

**Table S1.** Sequences of primers.

Primer	Sequence (5'-3')	Remarks
<i>TeAPI-1</i> -full-F	TCTCACCTGCCACCAAACCTA	Full-length gene cloning
<i>TeAPI-1</i> -full-R	TCACCGGCTTGTCGATCAGT	Full-length gene cloning
<i>TeAPI-2</i> -full-F	ACTCAACCCACCTCACCTACACA	Full-length gene cloning
<i>TeAPI-2</i> -full-R	GGCTCACTAGATCATTTTACGAAGG	Full-length gene cloning
<i>TeFUL1</i> -full-F	CGGAGATAGAAATGGGACGG	Full-length gene cloning
<i>TeFUL1</i> -full-R	ATACTACGGTGTCCAAACGT	Full-length gene cloning
<i>TeFUL2</i> -full-F	TAAGATGGGAAGAGGCAGAGTG	Full-length gene cloning
<i>TeFUL2</i> -full-R	GGCCTTCGGATTTTACTGGTTA	Full-length gene cloning
<i>TeFUL3</i> -full-F	TAAGCGGTGGTTGTTTCCGG	Full-length gene cloning
<i>TeFUL3</i> -full-R	CCGGCCGATAAAATTACATGCACAT	Full-length gene cloning
RT- <i>ACT</i> -F	GGGAAATGAATGCCAAAGCCAAG	QRT-PCR, Semi-PCR
RT- <i>ACT</i> -R	AAGACTTCACAACCACTCTCCAAT	QRT-PCR, Semi-PCR
qRT- <i>TeAPI-1</i> -F	GACACCGATACAACCTTCCTCA	QRT-PCR, Semi-PCR
qRT- <i>TeAPI-1</i> -R	CATCACCTCCTTCGCCGCTA	QRT-PCR, Semi-PCR
qRT- <i>TeAPI-2</i> -F	ATGCTGGCGGTGGTGGTGAA	QRT-PCR, Semi-PCR
qRT- <i>TeAPI-2</i> -R	TCATTTTACGAAGGAAAGCACC	QRT-PCR, Semi-PCR
qRT- <i>TeFUL1</i> -F	AGGAGAAAGAGTTAGAACAACAGGC	QRT-PCR, Semi-PCR
qRT- <i>TeFUL1</i> -R	GGTTGACCTTCTCTTGGGTTCTC	QRT-PCR, Semi-PCR
qRT- <i>TeFUL2</i> -F	CCAGCAGTGGACCATTCATTG	QRT-PCR
qRT- <i>TeFUL2</i> -R	GCGGCAGATACATTATGAGTTTGAG	QRT-PCR
qRT- <i>TeFUL3</i> -F	CTTATGGACCAGCACTCACAT	QRT-PCR, Semi-PCR
qRT- <i>TeFUL3</i> -R	GCATTTCTTCTGTTTCTCCGTTAC	QRT-PCR, Semi-PCR
RT- <i>TeFUL2</i> -F	ATAAGGCACTATGCTGGGAAGA	Semi-PCR
RT- <i>TeFUL2</i> -R	GCGGATCATCCATAGCGGAA	Semi-PCR
AD-F	CTATTCGATGATGAAGATACCCCAACCAACCC	Yeast two-hybrid
AD-R	GTGAACTTGCGGGGTTTTTCAGTATCTACGATT	Yeast two-hybrid
BD-F	TCATCGGAAGAGAGTAG	Yeast two-hybrid
BD-R	GAGTCACTTTAAATTTGTAT	Yeast two-hybrid
AD/BD- <i>TeAPI-1</i> -F	<b>CATATGATGGGTAGAGGTAAGGTACA</b>	Yeast two-hybrid
AD/BD- <i>TeAPI-1</i> -R	<b>GAATTCTTATGAAGGAAAACACCTCA</b>	Yeast two-hybrid
AD/BD- <i>TeAPI-2</i> -F	<b>CATATGATGGGTAGAGGTAAGGTACA</b>	Yeast two-hybrid
AD/BD- <i>TAPI-2</i> -R	<b>GAATTCTTACGAAGGAAAGCACCTCA</b>	Yeast two-hybrid
AD/BD- <i>TeFUL1</i> -F	<b>CATATGATGGGAAGAGGAAGAGTAACATTGA</b>	Yeast two-hybrid
AD/BD- <i>TeFUL1</i> -R	<b>GAATTCTTATATAATATGATCTACTGGCCGG</b>	Yeast two-hybrid
AD/BD- <i>TeFUL2</i> -F	<b>CATATGATGGGAAGAGGCAGAGTGC</b>	Yeast two-hybrid
AD/BD- <i>TeFUL2</i> -R	<b>GAATTCTTACTGGTTAATGTGGCGGA</b>	Yeast two-hybrid
AD/BD- <i>TeFUL3</i> -F	<b>CATATGATGGGAAGAGGAAGAGTAACATTGA</b>	Yeast two-hybrid
AD/BD- <i>TeFUL3</i> -R	<b>GAATTCTTATATAATATGATCTACTGGCCGG</b>	Yeast two-hybrid
AD/BD- <i>TeSEP1</i> -F	<b>CATATGATGGGTAGAGGAAGAGTTGAATTGA</b>	Yeast two-hybrid
AD/BD- <i>TeSEP1</i> -R	<b>GGATCCTCAAAGCATCCATCCAGGGA</b>	Yeast two-hybrid
AD/BD- <i>TeSEP3-1</i> -F	<b>CATATGATGGGAAAAGGAAGGTTAGAGTTGA</b>	Yeast two-hybrid
AD/BD- <i>TeSEP3-1</i> -R	<b>GGATCCTCATGCTGGCCAACCCTG</b>	Yeast two-hybrid

