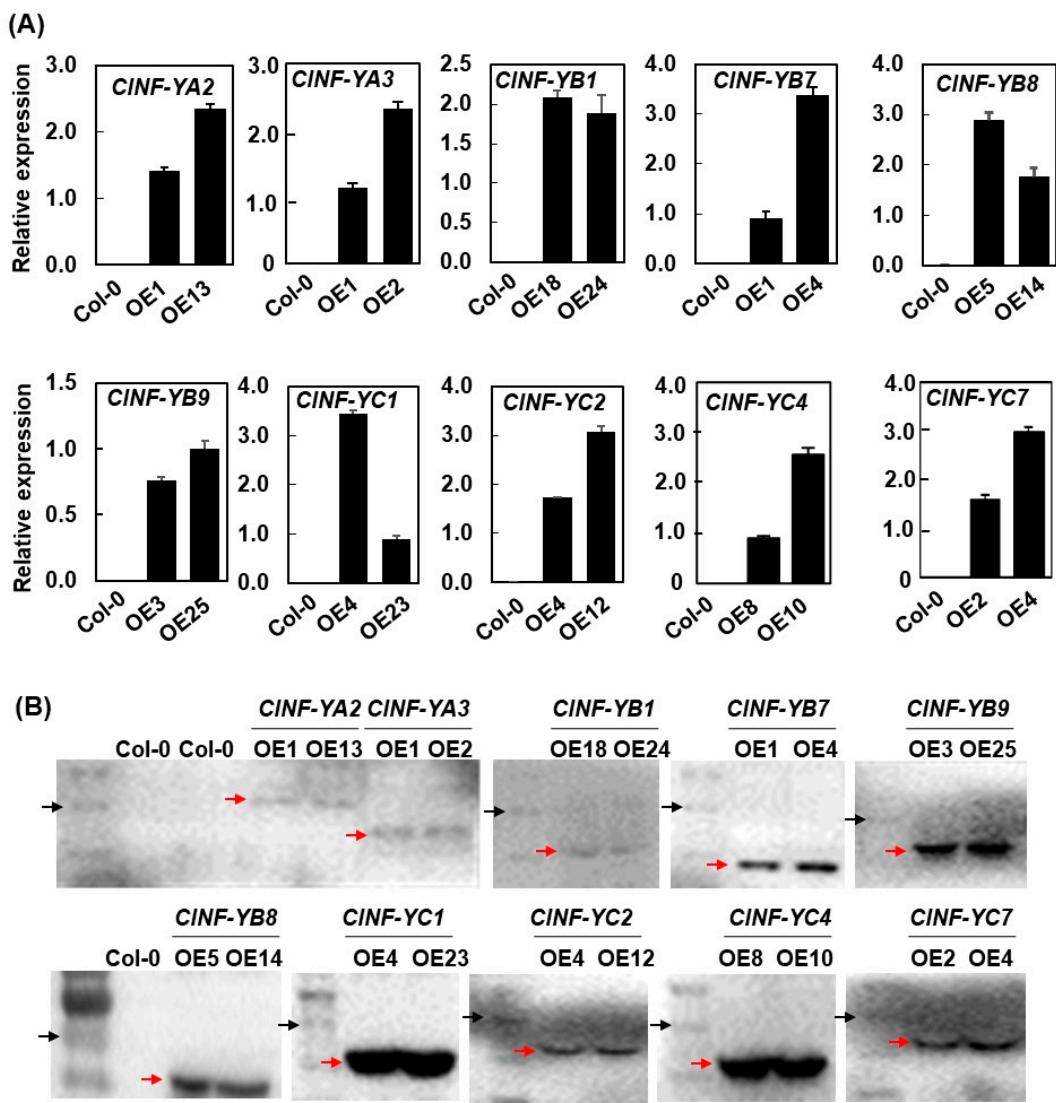


Figure S8. Characterization of the *CINF-Y*-overexpressing transgenic Arabidopsis lines. (A) Transcript levels of the *CINF-Y* genes in their corresponding transgenic Arabidopsis lines. Leaf samples were collected from four-week-old Arabidopsis plants, and qRT-PCR (B) analyses were performed with the Arabidopsis *AtActin* gene as an internal control. (B) Detection of the *CINF-Y*-GFP fusion proteins in transgenic Arabidopsis lines by Western blotting using anti-GFP antibody. Black arrows indicate the molecular weight of 63 kDa, while the red arrows indicate the target fusion proteins. Experiments were repeated three times with similar results and the data presented are the means \pm SE from three independent experiments.

Table S1. Ka/Ks ratio of the *CINF-Y* gene pairs.

Gene pairs	Ka	Ks	Ka/Ks	Types of selection
<i>CINF-YA2-CINF-YA3</i>	0.2122	0.9165	0.2315	Purifying selection
<i>CINF-YA2-CINF-YA5</i>	0.4201	1.2898	0.3257	Purifying selection
<i>CINF-YB2-CINF-YB10</i>	0.1909	1.701	0.1122	Purifying selection

Table S2. Collinear gene pairs between watermelon (*Citrullus lanatus*) and *Arabidopsis thaliana*, rice (*Oryza sativa*), and cucumber (*Cucumis sativus*), and their Ka/Ks ratios.

