Supplemental Table S1. Position of flower that showed senescence/abscission in the *35S:EDFs Arabidopsis*.

Construct	*35S:EDF1* n=47	*35S:EDF2* n=59	*35S:EDF3* n=59	*35S:EDF4* n=43	WT N=40
Position of flower senescence/abscission	3.35±0.43	2.9±0.5	3.2±0.52	3.2±0.58	5.1±0.55
Significance (TG/WT)	P≤0.01	P≤0.01	P≤0.01	P≤0.01	Not applicable

Statistic analysis was measured by student's T-test.

Supplemental Table S2. Position of flower that showed senescence/abscission in the *35S:EDFs+SRDX Arabidopsis*.

Construct	*35S:EDF1 +SRDX*, n=52	*35S:EDF2 +SRDX*, n=60	*35S:EDF3 +SRDX*, n=68	*35S:EDF4 +SRDX*, n=59	WT N=40
Position of flower senescence/abscission	2.97±0.53	2.52±0.33	2.65±0.23	2.62±0.29	5.1±0.55
Significance (TG/WT)	P≤0.01	P≤0.01	P≤0.01	P≤0.01	Not applicable

Statistic analysis was measured by student's T-test.

Supplemental Table S3. Position of flower that showed senescence/abscission in the *35S:EDFs+SRDX/etr1-1 Arabidopsis*.

Construct	*35S:EDF1+ SRDX/etr-1-1* n=15	*35S:EDF2+ SRDX/etr1-1* n=13	*35S:EDF3+ SRDX/etr-1-1* n=17	*35S:EDF4+ SRDX/etr-1-1* n=16	*etr1-1* n=10
Position of flower senescence /abscission	4.2±0.6	3.56±0.68	4.4±0.54	4.26±0.49	9.5±1.02
Significance (TG/*etr1-1*)	P≤0.01	P≤0.01	P≤0.01	P≤0.01	Not applicable

Statistic analysis was measured by student's T-test.

Supplemental Table S4. Position of flower that showed senescence/abscission in the *35S:EDFs+SRDX/ein2-1 Arabidopsis*.

Construct	*35S:EDF1+ SRDX/ein2-1* n=20	*35S:EDF2+ SRDX/ein2-1* n=23	*35S:EDF3+ SRDX/ein2-1* n=19	*35S:EDF4+ SRDX/ein2-1* n=15	*ein2-1* n=10
Position of flower senescence /abscission	4.66±0.38	3.98±0.78	5±0.71	4.86±0.55	9.2±0.92
Significance (TG/*ein2-1*)	P≤0.01	P≤0.01	P≤0.01	P≤0.01	Not applicable

Statistic analysis was measured by student's T-test.

Supplemental Table S5. Arabidopsis genes up-regulated in the *35S:FYF+GR Arabidopsis*.