AD/BD- <i>TeSEP3-2-F</i>	<b>CATATG</b> ATGGGAAGAGGAAGAGTAGAG	Yeast two-hybrid
AD/BD- <i>TeSEP3-2-R</i>	<b>GAATTCT</b> TAAACATGGCATCCATCCTT	Yeast two-hybrid
AD/BD- <i>TeSEP3-3-F</i>	<b>CATATG</b> ATGGGGAGAGGAAGA	Yeast two-hybrid
AD/BD- <i>TeSEP3-3-R</i>	<b>GAATTCT</b> CACTGAAACCATATTGACATGTAA	Yeast two-hybrid
AD/BD- <i>TeSEP4-F</i>	<b>CATATG</b> ATGGGAAGAGGCAGAGTTGAAC	Yeast two-hybrid
AD/BD- <i>TeSEP4-R</i>	<b>GGATCC</b> CTTATTTCTTAAGGCTTTATTTGTT	Yeast two-hybrid
AD/BD- <i>TeAGL6-F</i>	<b>CATATG</b> ATGGGGAGAGGACGAGTCG	Yeast two-hybrid
AD/BD- <i>TeAGL6-R</i>	<b>GGATCC</b> TCAAAGATTAACCCATCCATGGATA	Yeast two-hybrid
35S- <i>TeAPI-1-F</i>	<b>GGTACC</b> ATGGGTAGAGGTAAGGTACA	Ectopic expression vector
35S- <i>TeAPI-1-R</i>	<b>GGATCC</b> TATGAAGGAAAACACCTCA	Ectopic expression vector
35S- <i>TeAPI-2-F</i>	<b>GGTACC</b> ATGGGTAGAGGTAAGGTACA	Ectopic expression vector
35S- <i>TeAPI-2-R</i>	<b>GTCGAC</b> TTACGAAGGAAAGCACCTCA	Ectopic expression vector
35S- <i>TeFUL1-F</i>	<b>CCCGGG</b> ATGGGACGGGAAAAGGTAAC	Ectopic expression vector
35S- <i>TeFUL1-R</i>	<b>TCTAGAT</b> TACTTGCTAATGTGTTGAAG	Ectopic expression vector
35S- <i>TeFUL2-F</i>	<b>GGTACC</b> ATGGGAAGAGGCAGAGTGC	Ectopic expression vector
35S- <i>TeFUL2-R</i>	<b>GTCGAC</b> TTACTGGTTAATGTGGCGGA	Ectopic expression vector
35S- <i>TeFUL3-F</i>	<b>GGTACC</b> ATGGGAAGAGGAAGAGTAACATTGA	Ectopic expression vector
35S- <i>TeFUL3-R</i>	<b>GTCGAC</b> TTATATAATATGATCTACTGGCCGG	Ectopic expression vector
qRT- <i>FT-F</i>	TATCCCTGCTACAACCTGGAACAACC	QRT-PCR
qRT- <i>FT-R</i>	GCCTGCCAAGCTGTCTGAAACAATAT	QRT-PCR
qRT- <i>LFY-F</i>	TACTCTCCGCCGCTGGTGATTC	QRT-PCR
qRT- <i>LFY-R</i>	ACTTCCTCCTCCGCCGTTATTCC	QRT-PCR
qRT- <i>SCO1-F</i>	TGAAAGCGAAGTTTGGTCAAATAAGA	QRT-PCR
qRT- <i>SCO1-R</i>	TCTTGAAGAACAAGGTAACCCAATGA	QRT-PCR
qRT- <i>SEP3-F</i>	GTATCAGGGGCAACAAGATGGAAT	QRT-PCR
qRT- <i>SEP3-R</i>	AAAGAGAGGGATTGATTAAGTGAGAAAGA	QRT-PCR
qRT- <i>API-F</i>	AAATCCAGCATCCTTACATGCTCTC	QRT-PCR
qRT- <i>API-R</i>	CAGTTCGAGATCATTCCTCCTCATT	QRT-PCR
qRT- <i>SPL9-F</i>	CAAGGTTTCAGTTGGTGGAGGA	QRT-PCR
qRT- <i>SPL9-R</i>	TGAAGAAGCTCGCCATGTATTG	QRT-PCR
qRT- <i>SVP-F</i>	GAAGGACAGTCGTCGGAGTC	QRT-PCR
qRT- <i>SVP-R</i>	GCCTCTTCCATAGGCAGAAA	QRT-PCR
qRT- <i>TFL1-F</i>	GCACAACAGATGCTACGTTTGCC	QRT-PCR
qRT- <i>TFL1-R</i>	CCTATGCTTGGCCTTGGCAATTC	QRT-PCR
qRT- <i>AGL24-F</i>	GAAGGCTTTGGAGACAGAGTCGGTGA	QRT-PCR
qRT- <i>AGL24-R</i>	AGATGGAAGCCCAAGCTTCAGGGAA	QRT-PCR

Note: bold font is the sequence of enzyme cutting site. *TeAG1* (Acc. No. MT452648) and *TeAG2* (Acc. No. MT452649) are class C genes; *TeAGL11-1* (Acc. No. MT394168) and *TeAGL11-2* (Acc. No. MT394169) are class D genes; *TeSEP1* (Acc. No. MT394175), *TeSEP3-1* (Acc. No. MT394176), *TeSEP3-2* (Acc. No. MT394177), *TeSEP3-3* (Acc. No. MT394178), *TeSEP4* (Acc. No. MT394179) are class E genes. *TeAGL6* (Acc. No. MT394180) is *AGL6*-like gene.

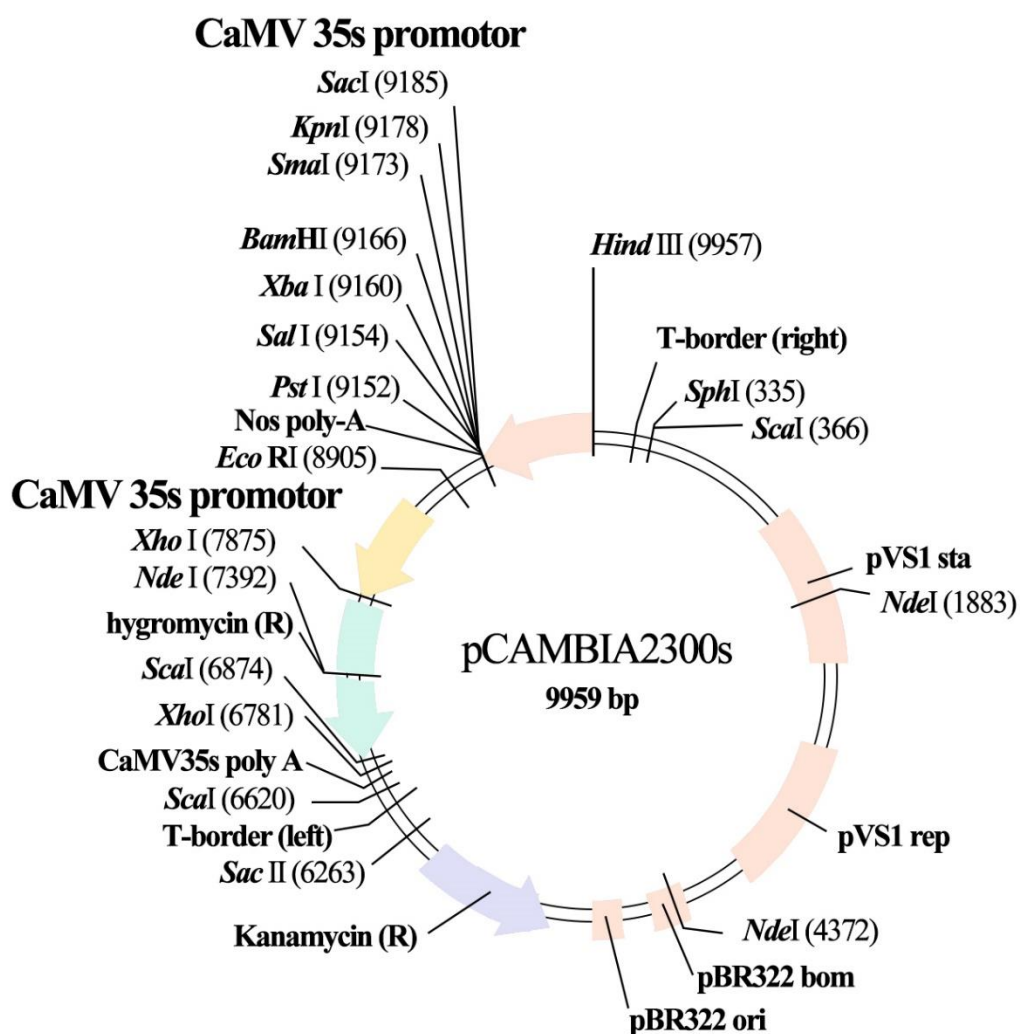
**Table S2.** Sequence information of AP1/FUL-like proteins used to construct evolutionary tree.