ID	Genes	ID	Genes	Ka	Ks	Ka/Ks
<i>Citrullus lanatus</i>		<i>Arabidopsis thaliana</i>				
Cla97C01G025170	<i>CINF-YA1</i>	AT1G30500	<i>AtNF-YA7</i>	Na	Na	Na
Cla97C01G025170	<i>CINF-YA1</i>	AT2G34720	<i>AtNF-YA4</i>	0.3314	1.8808	0.1762
Cla97C02G049270	<i>CINF-YA2</i>	AT3G20910	<i>AtNF-YA9</i>	0.3865	1.2602	0.3067
Cla97C02G049270	<i>CINF-YA2</i>	AT5G12840	<i>AtNF-YA1</i>	0.3597	2.0487	0.1756
Cla97C03G063440	<i>CINF-YA3</i>	AT3G20910	<i>AtNF-YA9</i>	0.3981	1.3213	0.3013
Cla97C03G063440	<i>CINF-YA3</i>	AT5G12840	<i>AtNF-YA1</i>	0.3820	1.5179	0.2517
Cla97C10G201180	<i>CINF-YA6</i>	AT5G06510	<i>AtNF-YA10</i>	0.3833	1.6131	0.2376
Cla97C02G039490	<i>CINF-YB2</i>	AT2G37060	<i>AtNF-YB8</i>	0.2017	3.9198	0.0515
Cla97C02G048360	<i>CINF-YB3</i>	AT2G27470	<i>AtNF-YB11</i>	Na	Na	Na
Cla97C03G067370	<i>CINF-YB4</i>	AT1G09030	<i>AtNF-YB4</i>	0.3787	1.9730	0.1919
Cla97C06G124610	<i>CINF-YB5</i>	AT5G08190	<i>AtNF-YB12</i> ,	Na	Na	Na
Cla97C09G168740	<i>CINF-YB7</i>	AT2G47810	<i>AtNF-YB5</i>	Na	Na	Na
Cla97C10G203800	<i>CINF-YB10</i>	AT2G37060	<i>AtNF-YB8</i>	0.0944	1.6693	0.0566
Cla97C10G203800	<i>CINF-YB10</i>	AT3G53340	<i>AtNF-YB10</i>	0.1578	1.8270	0.0864
Cla97C02G047110	<i>CINF-YC1</i>	AT1G07980	<i>AtNF-YC10</i>	Na	Na	Na
Cla97C03G067230	<i>CINF-YC3</i>	AT1G08970	<i>AtNF-YC9</i>	Na	Na	Na
Cla97C03G067230	<i>CINF-YC3</i>	AT1G54830	<i>AtNF-YC3</i> ,	Na	Na	Na
Cla97C06G127670	<i>CINF-YC4</i>	AT3G48590	<i>AtNF-YC1</i>	Na	Na	Na
Cla97C06G127670	<i>CINF-YC4</i>	AT5G63470	<i>AtNF-YC4</i>	0.0950	2.3127	0.0411
<i>Citrullus lanatus</i>		<i>Oryza sativa</i>				
Cla97C01G025170	<i>CINF-YA1</i>	LOC_Os12g41880	<i>OsNF-YA9</i>	0.2284	Na	Na
Cla97C10G201180	<i>CINF-YA6</i>	LOC_Os07g06470	<i>OsNF-YA5</i>	0.2892	Na	Na
Cla97C11G207940	<i>CINF-YA7</i>	LOC_Os02g53620	<i>OsNF-YA11</i>	0.3244	2.3306	0.1392
Cla97C02G039490	<i>CINF-YB2</i>	LOC_Os01g61810	<i>OsNF-YB2</i>	0.2157	Na	Na
Cla97C09G168740	<i>CINF-YB7</i>	LOC_Os01g70890	<i>OsNF-YB6</i>	0.1924	Na	Na
Cla97C10G203800	<i>CINF-YB10</i>	LOC_Os01g61810	<i>OsNF-YB2</i>	0.2101	Na	Na
Cla97C10G203800	<i>CINF-YB10</i>	LOC_Os05g38820	<i>OsNF-YB3</i>	0.0636	Na	Na
<i>Citrullus lanatus</i>		<i>Cucumis sativus</i>				
Cla97C01G025170	<i>CINF-YA1</i>	CsaV3_6G052320		0.0222	0.2111	0.1051
Cla97C02G049270	<i>CINF-YA2</i>	CsaV3_6G039350		0.0260	0.1527	0.1700
Cla97C02G049270	<i>CINF-YA2</i>	CsaV3_7G031020		0.5621	1.0997	0.5111
Cla97C03G063440	<i>CINF-YA3</i>	CsaV3_1G042800		0.0250	0.2033	0.1230
Cla97C04G068610	<i>CINF-YA4</i>	CsaV3_4G011610		0.1213	0.2783	0.4359
Cla97C09G166390	<i>CINF-YA5</i>	CsaV3_7G031020		0.0391	0.1883	0.2077
Cla97C10G201180	<i>CINF-YA6</i>	CsaV3_3G038100		0.0340	0.2110	0.1609
Cla97C02G035590	<i>CINF-YB1</i>	CsaV3_6G009670		0.0342	0.2858	0.1198
Cla97C02G039490	<i>CINF-YB2</i>	CsaV3_3G035490		0.1891	2.2902	0.0826

Cla97C02G039490	<i>CINF-YB2</i>	CsaV3_5G006310	0.0563	0.3626	0.1553
Cla97C02G048360	<i>CINF-YB3</i>	CsaV3_6G038390	0.0502	0.2052	0.2446
Cla97C03G067370	<i>CINF-YB4</i>	CsaV3_1G038920	0.1801	0.3509	0.5133
Cla97C06G124610	<i>CINF-YB5</i>	CsaV3_1G003510	0.0082	0.1965	0.0415
Cla97C07G136140	<i>CINF-YB6</i>	CsaV3_4G004940	0.0368	0.4065	0.0906
Cla97C07G136140	<i>CINF-YB6</i>	CsaV3_UNG179380	0.0368	0.4065	0.0906
Cla97C09G168740	<i>CINF-YB7</i>	CsaV3_7G028980	0.0693	0.3517	0.1971
Cla97C10G188720	<i>CINF-YB8</i>	CsaV3_3G004080	0.0228	0.3014	0.0758
Cla97C10G188900	<i>CINF-YB9</i>	CsaV3_3G004250	0.0422	0.4781	0.0882
Cla97C10G203800	<i>CINF-YB10</i>	CsaV3_3G035490	0.0124	0.0737	0.1690
Cla97C10G203800	<i>CINF-YB10</i>	CsaV3_5G006310	0.2230	1.4689	0.1518
Cla97C02G047110	<i>CINF-YC1</i>	CsaV3_6G021790	0.0788	0.1997	0.3949
Cla97C02G048620	<i>CINF-YC2</i>	CsaV3_6G038670	0.0496	0.2539	0.1953
Cla97C03G067230	<i>CINF-YC3</i>	CsaV3_1G039060	0.0067	0.1954	0.0341
Cla97C06G127670	<i>CINF-YC4</i>	CsaV3_1G000520	0.0039	0.2948	0.0133
Cla97C07G135160	<i>CINF-YC5</i>	CsaV3_4G006020	0.0260	0.5215	0.0499
Cla97C09G176240	<i>CINF-YC7</i>	CsaV3_7G006030	0.0097	0.2484	0.0390
Cla97C11G218950	<i>CINF-YC8</i>	CsaV3_5G029530	0.0264	0.2257	0.1168