Gene Name	**Description**	**PValueLogRatio**	**DEX treat after 3hr (Normalized Expression Ratio)**
At5g42040.1	Regulatory particle non-ATPase 12B (RPN12b)	0.0000009814	2.21
At1g52810.1	2-oxoglutarate-dependent dioxygenase-related similar to AOP1.2	0.0421979770	2.03
At5g40000.1	AAA-type ATPase family protein	0.0000006968	2.20
At2g13810.1	AGD2-like defense response protein 1	0.0000503158	2.35
At1g34050.1	Ankyrin repeat family protein contains ankyrin repeat domains	0.0000000001	3.16
At5g54710.1	Ankyrin repeat family protein contains ankyrin repeat domains	0.0000070965	2.01
At4g11000.1	Ankyrin repeat family protein contains ankyrin repeats	0.0000011824	2.16
At5g67340.1	beta-catenin repeat family protein	0.0000023224	2.10
At5g58680.1	beta-catenin repeat family protein	0.0000007333	2.20
At5g42410.1	Small auxin upregulated RNA 43(SAUR43)	0.0000003401	2.27
At2g14960.1	Encodes a protein similar to IAA-amido synthases (GH3.1)	0.0000001051	2.37
At1g27740.1	Basic helix-loop-helix (bHLH) family protein	0.0000035137	2.36
At5g56960.1	Basic helix-loop-helix (bHLH) family protein	0.0000020631	2.12
At5g43650.1	Basic helix-loop-helix (bHLH) family protein(bHLH92)	0.0000000003	2.99
At2g45760.1	BON1-associated protein (BAP1)	0.0000002139	2.30
At5g57010.1	Calmodulin-binding family protein	0.0000000244	2.50
At5g26920.1	Calmodulin-binding protein 60(CBP60)	0.0000031942	2.07
At1g27890.1	Polynucleotidyl transferase, ribonuclease H-like superfamily protein	0.0000034766	2.07
At1g61470.1	Polynucleotidyl transferase, ribonuclease H-like superfamily protein	0.0000013653	2.14
At1g27820.1	Polynucleotidyl transferase, ribonuclease H-like superfamily protein	0.0000065319	2.02
At1g63245.1	CLAVATA3/ESR-Related 14 (CLE14)	0.0005067724	2.21
At1g08860.1	Copine-like protein	0.0000037113	2.06
At3g48320.1	Cytochrome P450 71A21	0.0026060140	2.04
At2g45550.1	Cytochrome P450 family protein	0.0000618807	3.23
At4g31950.1	Cytochrome P450 family protein cytochrome P450 monooxygenase	0.0000000030	2.72
At1g74110.1	Cytochrome P450 family protein similar to Cytochrome P450 78A4	0.0006640643	2.25
At4g31970.1	Cytochrome P450 family protein similar to cytochrome P450 82C1	0.0000000802	2.40
At1g12740.1	Cytochrome P450 family protein similar to Cytochrome P450 90A1	0.0000008164	2.19
At2g21910.1	Cytochrome P450 family protein similar to Cytochrome P450 96A5	0.0000000284	2.51
At1g52900.1	Toll-Interleukin-Resistance (TIR) domain family protein	0.0000633215	2.11
At1g66090.1	Disease resistance protein (TIR-NBS class)	0.0000067894	2.01
At3g15960.1	DNA mismatch repair MutS family protein	0.0001509814	2.00
At4g26740.1	Embryo-specific protein 1 (ATS1)	0.0027421999	3.27
At3g23220.1	Ethylene-responsive element-binding protein(ERF95)	0.0000089198	2.81
At1g22810.1	DREB subfamily A-5 of ERF/AP2 transcription factor family(ERF19)	0.0000038062	2.06
At1g71450.1	DREB subfamily A-4 of ERF/AP2 transcription factor family(ERF21).	0.0004296007	2.25
At5g43410.1	Ethylene-responsive factor(ERF96)	0.0002813103	2.13
At3g23230.1	Ethylene-responsive factor98(ERF98)	0.0000009642	2.18
At3g09520.1	Exocyst subunit EXO70 family protein H4	0.0000000784	2.41
At4g01360.1	Encodes a protein related to BYPASS1 (BPS3)	0.0000018524	2.12