No.	Protein Name	Accession No.	Species	Plant Lineage
1	TeAP1-1	MT394170	<i>Tagetes erecta</i>	Asteraceae
2	TeAP1-2	MT394171	<i>Tagetes erecta</i>	Asteraceae
3	TeFUL1	MT394172	<i>Tagetes erecta</i>	Asteraceae
4	TeFUL2	MT394173	<i>Tagetes erecta</i>	Asteraceae
5	TeFUL3	MT394174	<i>Tagetes erecta</i>	Asteraceae
6	HaFUL	XP_021983861	<i>Helianthus annuus</i>	Asteraceae
7	HAM75	AF462152	<i>Helianthus annuus</i>	Asteraceae
8	HAM92	AY173071	<i>Helianthus annuus</i>	Asteraceae
9	CDM8	AAO22981	<i>Chrysanthemum morifolium</i>	Asteraceae
10	CDM41	AAO22980	<i>Chrysanthemum morifolium</i>	Asteraceae
11	CDM111	AAO22979	<i>Chrysanthemum morifolium</i>	Asteraceae
12	GSQUA1	CAA08805	<i>Gerbera hybrida</i>	Asteraceae
13	GSQUA2	CAX65661	<i>Gerbera hybrida</i>	Asteraceae
14	GSQUA3	CAX65662	<i>Gerbera hybrida</i>	Asteraceae
15	GSQUA5	CAX65663	<i>Gerbera hybrida</i>	Asteraceae
16	GSQUA6	CAX65664	<i>Gerbera hybrida</i>	Asteraceae
17	EuFUL	XP_022016988	<i>Antirrhinum majus</i>	Scrophulariaceae
18	DEFH28	AY040247	<i>Antirrhinum majus</i>	Scrophulariaceae
19	SQUA	X63701	<i>Antirrhinum majus</i>	Scrophulariaceae
20	AP1	NP_177074	<i>Arabidopsis thaliana</i>	Brassicaceae
21	CAL	NM_102395	<i>Arabidopsis thaliana</i>	Brassicaceae
22	FUL	NP_568929	<i>Arabidopsis thaliana</i>	Brassicaceae
23	PFG	AF176782	<i>Petunia hybrida</i>	Solanaceae
24	FBP26	AF176783	<i>Petunia hybrida</i>	Solanaceae
25	FBP29	AF335245	<i>Petunia hybrida</i>	Solanaceae
26	PhFUL	AY306172	<i>Petunia hybrida</i>	Solanaceae
27	CanMADS6	AF130118	<i>capsicum annuum</i>	Solanaceae
28	DcMADS1	AJ271147	<i>Daucus carota</i>	Apiaceae
29	OsMADS14	AF058697	<i>Oryza sativa</i>	Poaceae
30	OsMADS15	AF058698	<i>Oryza sativa</i>	Poaceae
32	ZAP1	L46400	<i>Zea mays</i>	Poaceae
33	TrmAP1	AY188331	<i>Triticum monococcum</i>	Poaceae
34	ORAP1-2	DQ104327	<i>Phalaenopsis amabilis</i>	Orchidaceae
35	DthyrFL1	AY927236	<i>Dendrobium thyrsiflorum</i>	Orchidaceae
36	AIFL	AY306138	<i>Allium sp.</i>	Liliaceae
37	GRCD2	CAH04878.1	<i>Gerbera hybrida</i>	Asteraceae
38	GRCD4	CAX65570.1	<i>Gerbera hybrida</i>	Asteraceae
39	PhAGL6	BAA94287.1	<i>Petunia hybrida</i>	Solanaceae
40	AGL6	NP_182089.1	<i>Arabidopsis thaliana</i>	Brassicaceae

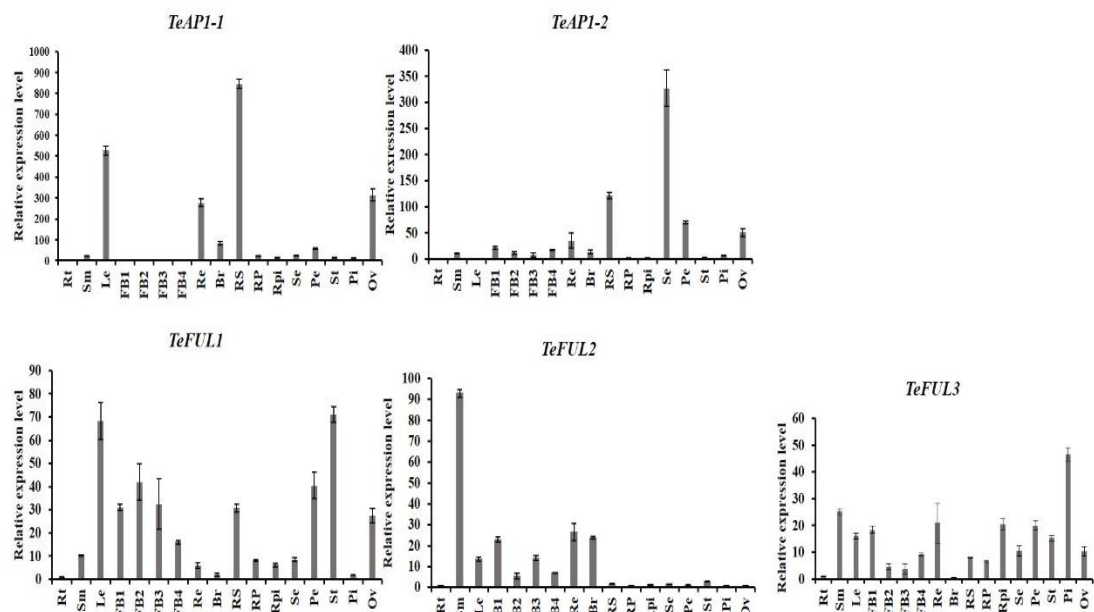
**Table S3.** Amino acid sequence alignment of TeAP1/FUL class proteins.

	TeAP1-1	TeAP1-2	TeFUL1	TeFUL2	TeFUL3
TeAP1-1	100%	89.92%	51.81%	49.80%	51.00%
TeAP1-2	89.92%	100%	49.19%	52.02%	49.60%
AP1	59.39%	59.14%	48.05%	53.52%	46.09%
CAL	55.00%	54.86%	42.35%	51.76%	43.53%
TeFUL1	51.81%	49.19%	100%	54.04%	61.16%
TeFUL2	49.80%	52.02%	54.04%	100%	50.21%
TeFUL3	51.00%	49.60%	61.16%	50.21	100%
FUL	54.25%	54.44%	52.89%	54.55%	54.07%
AGL79	44.84%	45.24	46.18%	49.40%	42.58%