Table S3. *Cis*-elements in promoters of the watermelon *CINF-Y* genes

Elements	Functions	<i>CINF-YAs</i>							<i>CINF-YBs</i>							<i>CINF-YCs</i>											
		1	2	3	4	5	6	7	1	2	3	4	5	6	7	8	9	10	1	2	3	4	5	6	7	8	
3-AF1	light responsive												1					1									
A-box	cis-acting regulatory element			1																				1		1	1
AAGAA-motif	development-related motifs	4	3	1	1	1	2		2	2	1	1		2		2				2	2	3		1	1		
ABRE3a	stress and hormonal response		1						1																		1
ABRE	abscisic acid responsiveness		5						4		1		3		2	2	1	4							1	1	2
ABRE4	stress and hormonal response		1						1																	1	
AC-II	vascular-specific expression			1																							
AACA	seed storage protein genes				1				1		1																
ACE	light responsiveness		1																							1	
AE-box	part of a module for light response								1				1		1	1				1	1				1	1	1
AP-1	regulation of ribonucleotide reductase		1																							1	
ARE	essential for anaerobic induction	4	1	2		1	3	2		5		2	1	1	5	1		1	3	6	1		2		2		
TATA	general <i>cis</i> -element		1			2		1		2	1	1	1	1	2		3								1	2	
AT~TATA-box	light responsive		1		10		5		1	3	5	15	2	2	13	2	3	2	1		1	14	1	2		5	
AT1 motif	light-responsive		1					1																			
AT-rich element	AT-rich DNA binding protein								1	1		1		1											1		
AT-rich	elicitor-mediated activation																1										
AAAC-motif	light responsive element	1															1										
ATCT-motif	light responsive					1			1								1	1							1		
AuxRR-core	auxin responsive								1		1						1									1	
Box 4	light responsive		5	3	3		2		1	1	1	4	2	2	2	2	7	4	2	1	2	1	5	1		4	
CAAT-box	common cis-acting element	22	41	27	27	14	35	33	30	23	28	37	43	21	24	38	32	24	25	17	24	26	30	48	26	33	

CAT-box	related to meristem expression						1	1					2					1								1
CARE	involved in viral DNA replication								1									1								
CCAAT-box	MYBHv1 binding site		1		1					1					1							1				
CCGTCC-motif	related to meristem specific activation		1																				1		1	1
CCGTCC-box	meristem specific activation			1																			1	1	1	
CGTCA-motif	MeJA-responsive			1		1	1		1			3					3	1			2	1		1	1	
CTAG-motif	rearrange the free energy						1			1	1										1					
DRE core	dehydration-responsive	1																	2		1					
F-box	involved in abiotic stress																								3	
ERE	ethylene-responsive				1	3	1				1			1	1	3	2	1	3	1			2	4		1
G-Box	light responsive		1						1		1			2		1	1		1	1				1		1
G-box	light responsive	2	3		1			4					3	1	2	1	1	2	1							1
GC-motif	waterlogging stress pathways																								1	
GA-motif	light responsive								1							1									1	
GARE-motif	gibberellin-responsive						1	1	1																1	
GATA-motif	part of a light responsive element	1		1	1	1	2			1					1	1		1	1							
GCN4_motif	involved in endosperm expression							1							2		1	1		1						
GT1-motif	light responsive	4	2	3			1	1	1	1	1	2					2	1	2	2	1				1	
Gap-box	necessary for light responsiveness				1													1				1				
I-box	part of a light responsive element	1												1	1							1		1		
LAMP-element	light responsive	1		1				1									1	1								
LTR	low-temperature responsive	1				3	1				1											2				
MBS	involved in drought-inducibility	2				1	1	2			2		1	1		1			1	1				1		
MBSI	flavonoid biosynthetic genes																							1		
MRE	light responsive	2			1			1					1	1	1		3				1		1			

Myc	water and drought responsive	2			1	1			1		1				1									1		
MYC	abiotic stress responses	2	1	1	3		5	3	2	4	1	4	3			3	4	1	1		5	5	3	9	3	6
Myb-binding site	activation of lysozyme enhancer	1		2		1	2	1	1							1			1		1			1	1	1
Myb	stress-associated	2	1	1		2	1	2			2		1	1		2			2		2					1
MYB	development and stress response	5	1	4		2	3	2	2	2	1	1	4	1	1	6	1	2	2	2	5	2	1	3	1	3
MYB recognition	DNA-binding specificities			1		1					1				1					1						
MYB-like	sequence-specific DNA binding	3	1	2			1	1		1	1		1			4	1	2	1	1		1		1		
MSA-like	cell cycle regulation																									
O2-site	zein metabolism regulation				2				1			1									1	1		1		
P-box	gibberellin-responsive element	2		1			1					1				1			1				1	1		
RY-element	seed-specific regulation					1											1									
Sp1	light responsive element								1					1				1								
TATA-box	core promoter element	15	38	12	52	39	20	22	9	26	36	61	50	33	54	20	39	16	24	27	25	56	35	29	10	68
TATC-box	gibberellin-responsive	1	1		1								1													
TC-rich repeats	defense and stress responsive		1			1		1			1			1									1			
TCA	salicylic acid responsive					1		1			2	1					1			2				1		
TCA-element	salicylic acid responsive						1	2				3	1	1		1	2		2	1	1		3		1	2
TCCC-motif	light responsive	1		1						1		1														
TCT-motif	part of a light responsive element	1	1						1	1		1		2				1					1		1	
TGA-element	auxin-responsive	1						1	1								2				2	1	1			
TGACG-motif	MeJA-responsive						1	1		1		3					3	1			2	1	1	1		
Unnamed 1	CGTGG	1	3						3		1		5	1	1	3	2		1	1					1	
Unnamed_1	GAATTAAATTAA																								1	
Unnamed_1	GGATTTCAGT																									
Unnamed_2	AACCTAACCT	1				1						1		1		1										

