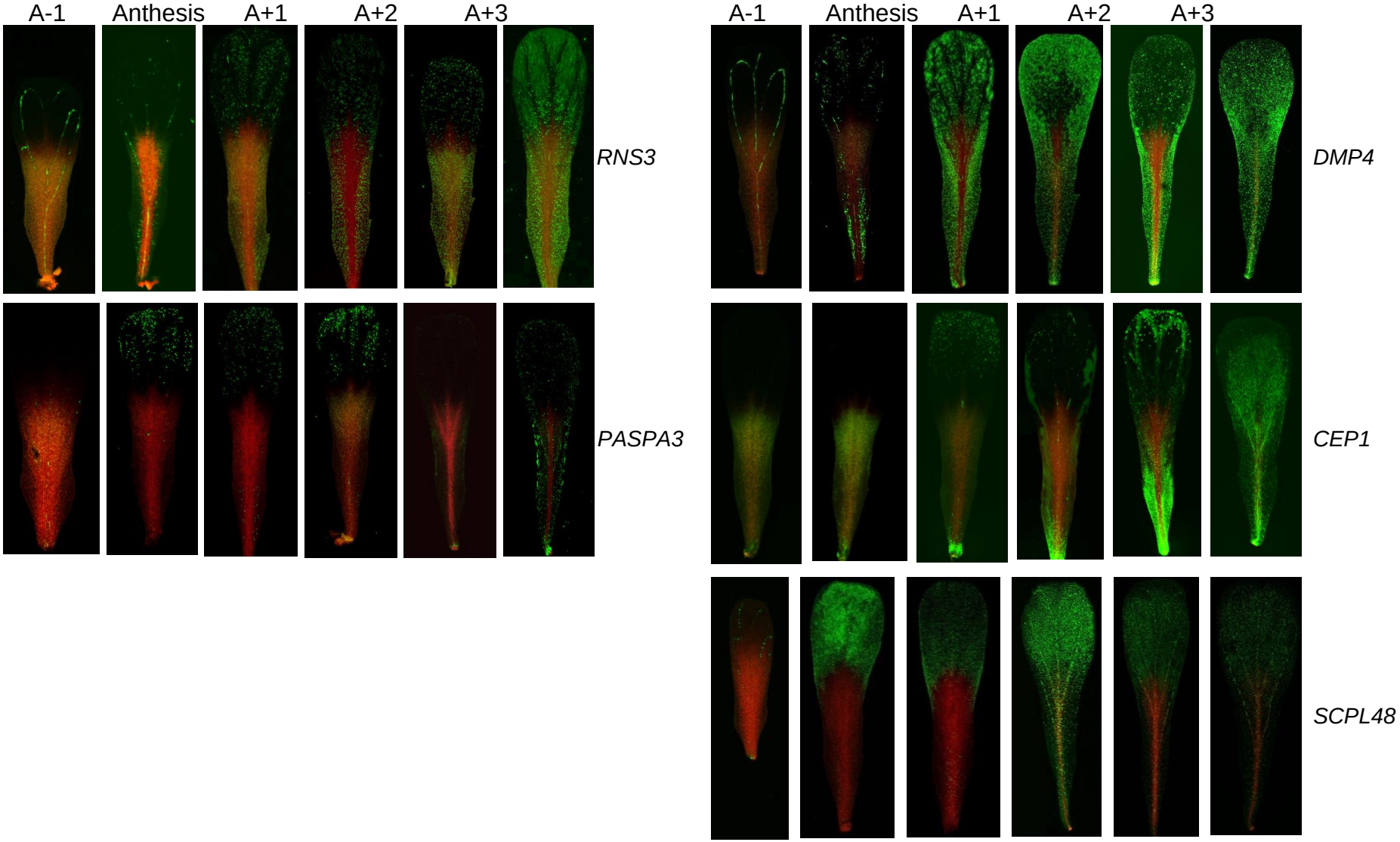
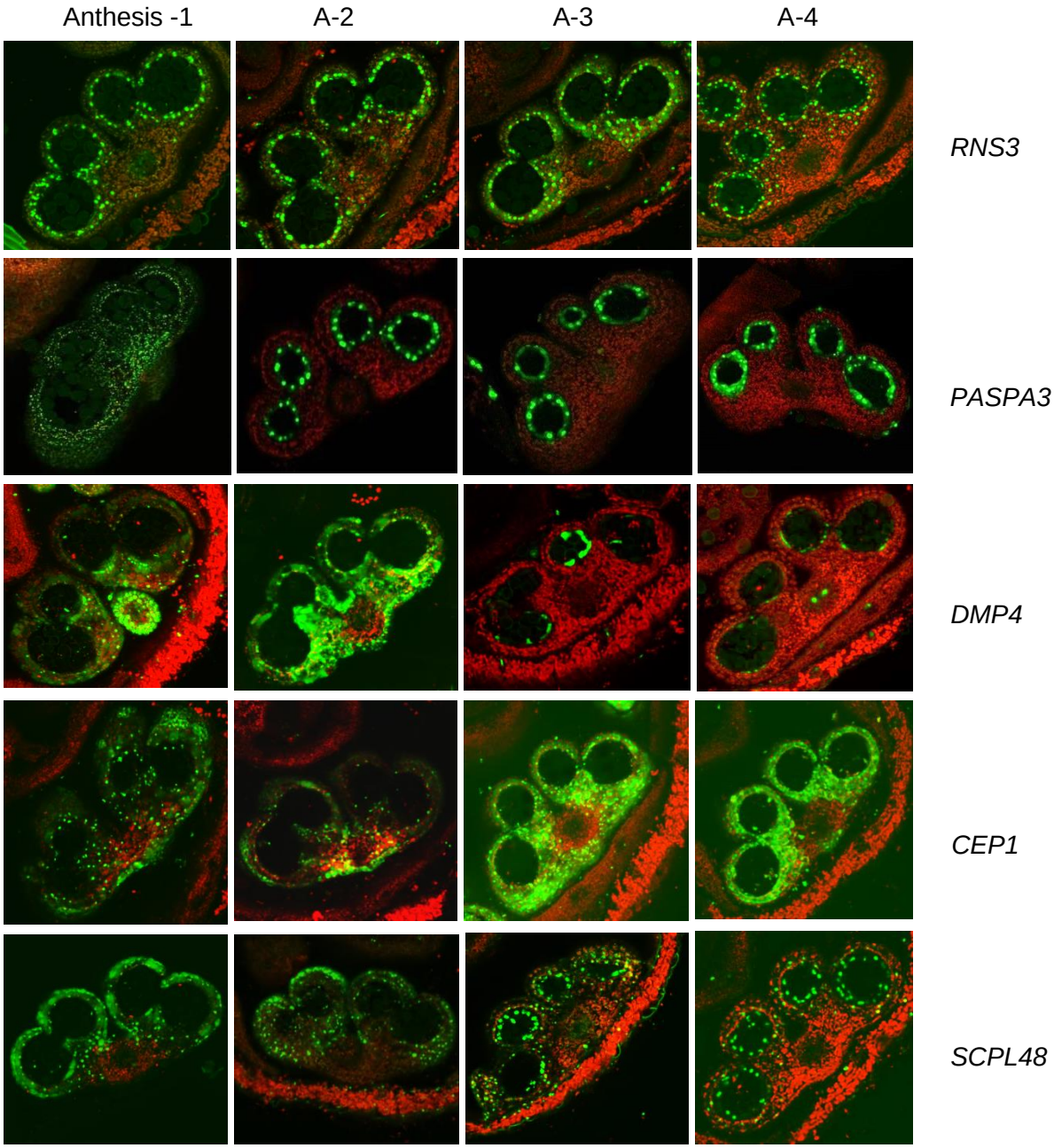
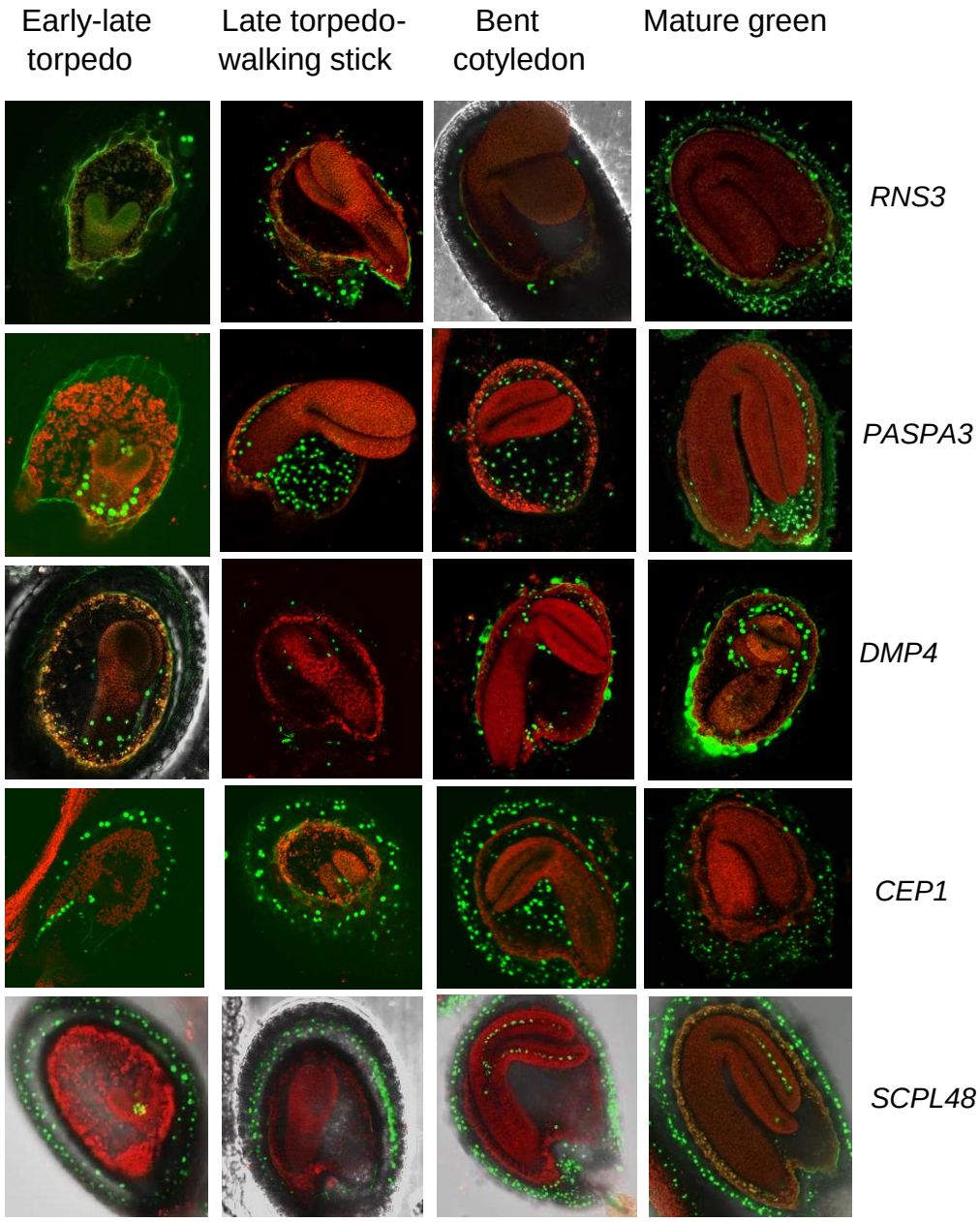