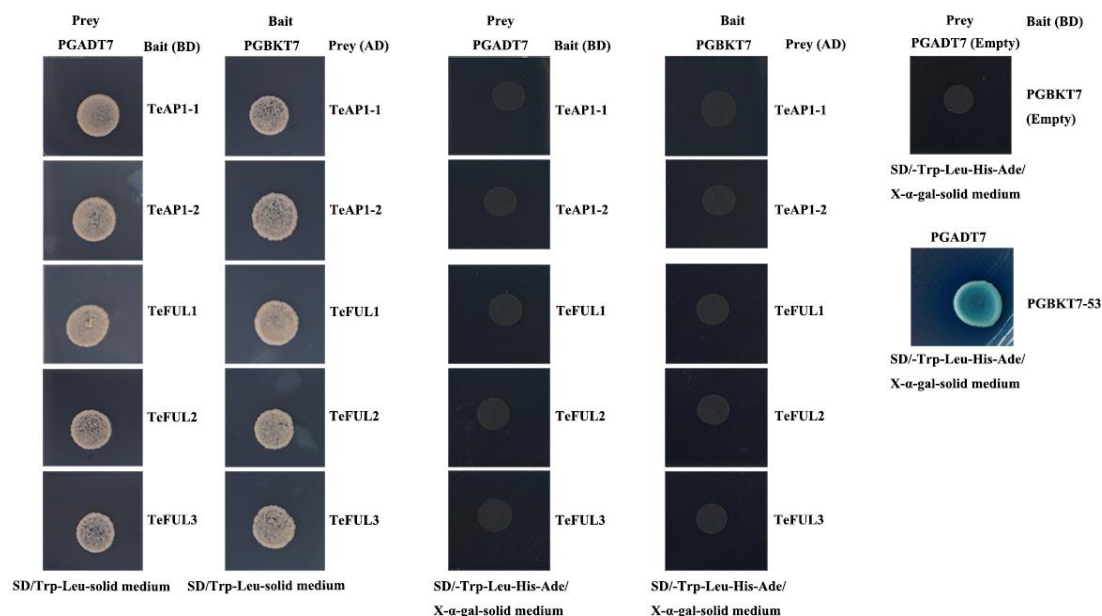
Note: the proteins AP1, FUL, CAL, and AGL79 are from Arabidopsis. TeAP1-1, TeAP1-2, TeFUL1, TeFUL2, and TeFUL3 were from marigold.



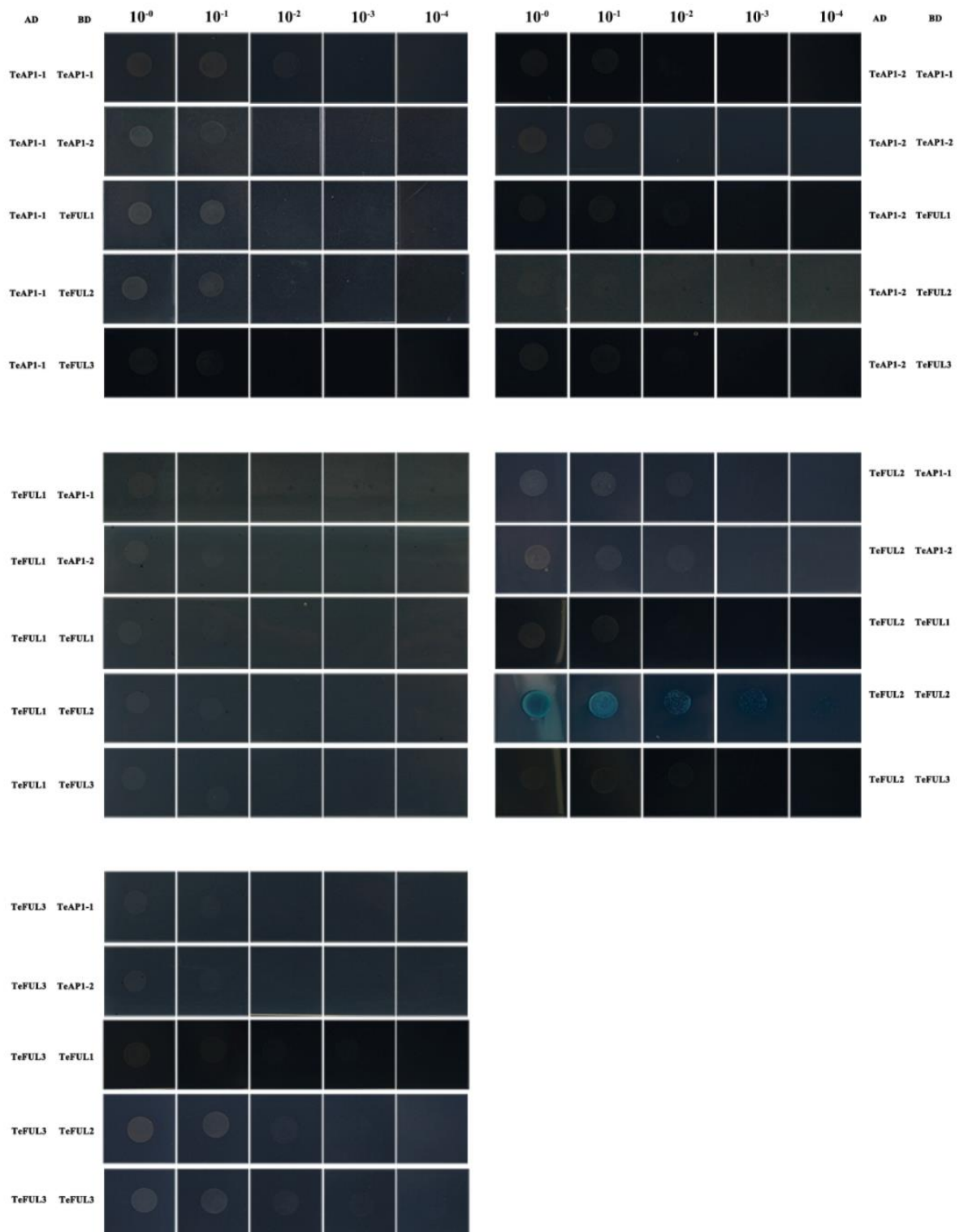
**Figure S1.** The map of pCambia2300s.