At5g03210.1	DBP interactin protein 2 (DIP2)	0.0000007187	2.20
At1g05880.1	Arabidopsis Ariadne 12 (ARI12)	0.0000000137	2.60
At1g13310.1	Endosomal targeting BRO1-like domain-containing protein	0.0000000018	2.80
At1g26390.1	FAD-binding domain-containing protein	0.0246118415	3.01
At1g30700.1	FAD-binding Berberine family protein	0.0000000004	2.94
At1g30720.1	FAD-binding Berberine family protein	0.0000000223	2.53
At2g39490.1	F-box family protein	0.0061853351	2.52
At2g02310.1	Phloem protein 2-B6 (PP2-B6)	0.0000000022	3.35
At2g02320.1	Phloem protein 2-B7 (PP2-B7);	0.0046575867	3.59
At1g14185.1	Glucose-methanol-choline (GMC) oxidoreductase family protein	0.0000148416	2.06
At5g11210.1	Glutamate receptor family protein (GLR2.5)	0.0000000026	2.89
At3g60120.1	Beta glucosidase 27 (BGLU27)	0.0000000484	2.56
At5g24540.1	Beta glucosidase 31 (BGLU31);	0.0000063019	2.03
At1g66280.1	Beta-glucosidase 22 (BGLU22)	0.0218837634	3.58
At5g63230.1	Glycosyl hydrolase family protein 17	0.0326333175	3.31
At5g59070.1	UDP-Glycosyltransferase superfamily protein	0.0000044476	2.05
At1g55780.1	Heavy-metal-associated domain-containing protein	0.0000000041	8.97
At5g46010.1	Homeodomain-like superfamily protein	0.0278535974	3.57
At1g69240.1	Hydrolase, alpha/beta fold family protein	0.0007482860	2.03
At1g74710.1	Isochorismate synthase 1 (ICS1)	0.0000008522	2.19
At1g35513.1	Isochorismate synthase-related / isochirismate mutase-related	0.0000008362	2.37
At4g39580.1	Galactose oxidase/kelch repeat superfamily protein	0.0000024551	2.12
At1g70130.1	Concanavalin A-like lectin protein kinase family protein	0.0000035963	2.07
At5g01560.1	Lectin protein kinase A4.3	0.0000010621	2.17
At1g66780.1	MATE efflux family protein	0.0000001601	2.41
At4g21840.1	Methionine sulfoxide reductase domain-containing protein	0.0000162807	2.03
At1g01560.1	MAPkinase 11(MPK11)	0.0000045875	2.04
At5g22380.1	NAC domain containing protein 90 (NAC090)	0.0000000000	3.31
At2g17040.1	NAC domain contain protein 36 (NAC036)	0.0000026773	2.09
At3g44350.1	NAC domain containing protein 61 (NAC061)	0.0000000010	2.94
At5g63130.1	Octicosapeptide/Phox/Bem1p (PB1) domain-containing protein	0.0000052365	2.03
At1g77530.1	O-methyltransferase family 2 protein	0.0000114345	2.07
At2g36690.1	Oxidoreductase, 2OG-Fe(II) oxygenase family protein	0.0000000200	4.44
At1g09935.1	Phosphoglycerate/bisphosphoglycerate mutase family protein	0.0000000000	4.87
At1g09932.1	Phosphoglycerate/bisphosphoglycerate mutase family protein	0.0000005024	2.23
At1g75830.1	Pathogenesis-related protein, belongs to the plant defensin (PDF) family	0.0378577718	2.05
At3g07195.1	RPM1-interacting protein 4 (RIN4) family protein	0.0000012513	2.16
At4g00970.1	Cysteine-rich receptor-like protein kinase 41	0.0000037483	2.06
At4g11470.1	Cysteine-rich receptor-like protein kinase 31	0.0000000005	2.98
At5g47850.1	CRINKLY4 related 4 (CCR4)	0.0000000132	2.58