Unnamed_4	CTCC	11	3	8	5	16	10	3	11	8	8	10	5	7	5	10	2	9	8	1	5	8	12	6	1	2	
Unnamed_6	taTAAATATCT		1				1		1				1				1									2	
Unnamed_8																										1	
Unnamed_10																										1	
Unnamed_12																										1	
Unnamed_14																										1	
W box	hormone-mediated signaling	1						1	2	1				2			2	2		2			1	1	1		
WUN-motif	wound-responsive		3			1		1					1	2						1					1	1	
box S	pathogen-inducible	1			1												1	1									
chs-CMA1a	light responsive		1											1									1			1	1
chs-CMA2a	light responsive												1	1					1		1						
circadian	circadian control																1										
STRE	stress response	2	2	2		2	4	1	2				2	2	2	1	1	1	4	3	1	1	3	1	5	1	
WRE3	stress responsive	1					1							1		2	1										
as-1	development-related motifs					1	1		1		3							3	1			2	1		1	1	
Plant Ap-2-like	floret development							1																			
re2f-1												1														1	
Subtotal	Excluding CAAT- and TATA-boxes	63	47	43	33	45	56	31	52	42	49	52	55	35	48	62	52	49	35	24	39	57	41	43	46	36	
TOTAL		100	126	82	112	98	111	86	91	91	113	150	148	89	126	120	123	89	84	68	88	139	106	120	82	137	

Note: Growth- and development-related *cis*-elements are labeled with red color; hormone-responsive *cis*-elements are indicated with blue color; abiotic and biotic stress-responsive *cis*-elements are shown in purple color.

Summary: Total *cis*-elements for *CINF-Y* gene promoters: 2679; total *cis*-elements for *CINF-Y* gene promoters excluding CAAT- and TATA-boxes: 1135; average of *cis*-elements for *CINF-Y* gene promoters excluding CAAT- and TATA-boxes: 45.4

Table S4. Primers used in this study.

Primer names	Sequence (5'-3')	Size (bp)
Cloning		
CINF-YA1-F	ATGGCCTCCTATATAATGGTGA	603
CINF-YA1-R	TCAGTTCTCTGACGAAGCAAG	
CINF-YA2-F	ATGCAGTCGAAGTCTAAAAGTG	1026
CINF-YA2-R	TCACTTGATGGCAAGACGCC	
CINF-YA3-F	ATGCAGTCAAAGTCTGAAACC	810
CINF-YA3-R	CTATTCTGAGGCCTGTTGT	
CINF-YA4-F	ATGATGAGCCCTGAAATAGAT	615
CINF-YA4-R	TCATATATGAGATAAATGTAG	
CINF-YA5-F	ATGCAATCAAAACCAGAAAATG	1026
CINF-YA5-R	TCAATTGATGGGGATGGCCCT	
CINF-YA6-F	ATGGCACCAACAACTGGCTATTG	1167
CINF-YA6-R	TTACTTCATACTTGATATCTGA	
CINF-YA7-F	ATGACAATGACTTGTCTGATAA	903
CINF-YA7-R	CTATGTTCCGTTCCGCCAT	
CINF-YB1-F	ATGGCGGATTCTGATAACGAATC	618
CINF-YB1-R	CTACCGGTGTCCGGTGCC	
CINF-YB2-F	ATGGCGGAGCCTCCCACCAAGT	498
CINF-YB2-R	TTAGAGAAGAGAGATTATTACTTG	
CINF-YB3-F	ATGGGAGATCAGCATAATGG	405
CINF-YB3-R	TTAAAATTGATTATTGTGTTCTG	
CINF-YB4-F	ATGAGCGGCCACAAACGAAAC	678
CINF-YB4-R	TCACCAACCAGAGCTCTGTT	
CINF-YB5-F	ATGGATGAAAACACAGGCATG	480
CINF-YB5-R	TCATGCATCATGATTATTATTAG	
CINF-YB6-F	ATGTTGCTGACCCCAAACAAGC	627
CINF-YB6-R	TCAAAGCTGGTACCAATTCC	
CINF-YB7-F	ATGGCTGACTCCGACAACGATTC	528
CINF-YB7-R	CTACCTGGGCCGACCCGTA	
CINF-YB8-F	ATGGCTGATGCTCCGGCGAGT	528
CINF-YB8-R	TTAATGCATATTATTATTCGAGAG	
CINF-YB9-F	ATGGAGAAAAAAAGTAGGTGCC	486
CINF-YB9-R	TCAGTTATCACTGGCGCCAAT	
CINF-YB10-F	ATGACAAAATTATCAAAGAG	411
CINF-YB10-R	TTAGCTCTCTAAACTTGCTCAG	
CINF-YC1-F	ATGGATCAGCAAGGGCATGGC	783
CINF-YC1-R	CTATTGATCAGGAGGGGTTG	
CINF-YC2-F	ATGGACACCAACAATCAAGCCC	663
CINF-YC2-R	CTACCTCTGACCATCAAGAT	
CINF-YC3-F	ATGAGGCAAGCGGGAGCAT	
CINF-YC3-R	TCAGCAAGGAATGGACATAGT	354