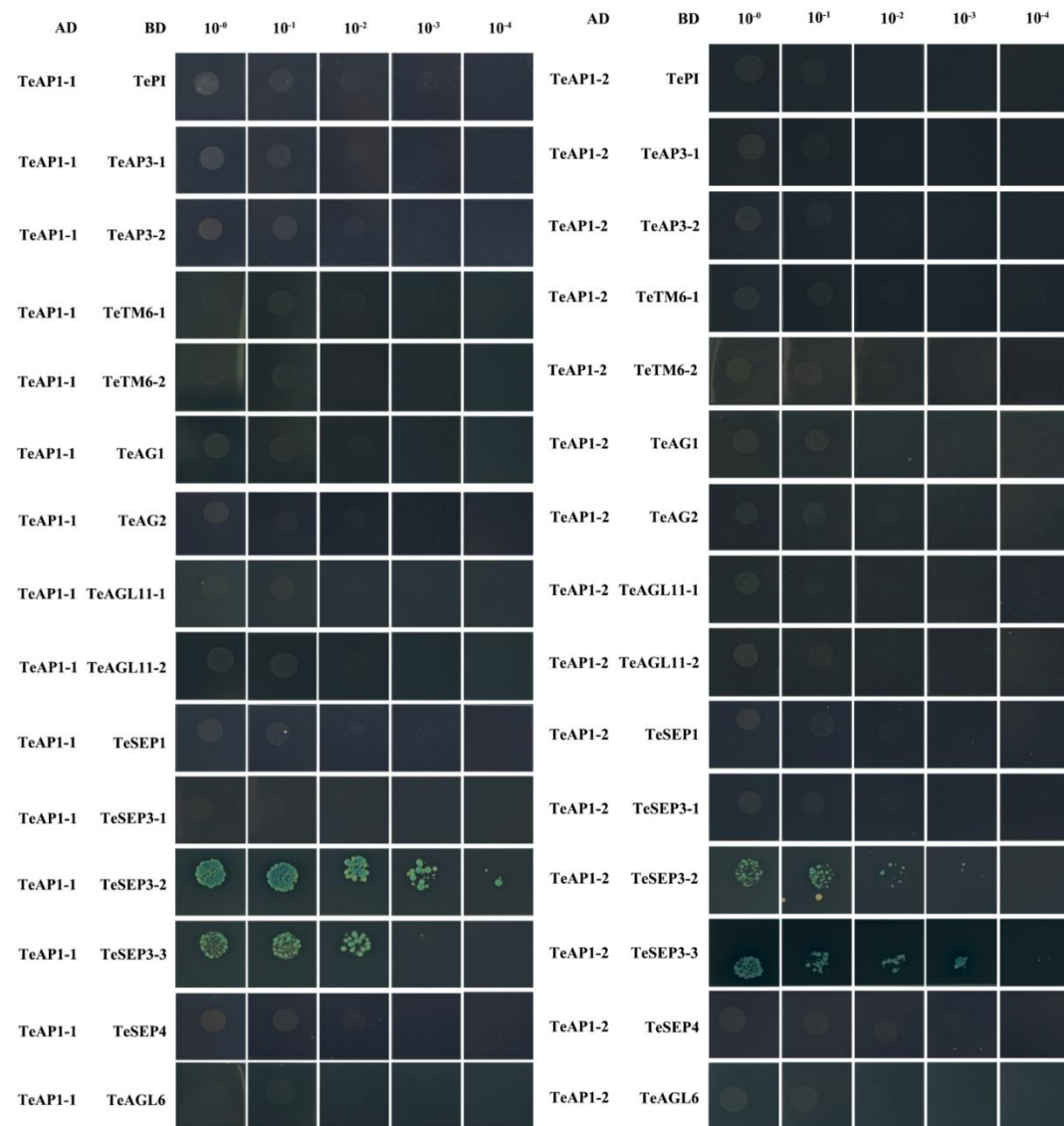


**Figure S2.** Expression levels of *TeAPI/FUL* in different tissues and organs. Rt: root; Sm: stems; Le: leaf; FB1-FB4: flower buds were 0-1mm, 2-3mm, 4-5 mm and 6-7mm in diameter, respectively; Re: receptacle; Br: bract; RS: sepal of ray floret; RP: petal of ray floret; RPi: pistil of ray floret; Se: sepal of disk floret; Pe: petal of disk floret; St: stamen of disk floret; Pi: pistil of disk floret; Ov: ovary.

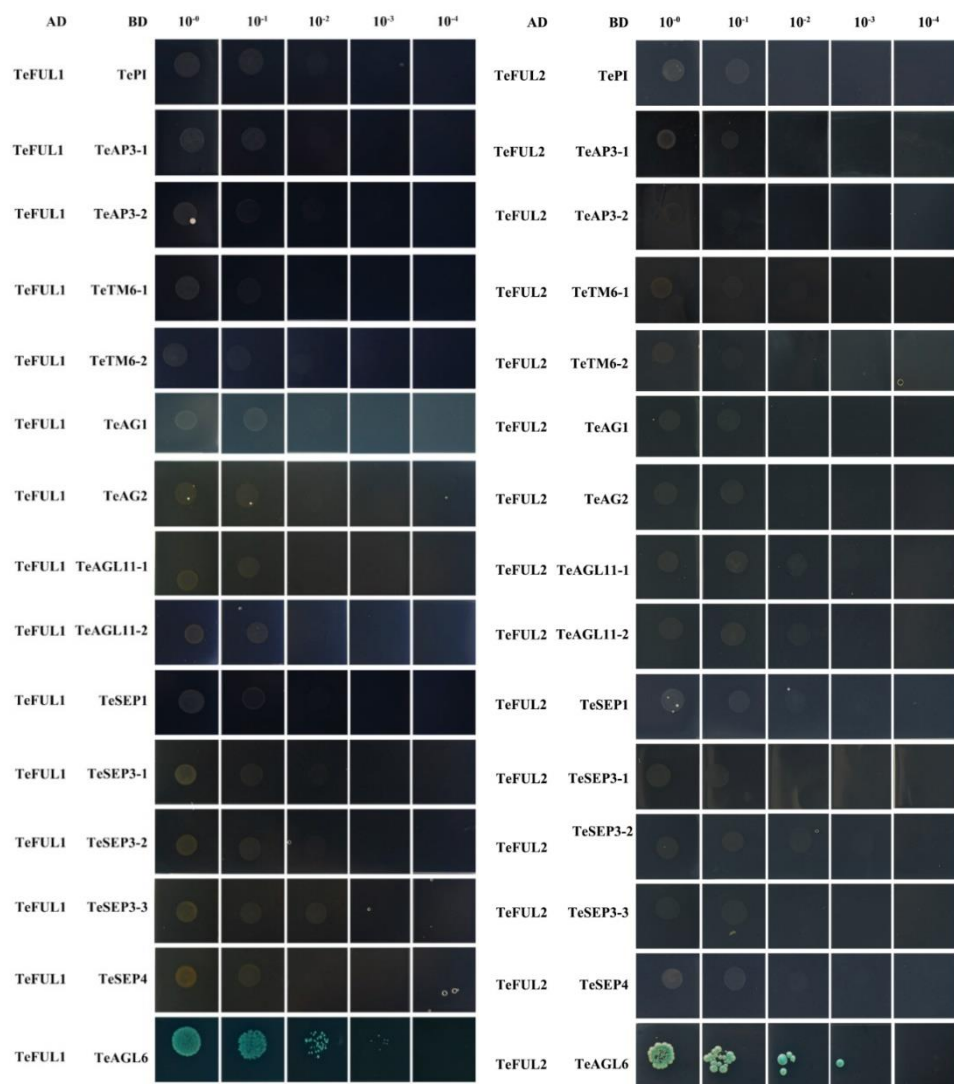


(a)