Supplemental Figure S1. Developmental series for petal senescence. The series starts one bud before anthesis (A-1), followed by the subsequent flowers before the dry stage (Anthesis, A+1 to A+4). Petals were dissected under a stereoscopic microscope, mounted in slides using Tween 0.01% dissolved in 1/10 MS and imaged in 2x4 tiles using confocal microscopy. The flowers were collected from one or two inflorescences from homozygous lines of the indicated transcriptional fusions with H2A-GFP cloned in a GAL4-UAS transactivation system.

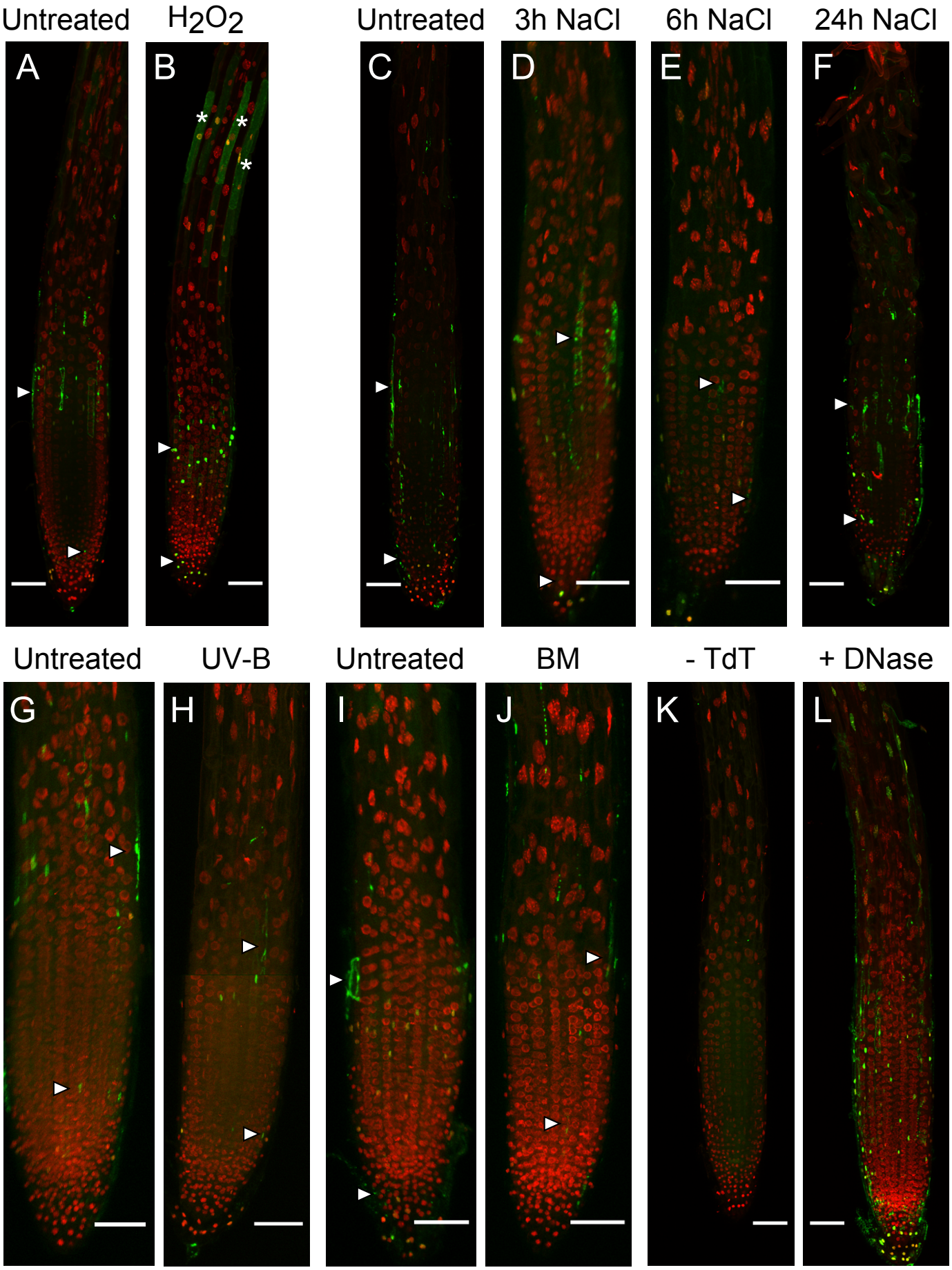


Supplemental Figure S2. Developmental series for tapetum differentiation. The series starts one bud before anthesis (Anthesis-1), and the previous floral buds around tapetum cell death (A-2 to A-4). Flowers at the indicated developmental stage were fixed for 2 hours at room temperature in a 3.7% Paraformaldehyde solution (dissolved in 50mM PIPES, 5mM EGTA and 1mM MgSO4 buffer), embedded in 5% agarose blocks and sectioned using a vibratome. They were mounted in slides with water and imaged using confocal microscopy. The flowers were collected from one or two inflorescences of the same plant using homozygous lines of the indicated transcriptional fusions with H2A-GFP in a GAL4-UAS transactivation system.