CINF-YC4-F	ATGGATCAATCAGAGCGTTCTC	801
CINF-YC4-R	CTATGCATCACTTGCTGCTGA	
CINF-YC5-F	ATGCAAGCTGATGAAGATGTAG	792
CINF-YC5-R	CTAACCTTCTCGTCGTAATCT	
CINF-YC6-F	ATGGCTTCATCCAAAAAGTC	603
CINF-YC6-R	CTATAACAACCAATGAAAATAGA	
CINF-YC7-F	ATGGAGGAAGAGGAAACC	423
CINF-YC7-R	CTATGACTCGTTGGTCTCCG	
CINF-YC8-F	ATGCAAGCAGATGAGGATGTTG	801
CINF-YC8-R	TTACTCCTCTTCATCATAATCTTC	
<hr/>		
<i>OE vectors</i>		
CINF-YA1-GFP-F	CCCGAGCTCATGGCCTCCTATATAATGGTGA	603
CINF-YA1-GFP-R	CCCGGTACCGTTCTCTGACGAAGCAAGATCG	
CINF-YA2-GFP-F	CCCGAGCTCATGCAGTCGAAGTCTAAAAGTG	1026
CINF-YA2-GFP-R	CCCGGTACCCTTGATGGCAAGACGCCTCTG	
CINF-YA3-GFP-F	CCCGAGCTCATGCAGTCAAAGTCTGAAACC	810
CINF-YA3-GFP-R	CCCGGTACCTCTGAGGCCCTGTTGTCAAG	
CINF-YA4-GFP-F	CCCGAGCTCATGATGAGCCCTGAAATAGAT	615
CINF-YA4-GFP-R	CCCGGTACCTATATATGCAGATAAAATGTAGTTG	
CINF-YA5-GFP-F	CCCGAGCTCATGCAATCAAAACCAGAAAATG	1026
CINF-YA5-GFP-R	CCCGGTACCATTGATGGGATGGCCCTCTG	
CINF-YA6-GFP-F	CCCGAGCTCATGGCACCAACTGGCTATTG	1167
CINF-YA6-GFP-R	CCCGGTACCCTTCATACTGATATCTGATTGG	
CINF-YA7-GFP-F	CCCGAGCTCATGACAATGACTTGTCTGATAA	903
CINF-YA7-GFP-R	CCCGGTACCTGTTCCGTTCCGCCATGTAC	
CINF-YB1-GFP-F	CCCGAGCTCATGGCGGATTCTGATAACGAATC	618
CINF-YB1-GFP-R	CCCGGTACCCCGGTGTCGGTGCCGGAAC	
CINF-YB2-GFP-F	CCCGAGCTCATGGCGGAGCCTCCCACCACT	498
CINF-YB2-GFP-R	CCCGGTACCGAGAAGAGAGATTATTACTTG	
CINF-YB3-GFP-F	CCCGAGCTCATGGGAGATCAGCATAATGG	405
CINF-YB3-GFP-R	CCCGGTACCAAATTGATTATTGTGTTCTTG	
CINF-YB4-GFP-F	AGCTTCGCGAGCTCGGTACCATGAGCGGCCACAAAC	678
	GAAAC	
CINF-YB4-GFP-R	GCCCTTGCTACCATGGTACCCAACCAGAGCTCTGTT	
	GAAG	
CINF-YB5-GFP-F	AGCTTCGCGAGCTCGGTACCATGGATGAAAACACAG	480
	GCATG	
CINF-YB5-GFP-R	GCCCTTGCTACCATGGTACCTGCATCATGATTATTATT	
	ATTAG	
CINF-YB6-GFP-F	CCCGAGCTCATGTTGCTGACCCAAACAAGC	627
CINF-YB6-GFP-R	CCCGGTACCAAGCTGGCTACCATTCCCCGC	
CINF-YB7-GFP-F	CCCGAGCTCATGGCTGACTCCGACAACGATTG	528
CINF-YB7-GFP-R	CCCGGTACCCCTGGGCCGACCCGTAGTAG	
CINF-YB8-GFP-F	CCCGAGCTCATGGCTGATGCTCCGGCGAGT	528

CINF-YB8-GFP-R	CCCGGTACCATGCATATTATTATTTCGAGAG	
CINF-YB9-GFP-F	CCCGAGCTCATGGAGAAAAAAGTAGGTGCC	486
CINF-YB9-GFP-R	CCCGGTACCGTTACTGGCGCCAATTTC	
CINF-YB10-GFP-F	CCCGAGCTCATGACCAAAATTATCAAAGAG	411
CINF-YB10-GFP-R	CCCGTACCGCTCTAAACTTGCTCAG	
CINF-YC1-GFP-F	AGCTTCGCGAGCTCGGTACCATGGATCAGCAAGGGC	783
	ATGGC	
CINF-YC1-GFP-R	GCCCTTGCTCACCATGGTACC	
	TTGATCAGGAGGGGTTGATC	
CINF-YC2-GFP-F	AGCTTCGCGAGCTCGGTACCATGGACACCAACAATCA	663
	AGCCC	
CINF-YC2-GFP-R	GCCCTTGCTCACCATGGTACC	
	CCTCTGACCATCAAGATTACC	
CINF-YC3-GFP-F	CCCGAGCTCATGAGGAAGCGGGAGCAT	354
CINF-YC3-GFP-R	CCCGTACCGCAAGGAATGGACATAG	
CINF-YC4-GFP-F	CCCGAGCTCATGGATCAATCAGAGCGTTCTC	801
CINF-YC4-GFP-R	CCCGTACCTGCATCACTTGCTGCTGAGTTG	
CINF-YC5-GFP-F	CCCGAGCTCATGCAAGCTGATGAAGATGTAG	792
CINF-YC5-GFP-R	CCCGTACACCTCTTCGTCGTAATCTTCC	
CINF-YC6-GFP-F	CCCGAGCTCATGGCTTCATCCAAAAAGTC	603
CINF-YC6-GFP-R	CCCGTACCTAACACCAATGAAAATAGAC	
CINF-YC7-GFP-F	AGCTTCGCGAGCTCGGTACCATGGAGGAAGAGGAAA	423
	CC	
CINF-YC7-GFP-R	GCCCTTGCTCACCATGGTACCTGACTCGTTGGCTCCG	
	C	
CINF-YC8-GFP-F	CCCGAGCTCATGCAAGCAGATGAGGATGTTG	801
CINF-YC8-GFP-R	CCCGTACCTCCTCTTCATCATAATCTTC	