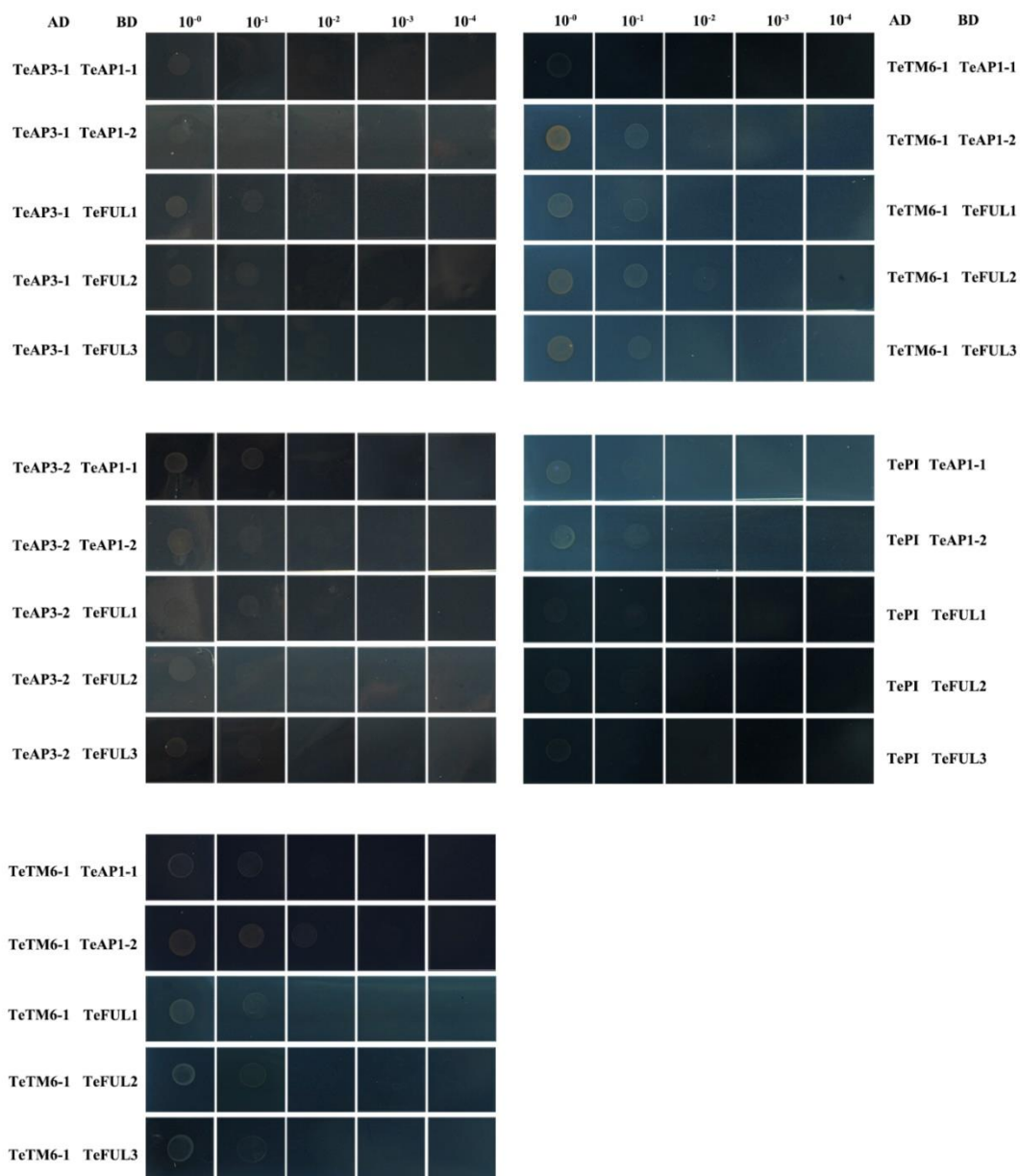


(b)

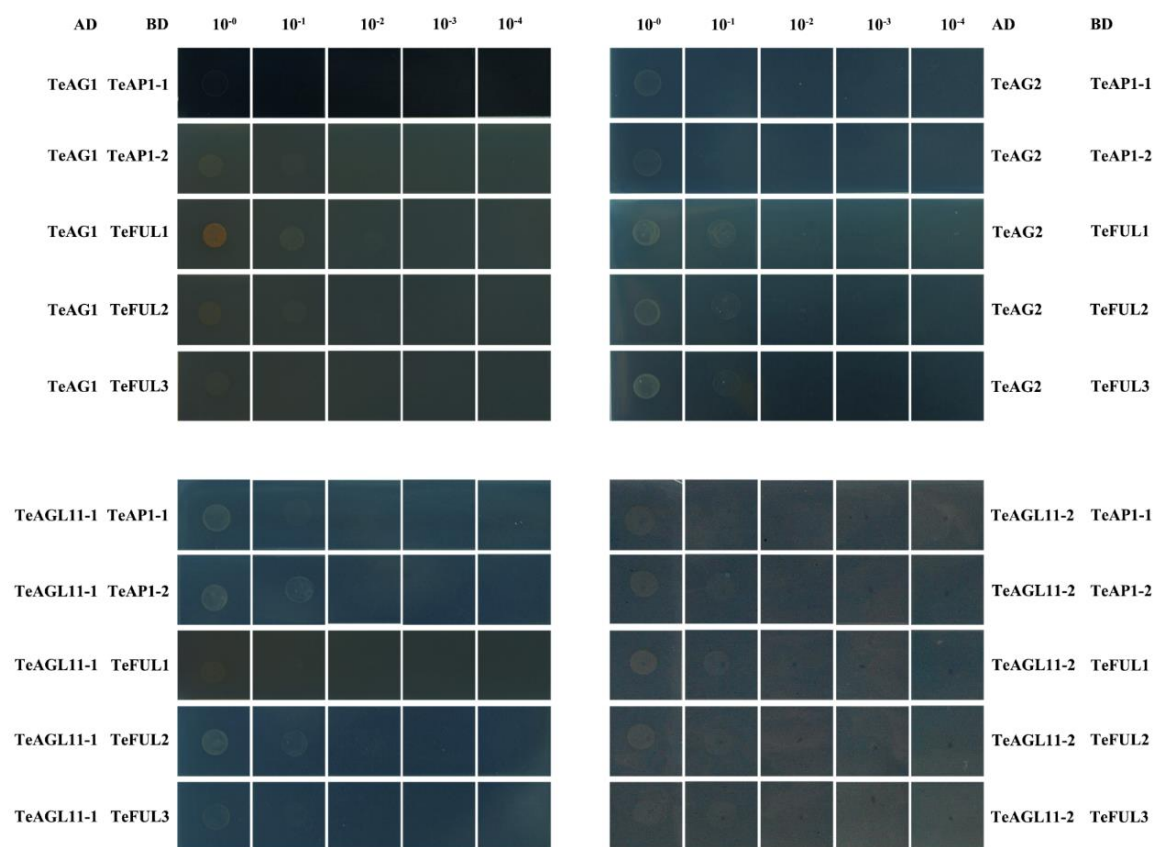




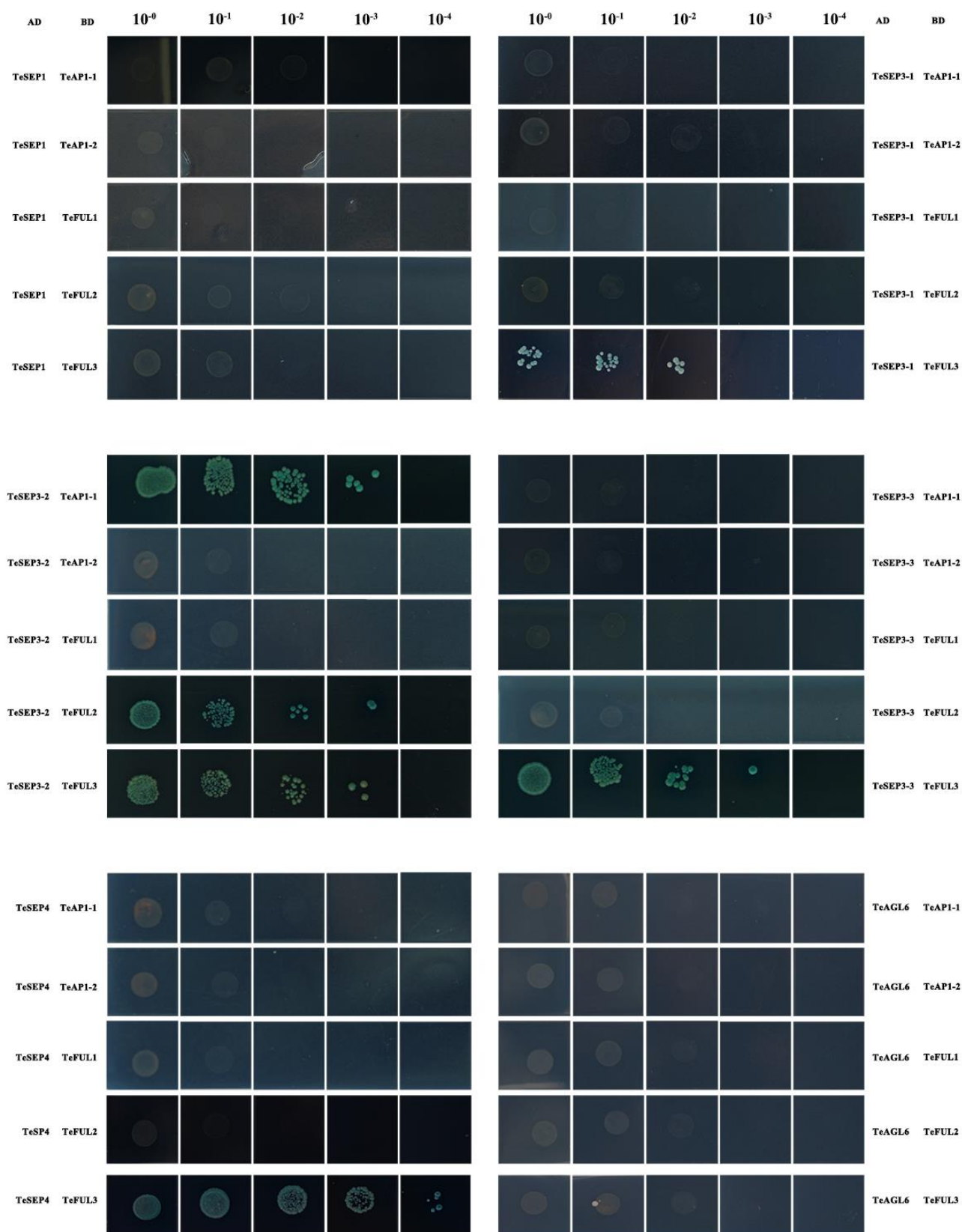
(c)