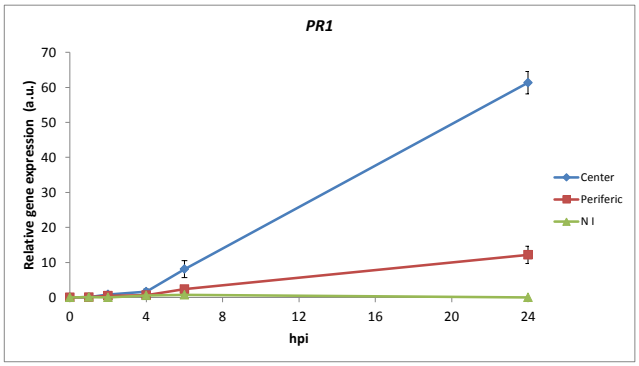


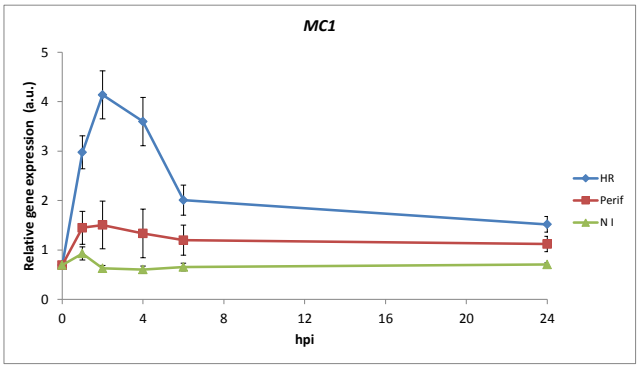
Supplemental Figure S3. Developmental series for seed development. Siliques at the indicated developmental stage were dissected in a stereoscopic microscope to remove the valves , fixed for 2 hours at room temperature in a 3.7% Paraformaldehyde solution (dissolved in 50mM PIPES, 5mM EGTA and 1mM MgSO4 buffer), embedded in 5% agarose blocks and sectioned using a vibratome. They were mounted with water in slides and imaged using CLSM. The siliques were collected from one or two stems of the same plant using homozygous lines of the indicated transcriptional fusions with H2A-GFP in a GAL4-UAS transactivation system.

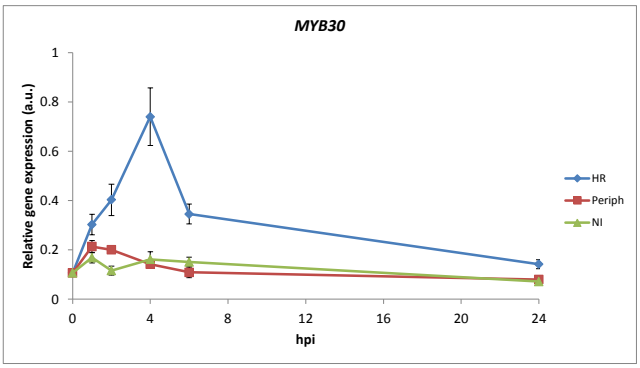
Supplementary Figure S4

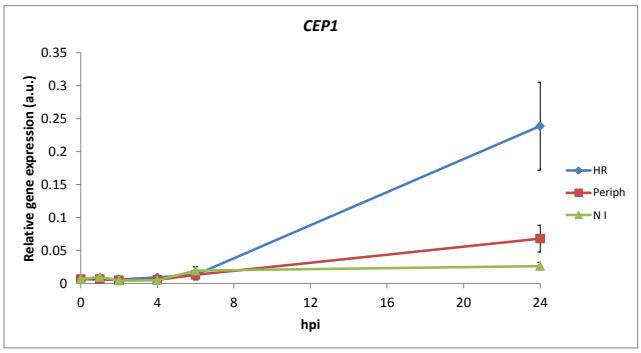


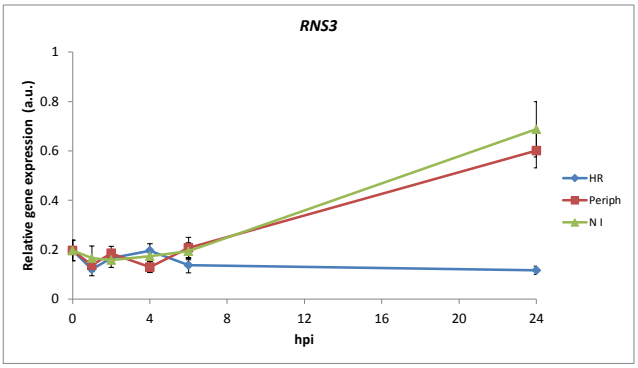
Supplemental Figure S4. Whole-mount TUNEL of 5-to 6-day old root tip after different abiotic stresses provoking cell death. TUNEL signals are in green, DAPI signals in red. A-B) Oxidative strss. A) untreated control. B) after treatment with 5mM H_2O_2 for 3h. C-F) salt stress. C) untreated control. D) after 3h, E) after 6h, F) after 24h of treatment with 140mM NaCl. G-H) ultraviolet radiation stress. G) non-radiated control. H) 8h after exposure to UV-B radiation. I-J) genotoxic stress, I) non-treated control, J) after 24h of treatment with 0.6ug/ml bleomycin. K) negative control without TdT enzyme. L) positive control after DNase treatment. Scale bars are 50um.