At1g07160.1	Protein phosphatase 2C family protein	0.0000019776	2.11
At5g43090.1	Pumilio proteins13 (PUM13) containing PUF domain	0.0002190484	3.51
At2g35770.1	Serine carboxypeptidase-like 28 (scpl28)	0.0013965508	2.34
At3g51680.1	Short-chain dehydrogenase/reductase (SDR) family protein	0.0000000312	2.91
At5g65165.1	Succinate dehydrogenase(SDH2-3)	0.0007416950	2.49
At1g16230.1	Target SNARE coiled-coil domain protein	0.0000683101	2.24
At5g48110.1	Terpene synthase/cyclase family protein	0.0000000122	2.61
At1g24420.1	HXXXD-type acyl-transferase family protein	0.0001136897	3.60
At1g01680.1	U-box domain-containing protein 54	0.0000000000	3.50
At3g61390.1	RING/U-box superfamily protein	0.0165444593	3.66
At2g23260.1	UDP-glucoronosyl/UDP-glucosyl transferase family protein	0.0000001124	2.45
At1g79680.1	Wall-associated kinase like 10	0.0000000441	2.49
At5g24110.1	WRKY family transcription factor 30	0.0000001021	2.37
At2g21900.1	WRKY family transcription factor 59	0.0227754116	2.40
At4g11070.1	WRKY family transcription factor 41	0.0000001114	2.39
At1g66550.1	WRKY family transcription factor 67	0.0001661204	4.09
At2g15390.1	Xyloglucan fucosyltransferase 4 (FUT4)	0.0000035152	2.09
At1g27730.1	Salt tolerance zinc finger (C2H2 type) family protein 10 (ZAT10)	0.0000054237	2.03
At3g46090.1	Salt tolerance zinc finger (C2H2 type) family protein 7 (ZAT7)	0.0000074257	2.00
At3g53600.1	Zinc finger (C2H2 type) family protein	0.0000029968	2.08
At4g09100.1	Zinc finger (C3HC4-type RING finger) family protein	0.0000000247	2.51
At1g43000.1	Zinc-binding family protein	0.0000000030	2.72
At3g46080.1	Zinc finger (C2H2 type) family protein	0.0000006011	2.21
At5g67450.1	Arabidopsis zinc finger (C2H2 type) protein 1 (AZF1)	0.0000021462	2.14
At2g42360.1	Zinc finger (C3HC4-type RING finger) family protein	0.0000019322	2.11
At1g53820.1	Zinc finger (C3HC4-type RING finger) family protein	0.0000000025	4.66
At2g46495.1	Zinc finger (C3HC4-type RING finger) family protein	0.0000006452	2.28

Supplemental Table S6. Arabidopsis genes down-regulated in the *35S:FYF+GR Arabidopsis*.

Gene Name	Description	PValueLogRatio	DEX treat after 3hr (Normalized Expression Ratio)
At2g04038.1	Basic leucine-zipper 48 (bZIP48)	0.0000000407	0.13
At1g48110.1	Evolutionarily conserved C-terminal region 7	0.0000000012	0.19
At4g19800.1	Glycosyl hydrolase family 18 protein	0.0002092207	0.14
At4g35170.1	Late embryogenesis family protein	0.0056002494	0.34
At5g65080.1	MADS-box family protein, agamous like 68(AGL68)	0.0160600295	0.27
At1g35515.1	Myb family transcription factor 8 (MYB8)	0.0000000003	0.05
At3g16360.1	phosphotransfer family protein (AHP4)	0.0050701954	0.45
At3g17910.1	Embryo deffective 3121	0.0000000000	0.07
At4g20370.1	Twin sister of FT protein (TSF) / TFL1 like protein	0.0329164375	0.50
At5g10970.1	zinc finger (C2H2 type) family protein	0.0007139490	0.50

Supplemental Table S7. Oligo nucleotide sequence of primers used in gene cloning and PCR analysis.