BiFC assays

CINF-YB1-P2YN-1F	CCCTTAATTAACATGGCGGATTCTGATAACGAATC	618
CINF-YB1-P2YN-1R	GGGACTAGTCCGGTGTCCGGTGCCG	
CINF-YB2-P2YN-1F	CCCTTAATTAACATGGCGGAGCCTCCCA	498
CINF-YB2-P2YN-1R	GGGACTAGTGAGAAGAGAGATTATTACTGAGTGTGTTA	
CINF-YB3-P2YN-1F	CCCTTAATTAACATGGGAGATCAGCATAATGGG	405
CINF-YB3-P2YN-1R	GGGACTAGTAAATTGATTATTGTGTTCTGTTCATC	
CINF-YB4-P2YN-1F	CCCTTAATTAACATGAGCGGCCACAAACGAAACT	678
CINF-YB4-P2YN-1R	GGGACTAGTCCAACCAGAGCTCTGTTGAAGATG	
CINF-YB5-P2YN-1F	CCCTTAATTAACATGGATGAAAACACAGGCA	480
CINF-YB5-P2YN-1R	GGGACTAGTTGCATCATGATTATTATTAGTATTA	
CINF-YB6-P2YN-1F	CCCTTAATTAACATGTTGCTGACCCAAACAAAGC	627
CINF-YB6-P2YN-1R	GGGACTAGTAAAGCTGGCTACCATTCCCCG	
CINF-YB7-P2YN-1F	CCCTTAATTAACATGGCTGACTCCGACAACGATC	528
CINF-YB7-P2YN-1R	GGGACTAGTCCTGGGCCGACCCGTAGTAGTA	
CINF-YB8-P2YN-F	CCCTTAATTAACATGGCTGATGCTCCGGC	528
CINF-YB8-P2YN-R	GGGACTAGTATGCATATTATTTCGAGAGTGTCTGT	

CINF-YB9-P2YN-F	CCCTTAATTAACATGGAGAAAAAAAGTAGGTGCCGG	486
CINF-YB9-P2YN-R	GGGACTAGTGTATCACTGGCGCCAATTTCAT	
CINF-YB10-P2YN-F	CCCTTAATTAACATGACCAAAATTATCAAAGAGATGTT	411
	ACC	
CINF-YB10-P2YN-R	GGGACTAGTGCTCTCTAAACTTGCTCAGGCTCC	
CINF-YC1-P2YC-F	CCCTTAATTAACATGGATCAGCAAGGGCATGG	783
CINF-YC1-P2YC-R	GGGACTAGTTGATCAGGAGGGTTGATCTTG	
CINF-YC2-P2YC-F	CCCTTAATTAACATGGACACCAACAATCAAGCC	663
CINF-YC2-P2YC-R	GGGACTAGTCCTCTGACCATCAAGATTACCC	
CINF-YC3-P2YC-F	CCCTTAATTAACATGAGGCAAGCGGGAGCA	354
CINF-YC3-P2YC-R	GGGACTAGTGCAAGGAATGGACATAGTTCAGTT	
CINF-YC4-P2YC-F	CCCTTAATTAACATGGATCAATCAGAGCGTTCTCAG	801
CINF-YC4-P2YC-R	GGGACTAGTTGCATCACTTGCTGCTGAGTTT	
CINF-YC5-P2YC-F	CCCTTAATTAACATGCAAGCTGATGAAGATGTAGGG	792
CINF-YC5-P2YC-R	GGGACTAGTACCTCTCGTCGTAATCTTCCTCG	
CINF-YC6-P2YC-F	CCCTTAATTAACATGGCTTCATCCAAAAAGTCAA	603
CINF-YC6-P2YC-R	GGGACTAGTTAACACCAATGAAAATAGACAGCAG	
CINF-YC7-P2YC-F	CCCTTAATTAACATGGAGGAAGAGGAAACCGG	423
CINF-YC7-P2YC-R	GGGACTAGTTGACTCGTTGGTCTCCGCC	
CINF-YC8-P2YC-F	CCCTTAATTAACATGCAAGCAGATGAGGATGTTG	801
CINF-YC8-P2YC-R	GGGACTAGTCTCCTCTTCATCATAATCTTCCTCTTC	