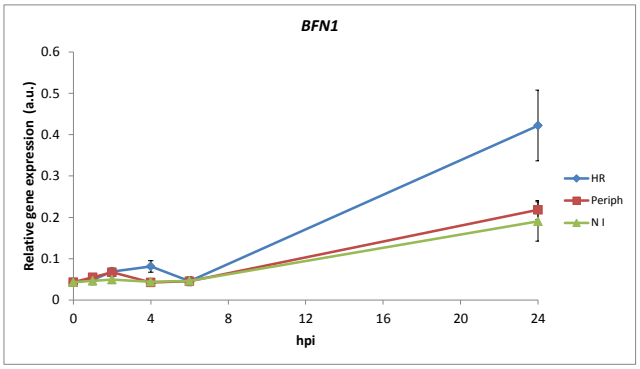


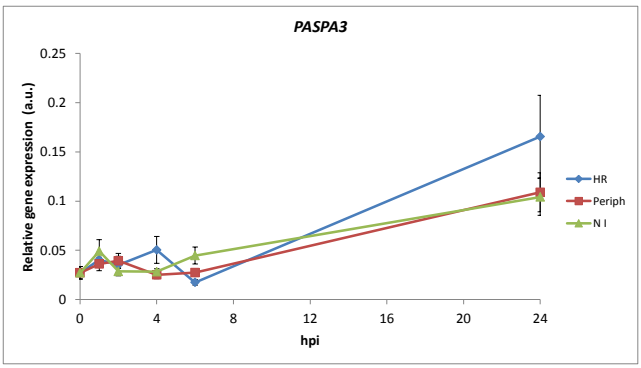


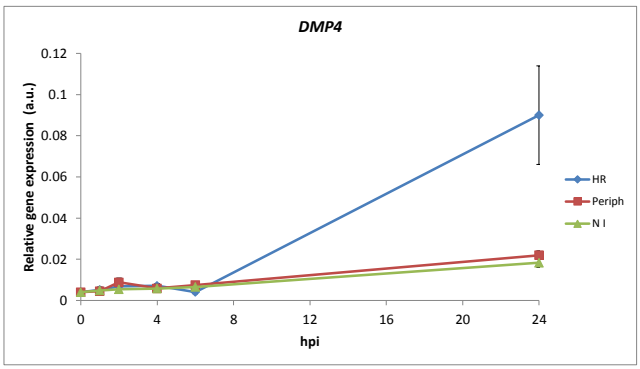


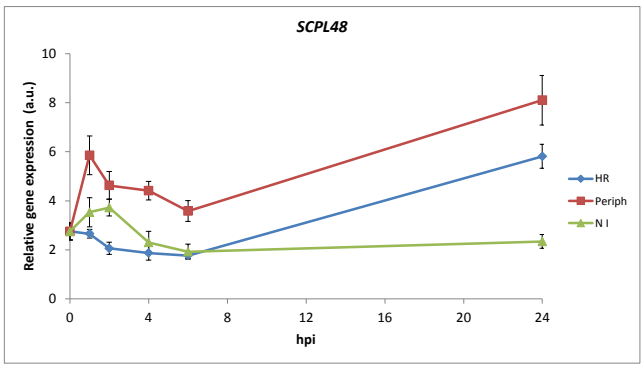


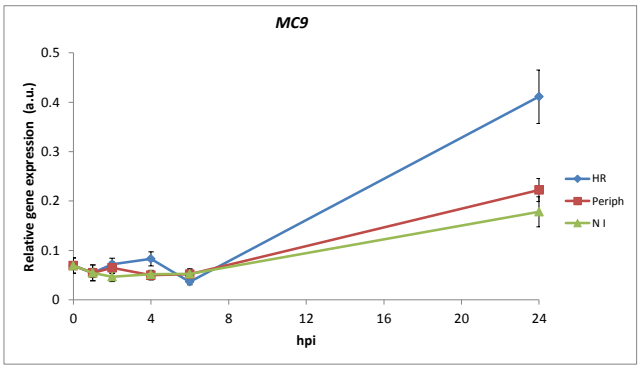












Supplemental Figure S4. dPCD marker genes are not transcriptionally regulated during HR-related ePCD. Arabidopsis Col-0 plants were inoculated with Pst AvrRpm1 (5 x 107 cfu/ml). Leaf samples were harvested at the indicated time points from areas inside the infiltrated zone that develops the HR (HR; blue), immediately neighboring the infiltrated zone (periph; red), and from non-inoculated tissues (NI; green) at the indicated time points. Relative expression of the indicated genes in the three zones was determined by Q-RT-PCR. PATHOGENESIS RELATED1 (PR1),METACASPASE1 (MC1), and MYB DOMAIN PROTEIN 30 (MYB30) were used as HR marker genes. Expression values were normalized using SAND family gene as internal standard. Mean and SEM values were calculated from 3 independent experiments with 3 replicates. hpi: hours after inoculation; a.u.: arbitrary units.

Supplemental Table S3. Detailed overview of the ATH1 microarray experiments used for the meta-analysis, describing the treatment leading to programmed cell death (PCD), the control treatment , the PCD subcategory, the presence/absence of a time course (TC) in the experiment, a summary description for the experiment, the experiment identifier and CEL file identifiers for the biological replicates. When a paper was referred for the experiment it is mentioned in the last column, otherwise it is marked as non-available (NA).

PCD	Control	PCD type	TC	Description	Identifier	CEL files	Ref.
Differentiating xylem	Cortex	Tracheary elements	No	sorted cells from 6 day-old roots, cell type specific- GFP expressing protoplast	GSE16468	GSM413912 -14, GSM413909- 11	(1)
VND6 and SND1 expressing cells	WT cells	Tracheary elements	No	cells treated with 2 µM estrogen for 12h	GSE20586	GSM517076 - 78, 82 -84, 88-90	(2)
35S:VND7-VP16-GR	Empty vector	Tracheary elements	No	10 day old seedlings treated with 10mM CHX for 2hrs followed by 10mM DEX for 4hrs	GSE24169	GSM594701-05, GSM594711-15	(3)
J3411:GFP, Lateral root cap plus epidermis	J0571:GFP, ground tissue (endodermis and cortex) and the QC	Lateral Root Cap	No	sorted cells from 4-5 day-old roots, cell type specific- GFP expressing protoplast	GSE5749	GSM133968-70 GSM133992-93	(4)
Peripheral endosperm-bending cotyledon stage	Embryo proper-bending cotyledon stage	Endosperm	No	Siliques containing bending cotyledon stage seeds were sectioned and the seed compartments were isolated using Laser Capture Microdissection (LCM)	GSE20039	GSM501159-60 GSM501157-58	(5)
Cellularized endosperm-linear cotyledon stage, Peripheral endosperm-bending cotyledon stage	Peripheral endosperm-globular stage, Peripheral endosperm-heart stage	Endosperm	No	Siliques containing seeds in the appropriate stage were sectioned and the seed compartments were isolated using LCM	GSE12403 GSE20039 GSE11262 GSE15160	GSM311289-90 GSM501159-60 GSM284390-91 GSM378649-50	(6)
General seed coat-bending cotyledon and linear cotyledon stage	LCM general seed coat at the heart stage	Seed coat	No	Siliques between 1.2 and 1.5 cm long, 1.6 and 1.9 cm long and 1.9-2.0 cm long were sectioned and the seed compartments isolated using LCM	GSE20039 GSE12403 GSE15160	GSM501165-66 GSM311295-96 GSM378657-58	(5)
Inducible overexpression ANAC059 and ANAC092	Empty vector	Senescence	No	3 weeks old shoots treated with 10µM estradiole and harvested 5 hours after induction	GSE14091	GSM353584-88 GSM353591-93	(7)
Partially senescent leaves, developmental stage: 6.0	Fully developed green leaves, developmental stage: 3.9	Senescence	No	Leaves were harvested at two stages to identify the senescence- enhanced genes	GSE5727	GSM133729-32	NA
Senescent leaf	Rosette leaf # 6	Senescence	No	AtGenExpress: Developmental series	GSE5630	GSM131513-15	NA

				(leaves)		GSM131537-39	
Flowers stage 15, petals	Flowers stage 12, petals	Senescence	No	AtGenExpress: Developmental series (flowers and pollen)	GSE5632	GSM131588-90 GSM131606-08	NA
Flowers stage 15, sepals	Flowers stage 12, sepals	Senescence	No	AtGenExpress: Developmental series (flowers and pollen)	GSE5632	GSM131585-87 GSM131603-05	NA
Senescing siliques of 20 days after anthesis	Mature green silique tissues of 10 days after anthesis	Senescence	No	Two pods collected from each plant and pooled from 20 plants	GSE5736	GSM133816-21	(8)
saul1 mutants transferred to low light treatment for 0, 48h	wt transferred to low light treatment for 0, 48h	Senescence	Yes	11 d old seedlings grown in permissive light (60 umol m-2 s-1) and then transferred to low light treatment	NA	NA	(9)
When 10-30 % cell death was observed in protoplasts the samples were harvested and pooled in one sample	No cell death	Biotic stress	No	6-day old, dark grown cell cultures were treated with 20uM Fumonisin B1 (mycotoxin that induces PCD by disrupting ceramide synthesis) or Methanol as mock treatment, pooled and then protoplasted	GSE5735	GSM133808-15	NA
cpr5 mutant	Wt	Biotic stress	No	Cpr5 mutant exhibits spontaneous cell death and heightened immunity	GSE40322	GSM991294-99	(10)
Wt	*rpp4* mutant	Biotic stress	Yes	2-week old leaves were inoculated with *Hyaloperonospora arabidopsidis* Emwa1. RNA extracted 0 and 6 days after inoculation. rpp4 mutant had the highest percentage of leaves with sporangiophores (SPP), confirming that its resistance to Hpa Emwa1 is completely compromised	GSE22274	GSM554311_rep1, _rep2 GSM554315_rep1, _rep2 GSM554316_rep1,_rep2 GSM554320_rep1,_rep2	(11)
30 h after inoculation	Before inoculation	Biotic stress	No	2 week old Wt roots were inoculated with *Phytophthora parasitica* 310 strain (10^6	GSE20226	GSM507047-48, GSM507055-56	(12)