Gene name	**Primer name**	**Primer sequence**	**Restriction site**	**Use**
EDF1	EDF1-F-2	5’-TCTAGAGCAACAAAAACTTAACCCATTTCTTCTTCT-3’	XbaI	cDNA cloning
At1g25560	EDF1-R-nos-2	5’-GGTACCCAAGATGTTGATAATCGCCTGCTTC-3’	KpnI	cDNA cloning
	EDF1-R-stop-2	5’-GGTACCTCACAAGATGTTGATAATCGCCTGCTTC-3’	KpnI	cDNA cloning
	EDF1-P-F1	5’-CTGCAGGTGGAAAAATTAGGTACTCTGCTCCG-3’	PstI	Promoter cloning
	EDF1-P-R1	5’-GGATCCATTTGTTGTGTTTGTGAGAGAGAAACAAAAAAAGAAG-3’	BamHI	Promoter cloning
	RT-EDF1-1	5'-TCACAAACACAACAAATATGGAATACAG-3'		Real time PCR
	RT-EDF1-2	5'-GCTTTGGAGTAGTAGAGATGGAGAG-3'		Real time PCR
EDF2	EDF2-F-2	5’-TCTAGACAACGTCACCTAAATCTCTCTCACC-3’	XbaI	cDNA cloning
At1g68840	EDF2-R-nos-2	5’-GGTACCCAAAGCATTGATTATCGCCTGCTTC-3’	KpnI	cDNA cloning
	EDF2-R-stop-2	5’-GGTACCTCACAAAGCATTGATTATCGCCTGCTTC-3’	KpnI	cDNA cloning
	EDF2-P-F1	5’-CTGCAGCCTCAAAGATAGTATTATACGTGTCTACG-3’	PstI	Promoter cloning
	EDF2-P-R1	5’-GGATCCTTTCTTTGTTTCAGTTTCTTGAAGATTCTCACC-3’	BamHI	Promoter cloning
	RT-EDF2-1	5'-CTAAACAACACGCCGAGAAACAC-3'		Real time PCR
	RT-EDF2-2	5'-GCCGAACCACCACCTGAACC-3'		Real time PCR
EDF3	EDF3-F-2	5’-GGATCCCACATATACATTCACATTACTAATCTCTCAAGATTTC-3’	BamHI	cDNA cloning
At3g25730	EDF3-R-nos-2	5’-GGTACCCAAAACTCGTTGCTTCTTACACCTTAAC-3’	KpnI	cDNA cloning
	EDF3-R-stop-2	5’-GGTACCTTACAAAACTCGTTGCTTCTTACACCTTAAC-3’	KpnI	cDNA cloning
	EDF3-P-F1	5’-CTGCAGGGTACTGTTGAGTGTTGACATATGATC-3’	PstI	Promoter cloning
	EDF3-P-R1	5’-GGATCCGTTATGAAACGAAATAAGAAACTGAGAGAAAATCAC-3’	BamHI	Promoter cloning
	RT-EDF3-1	5'-ACACATATACATTCACATTACTAATCTC-3'		Real time PCR
	RT-EDF3-2	5'-AATGGAATCTGTAGTTGTAGAGC-3'		Real time PCR
EDF4	EDF4-F-2	5’-TCTAGACACTTGCTGTTTCTTATTTCCCTCCC-3’	XbaI	cDNA cloning
At1g13260	EDF4-R-nos-2	5’-GGTACCCGAGGCGTGAAAGATGCGTTG-3’	KpnI	cDNA cloning
	EDF4-R-stop-2	5’-GGTACCTTACGAGGCGTGAAAGATGCGTTG-3’	KpnI	cDNA cloning
	EDF4-P-F1	5’-CTGCAGCCATCTATTTCTTTTTGTCGCATACCCAC-3’	PstI	Promoter cloning
	EDF4-P-R1	5’-GGATCCTAATCTGTGTTTTTTTTTATGGTTTGAAACAATGGAGAAAAC-3’	BamHI	Promoter cloning
	RT-EDF4-1	5'-CCGAAACATCACGCAGAGAAAC-3'		Real time PCR
	RT-EDF4-2	5'-AACCCGACCCGCATCTAAATC-3'		Real time PCR
FUF1	FUF-F-3	5'-TCTAGAACAACAAACACTCTTGAGCAAAAACT-3'	XbaI	cDNA cloning
At1g71450	FUF-R-4	5'-GGTACCCCCTTGTGGTAGACTATGAAAA-3'	KpnI	cDNA cloning
	FUF-P-F-1	5'-CTGCAGCGGACGAAAGGAGTGTACT-3'	PstI	Promoter cloning
	FUF-P-R-2	5'-GGATCCGAACACACACACACACGCA-3'	BamHI	Promoter cloning
	RT-FUF-1	5'-CAGCATTCGCATGGCAGTTC-3'		Real time PCR
	RT-FUF-2	5'-GACTCTGTTCCTTCGGTGGTG-3'		Real time PCR
UBQ10	RT-UBQ10-F	5'-CTCAGGCTCCGTGGTGGTATG-3'		Real time PCR
At4G05320	RT-UBQ10-4-2	5'-GTGATAGTTTTCCCAGTCAACGTC-3'		Real time PCR
BOP1	RT-BOP1-1	5'-CGAAGAAGGAAACAATAACAGTAACGATAA-3'		Real time PCR