Y3H assays

CINF-YA1-AD-F	GCCATGGAGGCCAGTGAATTCATGGCCTCCTATATAA	603
	TGGTGA	
CINF-YA1-AD-R	ATGCCCACCCGGGTGGAATTCTCAGTTCTCTGACGAAG	
	CAAGA	
CINF-YA2-AD-F	GCCATGGAGGCCAGTGAATTCATGCAGTCGAAGTCTA	1026
	AAAGTG	
CINF-YA2-AD-R	ATGCCCACCCGGGTGGAATTCTCACTTGATGGCAAGAC	
	GCC	
CINF-YA3-AD-F	GCCATGGAGGCCAGTGAATTCATGCAGTCAAAGTCTG	810
	AAACC	
CINF-YA3-AD-R	ATGCCCACCCGGGTGGAATT CCTATTCTGAGGCCTTGT	
	TTGT	
CINF-YA4-AD-F	GCCATGGAGGCCAGTGAATTCATGATGAGCCCTGAAA	615
	TAGATT	
CINF-YA4-AD-R	ATGCCCACCCGGGTGGAATTCTCATATATATGCAGATA	
	AATGTAG	
CINF-YA5-AD-F	CCCGAATTCATGCAATCAAACCAAGAAAATGT	1026
CINF-YA5-AD-R	CCCGAATTCTCAATTGATGGGGATGGCCCT	
CINF-YA6-AD-F	CCCGAATTCATGGCACCAAACTGGCTA	1167
CINF-YA6-AD-R	CCCGAATTCTTACTTCATACTTGATATCTGA	
CINF-YA7-AD-F	GCCATGGAGGCCAGTGAATTCATGACAATGACTTGTGTC	903
	TGATA	

CINF-YA7-AD-R	ATGCCACCCGGGTGGAATTCTATGTTCCGTTCCGC CAT	
CINF-YC1-BD-F	CCCGAATTCATGGATCAGCAAGGGCATGG	783
CINF-YC1-BD-R	CCCGAATTCTATTGATCAGGAGGGTTG	
CINF-YC2-BD-F	ATGCCATGGAGGCCAATTGACACCAACAATC AAGCC	663
CINF-YC2-BD-R	TCGACGGATCCCCGGGAATTCTACCTCTGACCATCAA GAT	
CINF-YC3-BD-F	CCCGAATTCATGAGGCAAGCAGGGAGCAT	354
CINF-YC3-BD-R	CCCGAATTCTCAGCAAGGAATGGACATAGT	
CINF-YC4-BD-F	CCCGAATTCATGGATCAATCAGAGCAGTCTC	801
CINF-YC4-BD-R	CCCGAATTCTATGCATCACTTGCTGCTGA	
CINF-YC5-BD-F	CCCGAATTCATGCAAGCTGATGAAGATGTAG	792
CINF-YC5-BD-R	CCCGAATTCTAACCTCTCGTCGTAATCT	
CINF-YC6-BD-F	CCCGAATTCATGGCTTCATCCAAAAAGTCAA	603
CINF-YC6-BD-R	CCCGAATTCTATAACAACCAATGAAAATAGA	
CINF-YC7-BD-F	ATGCCATGGAGGCCAATTGAGGAAGAGGAAA CCGG	423
CINF-YC7-BD-R	TCGACGGATCCCCGGGAATTCTATGACTCGTTGGTCT CCG	
CINF-YC8-BD-F	ATGGCCATGGAGGCCAATTGCAAGCAGATGAGG ATGTTG	801
CINF-YC8-BD-R	TCGACGGATCCCCGGGAATTCTACTCCTCTTCATCAT AATCTTC	
CINF-YB1-pBridge-F	CCCGAATTCATGGCGGATTCTGATAACGAA	618
CINF-YB1-pBridge-R	CCCGAATTCTACCGGTGTCCGGTGCC	
CINF-YB2-pBridge-F	TTGACTGTATGCCGGATTGAGCGGAGCCTCCCAC CAGT	498
CINF-YB2-pBridge-R	TCGACGGATCCCCGGGAATTCTTAGAGAAGAGAGATT ATTACTTG	
CINF-YB3-pBridge-F	CCCGAATTCATGGAGATCAGCATAATGG	405
CINF-YB3-pBridge-R	CCCGAATTCTAAAATTGATTATTGTGTTCTTG	
CINF-YB4-pBridge-F	TTGACTGTATGCCGGATTGAGCGGCCACAAACG AAAC	678
CINF-YB4-pBridge-R	TCGACGGATCCCCGGGAATTCTCACCAACCAGAGCTCT GTTG	
CINF-YB5-pBridge-F	CCCGAATTCATGGATGAAAACACAGGCATGTC	480
CINF-YB5-pBridge-R	CCCGAATTCTCATGCATCATGATTATTATTATTAG	
CINF-YB6-pBridge-F	TTGACTGTATGCCGGATTGAGCGGCCACAAACG CAAGC	627
CINF-YB6-pBridge-R	TCGACGGATCCCCGGGAATTCTCAAAGCTGGCTACCAT TCCCC	
CINF-YB7-pBridge-F	CCCGAATTCATGGCTGACTCCGACAAACGAT	528

CINF-YB7-pBridge-R	CCCGAATT CCTACCTGGGCCGACCCGTA	
CINF-YB8-pBridge-F	CCCGAATT CATGGCTGATGCTCCGGCGA	528
CINF-YB8-pBridge-R	CCCGAATT CTTAATGCATATTATTATTCGAGAG	
CINF-YB9-pBridge-F	TTGACTGTATGCCCGAATT CATGGAGAAAAAAAGTAG	486
	GTGCC	
CINF-YB9-pBridge-R	TCGACGGATCCCCGGGAATTCTCAGTTATCACTGGCGC	
	CAATT	
CINF-YB10--pBridge-F	CCCGAATT CATGACCAAAATTATCAAAGAGATG	411
CINF-YB10--pBridge-R	CCCGAATT CTTAGCTCTCTAAACTTGCTCAG	
CINF-YC1-pBridge-F	CCCGCGGCCGCAATGGATCAGCAAGGGCATGG	783
CINF-YC1-pBridge-R	CCCAGATCTCTATTGATCAGGAGGGGTTG	
CINF-YC2-pBridge-F	CCCGCGGCCGCAATGGACACCAACAATCAAGCC	663
CINF-YC2-pBridge-R	CCCAGATCTCTACCTCTGACCATCAAGAT	
CINF-YC3-pBridge-F	CCCGCGGCCGCAATGAGGCAAGCGGGAGCAT	354
CINF-YC3-pBridge-R	CCCAGATCTTCAGCAAGGAATGGACATAGT	
CINF-YC4-pBridge-F	CCCGCGGCCGCAATGGATCAATCAGAGCGTTCTC	801
CINF-YC4-pBridge-R	CCCAGATCTCTATGCATCACTTGCTGCTGA	
CINF-YC5-pBridge-F	CCCGCGGCCGCAATGCAAGCTGATGAAGATGTAG	792
CINF-YC5-pBridge-R	CCCAGATCTCTAACCTCTCGTCGTAATCT	
CINF-YC6-pBridge-F	CCCGCGGCCGCAATGGCTTCATCCAAAAAGTCAA	603
CINF-YC6-pBridge-R	CCCAGATCTCTATAACAACCAATGAAAATAGA	
CINF-YC7-pBridge-F	CCCGCGGCCGCAATGGAGGAAGAGGAAACCGG	423
CINF-YC7-pBridge-R	CCCAGATCTCTATGACTCGTTGGTCTCCG	
CINF-YC8-pBridge-F	CCCGCGGCCGCAATGCAAGCAGATGAGGATGTTG	801
CINF-YC8-pBridge-R	CCCAGATCTTACTCCTCTTCATCATAATCTTC	