				zoospores per Petri dish)			
Botrytis cinerea conidiospores	Mock treated	Biotic stress	Yes	Four 5 ul droplets of *Botrytis cinerea* conidiospores diluted to $5X10^5$ spores/ml or sterile potato dextrose broth were placed on each of 4-5 rosette leaves (4 week old) per plant. Laeves were harvested 18 hpi	GSE5684	GSM133025-36	(13)
Phytophthora infestans spores	Water drops on leaves	Biotic stress	Yes	*Phytophthora infestans* ($5x10^5$ spores) in water applied to 5 week old leaf surfaces. Tissue was harvested 6, 12, 24 hpi	GSE5616	GSM131160-68, GSM131151-59	NA
1 µM GST-NPP1 in water	1 µM GST in water	Biotic stress	No	5 week old leaves infiltrated, harvested 4 hours later	GSE5615	GSM131110, 12, 24, 26, 38, 40	NA
Chitosan 150 µg/ml	Mock solution (0.02% acetic acid)	Biotic stress	No	4 day-old seedlings were treated for 3 hours before RNA extraction	GSE17193	GSM429956,61 GSM429980-81,	(14)
10 µM HrpZ	leaves infiltrated with water	Biotic stress	No	5-weeks old rosette leaves treated for 4 hours	GSE5615	GSM131111, 22, 25, 36, 39,50	NA
*At*MYB30-ox	Arabidopsis AtMYB30-as	Biotic stress	No	4 weeks old leaves, 90-105 min after inoculation with a *Xanthomonas* strain, Xcc147	GSE9674	GSM244451-52, 58-59	(15)
Inoculation with *Pseudomonas syringae* pv. *tomato* (Pto) expressing the effector HopZ1a into Wt plants	Inoculation with *Pseudomonas syringae* pv. *tomato* (Pto) wt, into WT plants	Biotic stress	No	The effector HopZ1a is recognized in *Arabidopsis*, triggering the hypersensitive response (HR). Rosette leaf 1-5 harvested 6 hpi	GSE21920	GSM545364, 67, 72 84-86	NA
Cucumber mosaic virus (CMV) 2b counter-defense protein- expressing plants	Wt plants, mock treated	Biotic stress	No	The Cucumber mosaic virus (CMV) 2b counter-defense protein disrupts plant antiviral mechanisms mediated by RNA silencing and salicylic acid (SA)	GSE37921	GSM929932-33, 35, 36, 38, 39	(16)
Cell suspension cultures were exposed to high	Cell suspension cultures were kept at 50 microE/m2/s	Oxidative stress	No	200 mL of cultures with a cell density of approximately 150-200 mg/mL, kept at constant temperature	GSE22671	GSM562208-10, GSM562214-16	(17)

light during 30 minutes (1800 microE/m2/s)							
flu mutant	Wt	Oxidative stress	No	Plants grown under continuous light 90 mmol. m-2 . s-1 for 3 weeks, transferred to the dark for 8 h and rosette leaves were harvested 2 h after reillumination	GSE10812	GSM272985-88	(18)
Wt, 20mM hydrogen peroxide	Wt, sprayed with deionised water	Oxidative stress	No	2 week old seedlings were harvested 3 hr after treatment	GSE41136	GSM1009029-34	NA
Fumigation with 500 ppb ozone .	Fumigation with scrubbed air (filtered through charcoal and purafill)	Oxidative stress	No	2 week-old seedlings were harvested 6 hr after treatment. Flow rate was 910ml/min	GSE5722	GSM133705-10	NA
Wt seedlings treated with 5mM H2O2	Untreated	Oxidative stress	No	7d dark-grown seedlings were used to reduce the endogenous H2O2 level caused by light	GSE40574	GSM996955-58	(19)
Methyl viologen (10 uM final conc) was added to the media to induce Oxidative stress	Control plants were handled like the treated plants and harvested in parallel	Oxidative stress	Yes	18-day-old shoots were harvested 12 and 24 h after treatment	ME00340	OXIDATIVE_12H_SHOOT_REP1, REP2, OXIDATIVE_24H_SHOOT_REP1, REP2, OXIDATIVE_CONTROL_12H_SHOOT_REP1, REP2 OXIDATIVE_CONTROL_24H_SHOOT_REP1, REP2	NA
Methyl viologen (10 uM final conc) was added to the media to induce Oxidative stress	Control plants were handled like the treated plants and harvested in parallel	Oxidative stress	Yes	18-day-old roots were harvested 12 and 24 h after treatment	ME00340	OXIDATIVE_12H_ROOT_REP1, REP2, OXIDATIVE_24H_ROOT_REP1, REP2, OXIDATIVE_CONTROL_12H_ROOT_REP1, REP2 OXIDATIVE_CONTROL_24H_ROOT_REP1, REP2	NA

cat2 mutant, high light exposure in a sun simulator	*cat2*, Ambient growth conditions	Oxidative stress	Yes	6 week old leaves were harvested 0, 3 and 8 h after treatment	E-MEXP-449	pz220803_04, _05,_12, hyb1480, 81, 83	NA
*wee1*KO, transferred to medium with 2mM Hydroxyurea	*wee1*KO, transferred to control medium	Genotoxic stress	Yes	5d old roots were harvested 5 and 24 h after treatment	E-MEXP-3048, E-MEXP-3053	hyb2133-36, 39-42	(20)
1.5ug/ml bleomycin + 22 ug/ml mitomycin	Control- no treatment	Genotoxic stress	Yes	16 d old seedling shoots were harvested 12 and 24 h after treatment	GSE5620 GSE5625	GSM131251,52,55,56 GSM131375,76,79,80	NA
1.5ug/ml bleomycin + 22 ug/ml mitomycin	Control- no treatment	Genotoxic stress	Yes	16 d old seedling roots were harvested 12 and 24 h after treatment	GSE5620 GSE5625	GSM131253,54,57,58 GSM131377,78,81,82	NA
Thaxtomin A	Methanol	Genotoxic stress	No	suspension cell culture 6 h after treatment	GSE17824	GSM444737-44	NA
Isoxaben	Methanol	Genotoxic stress	No	Suspension cell culture, 6 h after treatment	GSE17824	GSM444745-52	NA
UV-1-day radiation	Continuos white light	UV stress	No	18 d old seedlings, shoots harvested 24h after treatment	GSE22951	GSM566614-16 GSM566623-25	NA
UV-B stress (15 min. 1.18 W/m2)	Control- no treatment	UV stress	Yes	16 d old seedlings, Shoots harvested 12 and 24 h after treatment	GSE5626	GSM131403-04 GSM131407-08	(17)
UV-B stress (15 min. 1.18 W/m2)	Control- no treatment	UV stress	Yes	16 d old seedlings Roots-12 and 24 h	GSE5626	GSM131405-06 GSM131409-10	(17)
30 h at 37 °C Heat stress, no recovery	No treatment, no recovery	Heat stress	No	3 week old seedling	GSE18666	GSM463683-86	(21)
55 C for 10 minutes	No treatment	Heat stress	No	6 d suspension cells	NASCARRAYS-30	NRID5299-NRID5304_Swidzinski	NA
250mM NaCl solution	Only water supply	Salt stress	No	5-week-old rosette leaves harvested 24 h after treatment	E-ATMX-30	E-ATMX-30.raw.1.zip/ WT-NaCl1.CEL / WT_NaCl2.CEL / WT-	(22)