At3G57130	RT-BOP1-2	5'-GTCATCTCCAATATCACGATTTGTAGCA-3'		Real time PCR
BOP2	RT-BOP2-1	5'-GCAACAACCAAAACAATGATAACAATACC-3'		Real time PCR
At2G41370	RT-BOP2-2	5'-CTGGACCCATCTGACCCGTACCT-3'		Real time PCR
IDA	IDA-F1	5'-TCTAGAATGGCTCCGTGTCGTAC-3'	xbaI	cDNA cloning
At1G68765	IDA-R1	5'-GGTACC TCAATGAGGAAGAGAGTTAACAAAAGAGTTG-3'	KpnI	cDNA cloning
	RT-IDA-1	5'-CATTCATTTACTCAAAGAAGTGGAAGTG-3'		Real time PCR
	RT-IDA-2	5'-GTGTCTCTTAGAAGGAGCAGAAGG-3'		Real time PCR
HAESA	RT-HAESA-1	5'-TGATTCAGAACTTGGAGATAAAGATATGG-3'		Real time PCR
At4G28490	RT-HAESA-2	5'-CTTCCGTGTAGTAAGGCGAGAG-3'		Real time PCR
HSL2	RT-HSL2-1	5'-TACATTCTCCCAATCTCAATCCTCTG-3'		Real time PCR
At5G65710	RT-HSL2-2	5'-CTGTTAATTGCGGGTATATGTCTTCC-3'		Real time PCR
HWS	RT-HWS-1	5'-GATATACTCAACGGGAGGCTCAG-3'		Real time PCR
At3G61590	RT-HWS-2	5'-CAGGTTAAAGAACACGGCATTGG-3'		Real time PCR
FYF	AGL42-1	5'-GGATCCATTCTAGGGCTCCTGACAGA-3'	BamHI	cDNA cloning
At5g62165	AGL42-2	5'-GGGATCCTCGCAGTTTCTATTTGGC-3	BamHI	cDNA cloning
	RT-AGL42-1	5'-AGCAATCACGACTCACAAATTCAC-3'		Real time PCR
	RT-AGL42-2	5'-AGCCTTTCTTTCTCGGACCTTTC-3'		Real time PCR
SAG12	RT-SAG12-1	5'-TCCAATTCTATTCGTCTGGTGTGT-3		Real time PCR
At5G45890	RT-SAG12-2	5'-CCACTTTCTCCCCATTTTGTTC-3		Real time PCR
α-VPE	RT-α-VPE-1	5'-GAGAACCGCTTGTTGACGATTG -3		Real time PCR
At2G25940	RT-α-VPE-2	5'-TTGCTGCCTCCTCCATTGC-3		Real time PCR
β-VPE	RT-β-VPE-1	5'-AATTAACTGAGACAACAAGGCATAGG-3		Real time PCR
At1G62710	RT-β-VPE-2	5'-CATTCCCAATCGTCAACCAAAGG-3		Real time PCR
AtMC1	RT-MC1-1	5'-GGTGGTAGTGGTGGAGTTGTG-3		Real time PCR
At1G02170	RT-MC1-2	5'-TGGCAAGCAGTCAGTTGAGG-3		Real time PCR
AtMC9	RT-MC9-1	5'-CATGATCTCTGATTCTTGCCATAGTG-3		Real time PCR
At5G04200	RT-MC9-2	5'-TTATAGTCTTGTTCGTTGTCTCAATAGC-3		Real time PCR