(d)



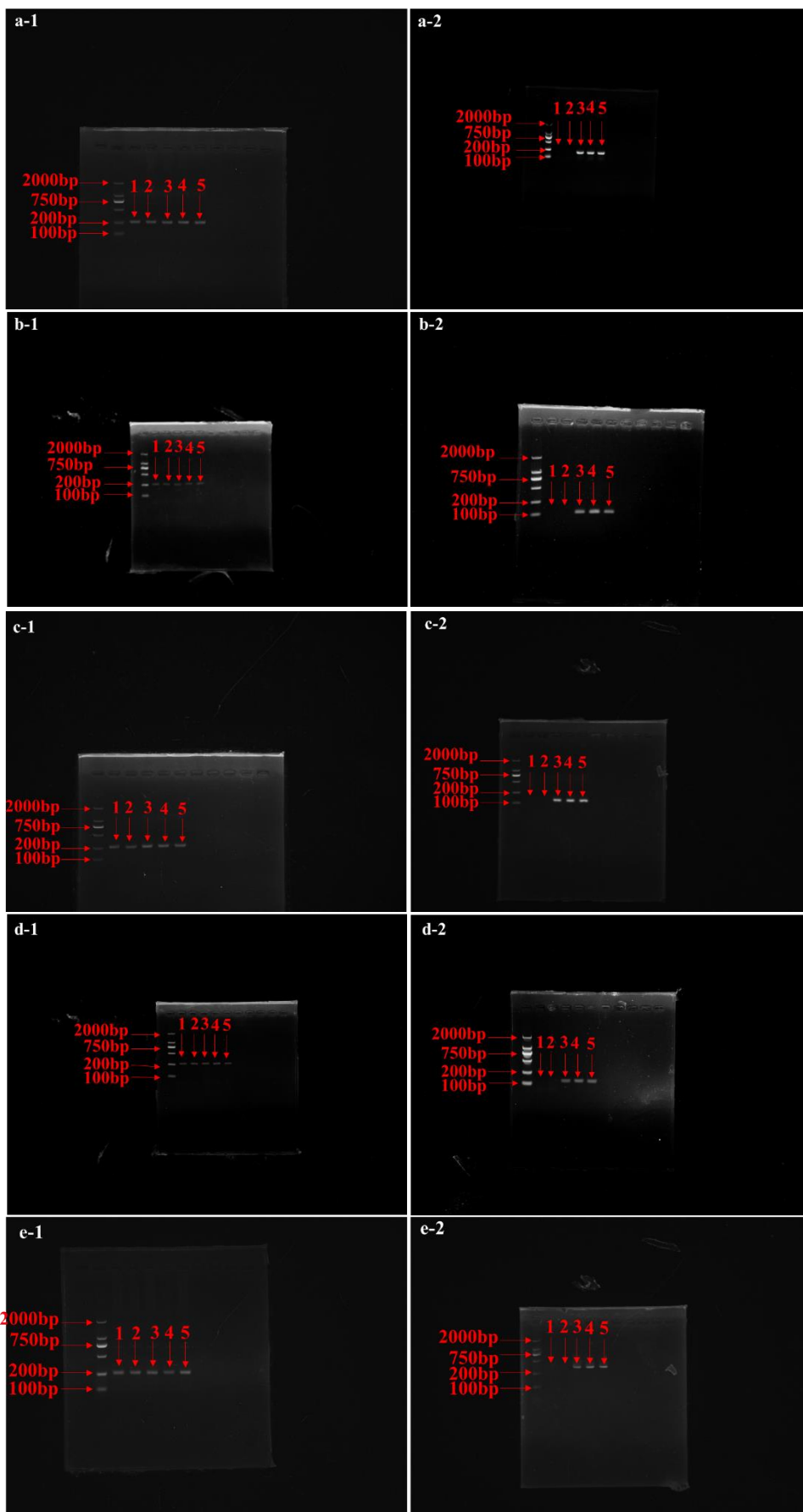
(e)