						1.CEL /WT-2	
140 mM NaCl	No treatment	Salt stress	Yes	whole seedling roots ,5 days after germination, were harvested 16 and 32 h after treatment	GSE7642	GSM184925-26, GSM184933-36	(23)
Nacl 150 mM	No treatment	Salt stress	Yes	16 d old seedling shoots were harvested 12 and 24 h after treatment	GSE5623	GSM131323-24, GSM131327-28	(17)
Nacl 150 mM	No treatment	Salt stress	Yes	16 d old seedling roots were harvested 12 and 24 h after treatment	GSE5623	GSM131325-26, GSM131329-30	(17)
Wildtype_24H 0°C_Rep1	Wildtype_no treatment_Rep2	Cold stress	No	10 day old seedlings-grown in plate	GSE3326	GSM74900-01, GSM748995	(24)
4°C_under continuous light (~25 umol m-2 s-1)	24°C_under continuous light (~25 umol m-2 s-1)	Cold stress	No	10 day old seedlings-grown in plate 18 days old, aerial parts, soil grown	GSE5534 GSE5535	GSM128789-90, GSM128795-96, GSM128797-98 GSM128803-04	NA
0.3 M mannitol	Control- no treatmen	Osmotic stress	Yes	16-day-old seedlings, Shoots harvested 12 and 24 h after treatment	GSE5622	GSM131299-300 GSM131303-304	(17)
0.3 M mannitol	Control- no treatment	Osmotic stress	Yes	16-day-old seedlings, Shoots harvested 12 and 24 h after treatment	GSE5622	GSM131301-302 GSM131305-306	(17)
0.3M mannitol	Mock treated	Osmotic stress	No	30 d old leaf, 10 day treatment	GSE36789	GSM901069-71 GSM901075-77	(25)
0.3M mannitol	Mock treated	Osmotic stress	No	30 d old root, 10 day treatment	GSE36789	GSM901072-74 GSM901078-80	(25)
ACC (10 uM) ethylene precursor	Mock (3 hours)	Hormone (Ethylene)	No	7-day-old seedling, 3 h after treatment	ME00334	RIKEN-GODA23A, 23B RIKEN-GODA17BA,17AA	NA
5 ppm ethylene	Air	Hormone (Ethylene)	No	Petiole harvested 3 h after treatment	NASC ARRAYS-32	Millenaar_A2_ETH_Rep1, Rep2, Millenaar_A5_ETH_Rep3, Millenaar_A1_AIR_Rep1, Rep2 Millenaar_A4_AIR_Rep3	NA
10 ppm ethylene	Air	Hormone (Ethylene)	No	7-day-old seedling, 3 h after treatment	ME00364	RIKEN-GODA21AH, BH RIKEN-GODA1AH, BH	(26)
Salicylic acid (10 uM, 3 hours)	Mock (3 hours)	Hormone (Salicylic acid)	No	3 week old plants, 4 h after treatment	GSE14247	GSM356823-26	NA
2 mM SA treated	Water treated	Hormone (Salicylic acid)	No	9-day-old seedling, 24 h after treatment	GSE14961	GSM373532-36	NA

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Supplemental Table S4. Overview of the number of up- and down-regulated genes per condition in the experiments used in the meta-analysis. For each condition the associated experiment number is indicated.

1) Developmental induced cell death

		Number of genes			*Condition*	*Experiment*
1.1 Differentiation induced PCD		Down	Up	Total		
e-1 vs e-2	Xylem vs cortex	3124	2208	5332	*1*	*1*
e-3 vs e-5	VND6 vs Wt	995	1273	2268	*2*	*2*
e-4- vs e-5	SND1 vs Wt	371	1030	1401	*3*	*2*
e-6 vs e-7	VND7 vs mock	64	133	197	*4*	*3*
e-8 vs e-9	LRC vs ground	994	1108	2102	*5*	*4*
e-10 vs e-11	End vs embryo, bending cotyledon stage	2793	1834	4627	*6*	*5*
e-13 vs e-15	Linear cotyledon vs globular stage, endosperm	2983	2907	5890	*7*	*6*
e-14 vs e-12	Bending cotyledon vs heart stage, endosperm	2850	2120	4970	*8*	*6*
e-16 vs e-18	Bending cotyledon vs heart stage,seed coat	2265	1770	4035	*9*	*7*
e-17 vs e-18	Linear cotyledon vs heart stage,seed coat	1611	1643	3254	*10*	*7*
1.2 Senescence induced PCD						
e-19 vs e-21	Inducible ANAC059 vs empty vector	27	46	73	*11*	*8*
e-20 vs e-21	Inducible ANAC092 vs empty vector	60	180	240	*12*	*8*
e-22 vs e-23	Mature green vs senescing siliques	1513	1383	2896	*13*	*9*
e-24 vs e-25	Rosette, green vs senescing leaves	2338	2572	4910	*14*	*10*
e-26 vs e-27	Flower stage 15 vs stage 12, petals	2478	2217	4695	*15*	*11*
e-28 vs e-29	Flower stage 15 vs stage 12, sepals	1794	1435	3229	*16*	*12*
e-30 vs e-31	Leaf stage 6 vs 3.9, partially senescent vs mature green	1485	1748	3233	*17*	*13*
e-32 vs e-34	*saul* vs wt, time 0, low light	1	26	27	*18*	*14*
e-33 vs e-35	*saul* vs wt, time 48 h, low light	2677	2172	4849	*19*	*14*

2) Environmental induced cell death

2.1 Biotic induced PCD		Down	Up	Total	*Contrast*	*Experiment*
e-36 vs e-37	Fumonisin B1 vs mock, protoplast	21	39	60	*20*	*15*
e-38 vs e-39	*cpr5* vs wt	129	751	880	*21*	*16*
e-40 vs e-42	*rpp4* vs wt, time 0	354	256	610	*22*	*17*
e-41 vs e-43	*rpp4* vs wt, 6 days after inoculation	174	84	258	*23*	*17*
e-44 vs e-45	*Phytophthora* inoculated root vs control, 30 hpi	1634	1303	2937	*24*	*18*
e-46 vs e-48	*Botrytis* inoculated leaves, vs control, 18 hpi	73	539	612	*25*	*19*
e-47 vs e-49	*Botrytis* inoculated leaves, vs control, 48 hpi	1597	1287	2884	*26*	*19*
e-50 vs e-53	*Phytophthora* inoculated leaves, vs control, 6 hpi	1190	1051	2241	*27*	*20*
e-51 vs e-54	*Phytophthora* inoculated leaves, vs control, 12 hpi	333	658	991	*28*	*20*
e-52 vs e-55	*Phytophthora* inoculated leaves, vs control, 24 hpi	356	563	919	*29*	*20*
e-56 vs e-57	NPP1 treated leaves vs mock, 4h	241	722	963	*30*	*21*
e-58 vs e-59	chitosan vs mock,seedlings, 3h	501	634	1135	*31*	*22*
e-60 vs e-61	HrpZ treated leaves vs mock, 4h	1141	1374	2515	*32*	*23*
e-62 vs e-63	AtMYB30-ox vs AtMYB30-as, *Xanthomonas* inoculated, 90-105 min after inoc	35	53	88	*33*	*24*