RT-qPCR

CINF-YA1-RT-F	GGTGGACGGTTCTCAA	110
CINF-YA1-RT-R	GCAAGATCGCTTCTATCAGA	
CINF-YA2-RT-F	GCAGTAGCCAATTCCATAA	105
CINF-YA2-RT-R	CACTTCGCTGCTGTCCC	
CINF-YA3-RT-F	TGGAGGACGTTTGCTA	112
CINF-YA3-RT-R	GCTTCCGTTCTGCTGTT	
CINF-YA4-RT-F	GATGATGATGATGTGGAAGG	100
CINF-YA4-RT-R	CAGATAAAATGTAGTTGGGAAG	
CINF-YA5-RT-F	ACTCAAAATATGCAGATAACAC	144
CINF-YA5-RT-R	TGGAGCCCCATTCACTT	
CINF-YA6-RT-F	GATAGTCCCCGCGTTG	130
CINF-YA6-RT-R	GGATGATTCTTGTGTTCTC	
CINF-YA7-RT-F	GAUTGCAACTTGCTCCG	115
CINF-YA7-RT-R	ATACTGCTCCATTCTCCC	
CINF-YB1-RT-F	CGGCAGTGGGACAAATA	149
CINF-YB1-RT-R	CACCAGCACCATAAACG	
CINF-YB2-RT-F	CGACGTTGGGATTGAG	148

C1NF-YB2-RT-R	TGCTGGGAATTTGACC	
C1NF-YB3-RT-F	ATGGCTTAGATAACTATGCTG	109
C1NF-YB3-RT-R	TGTAGTTGTTGAGTAATTTC	
C1NF-YB4-RT-F	TCAGGGAAACCAGAAGA	131
C1NF-YB4-RT-R	GAAGATGAGCCGCCATA	
C1NF-YB5-RT-F	TGATGATATTGCTGTGCT	119
C1NF-YB5-RT-R	ATCCCTTATTGTTGAGC	
C1NF-YB6-RT-F	GCATTTCAAATAGGGCACG	105
C1NF-YB6-RT-R	AAGCTGGCTACCATTCC	
C1NF-YB7-RT-F	GGCGGTGGGAATTGG	112
C1NF-YB7-RT-R	ACCTGGGCCACCCGTAGT	
C1NF-YB8-RT-F	CTGCTAAAGGTGGTGATGC	139
C1NF-YB8-RT-R	AGTACTTGAGAACTCGCATAA	
C1NF-YB9-RT-F	GCAAGAATGCCGGAAAG	117
C1NF-YB9-RT-R	TCGGCTTCATCATTATCC	
C1NF-YB10-RT-F	AAGGTGGGAAGTGGAGTA	115
C1NF-YB10-RT-R	GCTTCGGTGCAGTGT	
C1NF-YC1-RT-F	GGTAAGCCTGTGATGGAC	100
C1NF-YC1-RT-R	GATCAGGAGGGGTTGA	
C1NF-YC2-RT-F	GGAGACCGGCAATGGAT	103
C1NF-YC2-RT-R	CCACTCGCGTAAGAAC	
C1NF-YC3-RT-F	GGCCACTGATGTTTCG	101
C1NF-YC3-RT-R	AGCAAGGAATGGACATAGTT	
C1NF-YC4-RT-F	ATGGGAAGCAATTAGAT	104
C1NF-YC4-RT-R	TGCTGCTGAGGTTGAGTAT	
C1NF-YC5-RT-F	CGAATATCCTGGTGGTC	102
C1NF-YC5-RT-R	TCGTAATCTCCTCGTCAT	
C1NF-YC6-RT-F	ATCGGATCAAGAAAATCAT	132
C1NF-YC6-RT-R	GAGCACAGCACGCATAT	
C1NF-YC7-RT-F	ACTCGCACTGTCGTTGA	105
C1NF-YC7-RT-R	CTATGACTCGTTGGTCTCC	
C1NF-YC8-RT-F	TACCACCACCACCAAGCAG	101
C1NF-YC8-RT-R	AGGCCAGGCAGGGAATT	
C1GAPDH-F	ATGGGCAAAGTTAAGATCGGCATCA	91
C1GAPDH-R	CCAATTGATATCATCACTCTGC	
AtPR1-RT-F	TCGTCTTGTAGCTCTGTAGGTG	120
AtPR1-RT-R	TAGATTCTCGTAATCTCAGCTCT	
AtPR5-RT-F	ATGGCA AATATCTCCAGTATTACA	125
AtPR5-RT-R	ATGTCGGGCAAGCCCGTTGAGG	
AtActin-F	GGCGATGAAGCTCAATCCAAACG	110
AtActin-R	GGTCACGACCAGCAAGATCAAGACG	