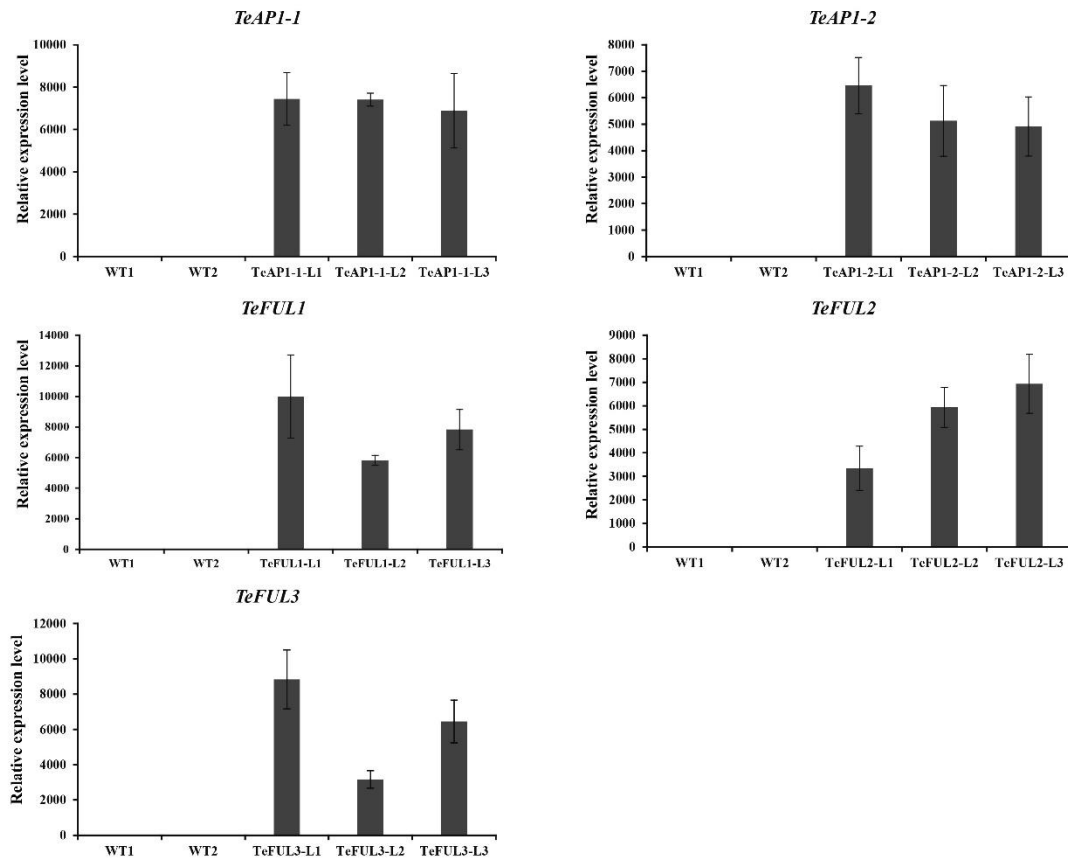
**(f)**

**Figure S3.** Interactions of TeAP1/FUL proteins with class A, B, C, D and, E proteins of marigold by yeast two-hybrid assays. **(a)** Assessing of Self-activation and auto-action of AD and BD constructs. **(b)** Interactions of TeAP1/FUL proteins with class B, C, D, and E proteins

of marigold by yeast two-hybrid assays. Ten-fold serial dilutions from  $10^{-1}$  to  $10^{-5}$  of each culture were spotted on the selected SD -Leu/-Trp/-His/-Ade plates with X- $\alpha$ -gal. **(c)** Interactions of TeAP1/FUL with class A, B, C, D, and E proteins of marigold by yeast two-hybrid assays. Ten-fold serial dilutions from  $10^{-1}$  to  $10^{-5}$  of each culture were spotted on the selected SD -Leu/-Trp/-His/-Ade plates with X- $\alpha$ -gal. Class B proteins: TeAP3-1, TeAP3-2, TePI, TeTM6-1, TeTM6-2. Class C proteins: TeAG1 and TeAG2 proteins; Class D proteins: TeAGL11-1 and TeAGL11-2; Class E proteins: TeSEP1, TeSEP3-1, TeSEP3-2, TeSEP3-3, TeSEP4 and TeAGL6 proteins. **(d)** Interactions of class B proteins and TeAP1/FUL proteins of marigold by yeast two-hybrid assays. Ten-fold serial dilutions from  $10^{-1}$  to  $10^{-5}$  of each culture were spotted on the selected SD -Leu/-Trp/-His/-Ade plates with X- $\alpha$ -gal. Class B proteins: TeAP3-1, TeAP3-2, TePI, TeTM6-1, TeTM6-2. **(e)** Interactions of class C and D proteins with TeAP1/FUL proteins of marigold by yeast two-hybrid assays. Ten-fold serial dilutions from  $10^{-1}$  to  $10^{-5}$  of each culture were spotted on the selected SD -Leu/-Trp/-His/-Ade plates with X- $\alpha$ -gal. Class C proteins: TeAG1 and TeAG2 proteins; Class D proteins: TeAGL11-1 and TeAGL11-2. **(f)** Interactions of class E proteins and TeAP1/FUL proteins of marigold by yeast two-hybrid assays. Ten-fold serial dilutions from  $10^{-1}$  to  $10^{-5}$  of each culture were spotted on the selected SD -Leu/-Trp/-His/-Ade plates with X- $\alpha$ -gal. Class D proteins: Class E proteins: TeSEP1, TeSEP3-1, TeSEP3-2, TeSEP3-3, TeSEP4 and TeAGL6 proteins.



**f**



**Figure S4.** Expression of *TeAPI-1*, *TeAPI-2*, *TeFUL1*, *TeFUL2* and *TeFUL3* in seedlings of T<sub>1</sub> transgenic plants. (a-e) Expression of *TeAPI-1*, *TeFUL1*, and *TeFUL3* in seedlings of T<sub>1</sub> transgenic lines by semi-quantitative RT-PCR. (a) Semi-qRT-PCR analysis of transgenes in wild-type Arabidopsis and *35S:TeAPI-1* transgenic plants. (a-1) The picture was the constitutive gene is Arabidopsis house-keeping gene *AtEF1a*. (a-2) The picture was the expression level of *TeAPI-1* in transgenic lines, the band size was 180 bp. The number of 1-5 indicate wild-type Arabidopsis plant 1, wild-type Arabidopsis plant 2, *35S:TeAPI-1* transgenic Arabidopsis line 1, *35S:TeAPI-1* transgenic Arabidopsis line 2, and *35S:TeAPI-1* transgenic Arabidopsis line 3, respectively. (b) Semi-qRT-PCR analysis of transgenes in wild-type Arabidopsis and *35S:TeAPI-2* transgenic plants. (b-1) The picture was the constitutive gene is Arabidopsis house-keeping gene *AtEF1a*. (b-2) The picture was the expression level of *TeAPI-2* in transgenic lines, the band size was 106 bp. The number of 1-5 indicate wild-type Arabidopsis plant 1, wild-type Arabidopsis plant 2, *35S:TeAPI-2* transgenic Arabidopsis line 1, *35S:TeAPI-2* transgenic Arabidopsis line 2, and *35S:TeAPI-1* transgenic Arabidopsis line 3, respectively. (c) Semi-qRT-PCR analysis of transgenes in wild-type Arabidopsis and *35S:TeFUL1* transgenic plants. (c-1) The picture was the constitutive gene is Arabidopsis house-keeping gene *AtEF1a*. (c-2) The picture was the expression level of *TeFUL1* in transgenic lines, the band size was 139 bp. The number of 1-5 indicate wild-type Arabidopsis plant 1, wild-type Arabidopsis plant 2, *35S:TeFUL1* transgenic Arabidopsis line 1, *35S:TeFUL1* transgenic Arabidopsis line 2, and *35S:TeFUL1* transgenic Arabidopsis line 3, respectively. (d) Semi-qRT-PCR analysis of transgenes in wild-type Arabidopsis and *35S:FUL2* transgenic plants. (d-1) The picture was the constitutive gene is Arabidopsis house-keeping gene *AtEF1a*. (d-2) The

picture was the expression level of *TeFUL2* in transgenic lines, the band size was 127 bp. The number of 1-5 indicate wild-type Arabidopsis plant 1, wild-type Arabidopsis plant 2, *35S:TeFUL2* transgenic Arabidopsis line 1, *35S:TeFUL2* transgenic Arabidopsis line 2, and *35S:TeFUL2* transgenic Arabidopsis line 3, respectively. (e) Semi-qRT-PCR analysis of transgenes in wild-type Arabidopsis and *35S:FUL3* transgenic plants. (e-1) The picture was the constitutive gene is Arabidopsis house-keeping gene *AtEF1α*. (e-2) The picture was the expression level of *TeFUL3* in transgenic lines, the band size was 377 bp. The number of 1-5 indicate wild-type Arabidopsis plant 1, wild-type Arabidopsis plant 2, *35S:TeFUL3* transgenic Arabidopsis line 1, *35S:TeFUL3* transgenic Arabidopsis line 2, and *35S:TeFUL3* transgenic Arabidopsis line 3, respectively. (f) Expression of *TeAP1-1*, *TeAP1-2*, *TeFUL1*, *TeFUL2* and *TeFUL3* in seedlings of T<sub>1</sub> transgenic lines by quantitative real-time PCR.