e-64 vs e-65	*Pseudomonas* expressing HopZ1a, into Wt plants vs *Pseudomonas* Wt , into Wt plants	754	693	1447	*34*	*25*
e-66 vs e-67	Cucumber mosaic virus (CMV) 2b counter-defense protein- expressing plants vs wt plants	78	391	469	*35*	*26*
2.2 Oxidative stress		Down	Up	Total	*Contrast*	*Experiment*
e-68 vs e-69	HL exposed cultures, vs control, 30 min	42	277	319	*36*	*27*
e-70 vs e-71	*flu* vs wt, continuos light-dark-light, leaves	386	1261	1647	*37*	*28*
e-72 vs e-73	20mM hydrogen peroxide vs control, 3 h, seedling	45	198	243	*38*	*29*
e-74 vs e-75	500 ppb ozone vs control, 6h, seedling	860	1538	2398	*39*	*30*
e-76 vs e-77	5mM H2O2 vs control, seedling dark grown	205	693	898	*40*	*31*
e-78 vs e-80	Methyl viologen vs control, 12h, shoots	0	73	73	*41*	*32*
e-79 vs e-81	Methyl viologen vs control, 24h, shoots	8	274	282	*42*	*32*
e-82 vs e-84	Methyl viologen vs control, 12h, roots	3	1	4	*43*	*33*
e-83 vs e-85	Methyl viologen vs control, 24h, roots	99	21	120	*44*	*33*
e-86 vs e-88	*cat2* mutant, high light, vs control, 3h	563	593	1156	*45*	*34*
e-87 vs e-88	*cat2* mutant, high light, vs control, 8h	1326	1674	3000	*46*	*34*
2.3 Genotoxic stress						
e-89 vs e-91	*wee1* KO- Hydroxyurea, vs control,5h	3	60	63	*47*	*35*
e-90 vs e-92	*wee1* KO- Hydroxyurea, vs control,24h	49	138	187	*48*	*35*
e-93 vs e-95	bleomycin +mitomycin vs control, shoots, 12 h	25	158	183	*49*	*36*
e-94 vs e-96	bleomycin +mitomycin vs control, shoots, 24 h	16	152	168	*50*	*36*
e-97 vs e-99	bleomycin +mitomycin vs control, roots, 12 h	116	223	339	*51*	*37*
e-98 vs e-100	bleomycin +mitomycin vs control, roots, 24 h	175	283	458	*52*	*37*
e-101 vs e-102	TA, cell cultures vs mock, 6h	1	189	190	*53*	*38*
e-103 vs e-104	IXB, cell cultures vs mock, 6h	0	37	37	*54*	*39*
2.4 UV stress						
e-105 vs e-106	UV-1-day radiation vs white light, shoots 18d, 24h	483	570	1053	*55*	*40*
e-107 vs e-95	UV-15min vs control, shoots 16d , 12 h	89	358	447	*56*	*41*
e-108 vs e-96	UV-15min vs control, shoots 16d , 24 h	87	314	401	*57*	*41*
e-109 vs e-99	UV-15min vs control, roots 16d , 12 h	3	4	7	*58*	*42*
e-110 vs e-100	UV-15min vs control, roots 16d , 24 h	88	155	243	*59*	*42*
2.5 Heat stress						
e-111 vs e-112	30 h, 37 °C- no recovery vs control, 3week seedling	2125	2170	4295	*60*	*43*
e-113 vs e-115	10m , 55 °C vs mock,suspension cells	610	759	1369	*61*	*44*
2.6 Salt stress						
e-116 vs e-117	250mM NaCl vs control, rosette leaves, 24 h	1251	965	1351	*62*	*45*
e-118 vs e-120	140mM NaCl vs control, seedling root, 16 h	162	334	496	*63*	*46*
e-119 vs e-120	140mM NaCl vs control, seedling root, 32 h	112	300	412	*64*	*46*
e-121 vs e-95	250mM NaCl vs control, shoots 16d , 12 h	342	449	791	*65*	*47*
e-122 vs e-96	250mM NaCl vs control, shoots 16d , 24 h	874	953	1827	*66*	*47*
e-123 vs e-99	250mM NaCl vs control, roots 16d , 12 h	1652	1613	3265	*67*	*48*

e-124 vs e-100	250mM NaCl vs control, roots 16d , 24 h	1269	1618	2887	*68*	*48*
2.7 Cold stress						
e-125 vs e-126	Wildtype_24h 0°C vs control, 24 h	938	1123	2061	*69*	*49*
e-127 vs e-129	4°C vs 24°C, 7days treated, seedlings 10d old	784	718	1502	*70*	*50*
e-128 vs e-130	4°C vs 24°C, 7days treated, seedlings 18d old	368	358	726	*71*	*50*
2.8 Osmotic stress						
e-131 vs e-95	300 mM Mannitol-12 h vs control, shoots, 16 d	1901	1657	3558	*72*	*51*
e-132 vs e-96	300 mM Mannitol-24 h vs control, shoots, 16 d	2439	2168	4607	*73*	*51*
e-133 vs e-99	300 mM Mannitol-12 h vs control, roots, 16 d	1501	1196	2697	*74*	*52*
e-134 vs e-100	300 mM Mannitol-24 h vs control, roots, 16 d	1290	1073	2363	*75*	*52*
e-135 vs e-136	300 mM Mannitol-10 d vs control, 30 d old , leaf	331	533	864	*76*	*53*
e-137 vs e-138	301 mM Mannitol-10 d vs control, 30 d old , leaf	642	857	1499	*77*	*54*
2.9 Hormone		Down	Up	Total	*Contrast*	*Experiment*
e-139 vs e-140	ACC (10 uM, 3 h), seedling	14	53	67	*78*	*55*
e-141 vs e-142	5 ppm ethylene, 3h, petiole	149	244	393	*79*	*56*
e-143 vs e-144	Salicylic acid (SA, 10 uM, 3 h), seedling	96	403	499	*80*	*57*
e-145 vs e-146	10 ppm ethylene vs air, 3 week old, 4h	2969	3027	5996	*81*	*58*
e-147 vs e-148	2 mM SA vs control, seedling, 24h	1543	1558	3101	*82*	*59*

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Supplemental Tables S6.1 – S6.6

Supplemental Tables S6.1. Performance results of SVM and RF classification of dPCD versus ePCD instances based on the expression profiles of various gene (feature) sets in various experiment subsets. The SVM and RF parameter settings for all analyses can be found in Supplemental Tables S6.2 and S6.3, respectively (linked to the identifiers in the first column). The performance scores displayed are MCC scores generated by 10-fold cross-validation (or 5-fold cross-validation when the number of contrasts in one of the classes was < 10). No optimal settings are reported for the sampled entries (C1.SVM-D4.SVM and C1.RF-D4.RF) since the results are averaged over a hundred runs.

Identifier	dPCD Class	ePCD Class	#dPCD contrasts	#ePCD contrasts	Balanced	Gene Selection	Algorithm	MCC (Matthews Correlation Coefficient)
A1.SVM	All dPCD	All ePCD	19	64	No	All	SVM	0.75
A1.RF							RF	0.71
A2.SVM	All dPCD	All ePCD	19	64	No	Curated	SVM	0,71
A2.RF							RF	0,76
A3.SVM	All dPCD	Osmotic+genotoxic+biotic	19	30	No	All	SVM	0.75
A3.RF							RF	0.79
A4.SVM	All dPCD	Osmotic+genotoxic+biotic	19	30	No	Curated	SVM	0,79
A4.RF							RF	0,83
B1.SVM	Differentiation dPCD	All ePCD	10	64	No	All	SVM	0.88
B1.RF							RF	0.82
B2.SVM	Differentiation dPCD	All ePCD	10	64	No	Curated	SVM	0,88
B2.RF							RF	0,77
B3.SVM	Differentiation dPCD	Osmotic+genotoxic+biotic	10	30	No	All	SVM	0.93
B3.RF							RF	0.87
B4.SVM	Differentiation dPCD	Osmotic+genotoxic+biotic	10	30	No	Curated	SVM	0,93
B4.RF							RF	0,87

Supplemental Table S6.1 (continued):

C1.SVM	All dPCD	Sampled from all ePCD	19	19	Yes	All	SVM	0.74
C1.RF							RF	0.77
C2.SVM	All dPCD	Sampled from all ePCD	19	19	Yes	Curated	SVM	0,77
C2.RF							RF	0,81
C3.SVM	All dPCD	Sampled from Osmotic+genotoxic+biotic	19	19	Yes	All	SVM	0.73
C3.RF							RF	0.79
C4.SVM	All dPCD	Sampled from Osmotic+genotoxic+biotic	19	19	Yes	Curated	SVM	0,76
C4.RF							RF	0,83
D1.SVM	Differentiation dPCD	Sampled from all ePCD	10	10	Yes	All	SVM	0.75
D1.RF							RF	0.8
D2.SVM	Differentiation dPCD	Sampled from all ePCD	10	10	Yes	Curated	SVM	0,79
D2.RF							RF	0,81
D3.SVM	Differentiation dPCD	Sampled from Osmotic+genotoxic+biotic	10	10	Yes	All	SVM	0.71
D3.RF							RF	0.79
D4.SVM	Differentiation dPCD	Sampled from Osmotic+genotoxic+biotic	10	10	Yes	Curated	SVM	0.77
D4.RF							RF	0.82

Supplemental Table S6.2. Optimized SVM parameter settings for the analyses in Supplemental Table S6.1

Identifier	Kernel Type	Gamma	Nu	Eps
A1.SVM	RBF	0	0.2	0.001
A2.SVM	RBF	0,125	0,2	0,001
A3.SVM	Linear	0	0.1	0.001
A4.SVM	RBF	0,5	0,2	0,001
B1.SVM	RBF	0	0.1	0.001
B2.SVM	RBF	0,125	0,1	0,001
B3.SVM	RBF	0.5	0.2	0.001
B4.SVM	RBF	0,5	0,2	0,001

Supplemental Table S6.3. Optimized RF parameter settings for the analyses in Supplemental Table S6.1

Identifier	max-depth	min instances	num trees
A1.RF	2	7	20
A2.RF	2	5	30
A3.RF	2	4	10
A4.RF	2	3	100
B1.RF	1	10	30
B2.RF	1	10	30
B3.RF	1	10	30
B4.RF	1	10	30

Supplemental Table S6.4. The performance of binary classifiers discriminating a particular PCD subclass from all other subclasses. N/A indicates that the MCC could not be calculated by lack of positives or negatives, and thus indicates very poor performance. The SVM and RF parameter settings for all analyses can be found in Supplemental Tables S6.5 and S6.6, respectively (linked to the identifiers in the first column).

Identifier	Class 1	Class 2	#Contrasts Class 1	#Contrasts Class 2	Gene Selection	Algorithm	MCC
E1.SVM	Senescence dPCD	All - Senescence dPCD	9	74	All	SVM	0.46
E1.RF						RF	0.46
E2.SVM	Senescence dPCD	All - Senescence dPCD	9	74	Curated	SVM	0.73
E2.RF						RF	0.4
F1.SVM	Differentiation dPCD	All - Differentiation dPCD	10	73	All	SVM	0.88
F1.RF						RF	0.75
F2.SVM	Differentiation dPCD	All - Differentiation dPCD	10	73	Curated	SVM	0.88
F2.RF						RF	0.82
G1.SVM	Genotoxic ePCD	All - Genotoxic ePCD	9	74	All	SVM	0.73
G1.RF						RF	0.8
G2.SVM	Genotoxic ePCD	All - Genotoxic ePCD	9	74	Curated	SVM	0.8
G2.RF						RF	0.8
H1.SVM	Oxidative ePCD	All - Oxidative ePCD	10	73	All	SVM	0.3
H1.RF						RF	N/A
H2.SVM	Oxidative ePCD	All - Oxidative ePCD	10	73	Curated	SVM	0.29
H2.RF						RF	N/A
I1.SVM	UV ePCD	All - UV ePCD	5	78	All	SVM	N/A
I1.RF						RF	N/A
I2.SVM	UV ePCD	All - UV ePCD	5	78	Curated	SVM	N/A
I2.RF						RF	N/A

Supplemental Table S6.4 (continued)

J1.SVM	Temperature ePCD	All - Temperature ePCD	6	77	All	SVM	N/A
J1.RF						RF	N/A
J2.SVM	Temperature ePCD	All - Temperature ePCD	6	77	Curated	SVM	0.39
J2.RF						RF	0.39
K1.SVM	Osmotic/Salt ePCD	All - Osmotic/Salt ePCD	13	70	All	SVM	0.77
K1.RF						RF	0.82
K2.SVM	Osmotic/Salt ePCD	All - Osmotic/Salt ePCD	13	70	Curated	SVM	0.96
K2.RF						RF	0.86
L1.SVM	Hormone ePCD	All - Hormone ePCD	5	78	All	SVM	N/A
L1.RF						RF	0.44
L2.SVM	Hormone ePCD	All - Hormone ePCD	5	78	Curated	SVM	0.62
L2.RF						RF	0.17
M1.SVM	Biotic ePCD	All - Biotic ePCD	16	67	All	SVM	0.62
M1.RF						RF	0.49
M2.SVM	Biotic ePCD	All - Biotic ePCD	16	67	Curated	SVM	0.66
M2.RF						RF	0.46

Supplemental Table S6.5. Optimized SVM parameter settings for the analyses in Supplemental Table S6.4

Identifier	Kernel Type	Gamma	Nu	Eps
E1.SVM	RBF	0	0.1	0.001
E2.SVM	RBF	0.03	0.1	0.001
F1.SVM	RBF	0	0.1	0.001
F2.SVM	RBF	0.03	0.1	0.001
G1.SVM	RBF	0.03	0.1	0.001
G2.SVM	RBF	0	0.1	0.001
H1.SVM	RBF	0.5	0.1	0.001
H2.SVM	RBF	0.5	0.1	0.001
I1.SVM	N/A	N/A	N/A	N/A
I2.SVM	N/A	N/A	N/A	N/A
J1.SVM	N/A	N/A	N/A	N/A
J2.SVM	RBF	2	0.1	0.001
K1.SVM	RBF	0	0.1	0.001
K2.SVM	RBF	0.5	0.2	0.001
L1.SVM	N/A	N/A	N/A	N/A
L2.SVM	RBF	2	0.1	0.01
M1.SVM	RBF	0	0.1	0.001
M2.SVM	RBF	0.5	0.1	0.001

Supplemental Table S6.6. Optimized RF parameter settings for the analyses in Supplemental Table S6.4

Identifier	max-depth	min instances	num trees
E1.RF	1	8	20
E2.RF	3	1	30
F1.RF	1	1	10
F2.RF	2	1	30
G1.RF	1	8	10
G2.RF	1	8	10
H1.RF	N/A	N/A	N/A
H2.RF	N/A	N/A	N/A
I1.RF	N/A	N/A	N/A
I2.RF	N/A	N/A	N/A
J1.RF	N/A	N/A	N/A
J2.RF	1	2	200
K1.RF	1	1	10
K2.RF	1	1	10
L1.RF	1	5	20
L2.RF	4	2	30
M1.RF	2	6	10
M2.RF	1	9	10

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Supplemental Table S7. Phytozome blast search for putative homologs of the Arabidopsis dPCD marker genes MC9, BFN1, PASPA3, RNS3, and SCPL48

	MC9 (325AA)				BFN1 (305AA)				PASPA3 (508AA)			
	best blast hit	%ID	blast length	e-value	best blast hit	%ID	blast length	e-value	best blast hit	%ID	blast length	e-value
Arabidospis *lyrata*	scaffold_600361.1	95.3	319	1.2e-163	fgenesh2_kg.1	98.69	305	4.6e-169	fgenesh2_kg.6	95.67	508	1.1e-268
Medicago *truncatula*	AES66180	42.4	300	3.5e-42	AES63715	68.67	300	2.2e-113	AES92659	63.08	520	5.8e-184
Solanum *lycopersicum*	Solyc10g081300.1.1	53.5	331	8.9e-83	Solyc02g078910.2.1	69.00	300	1.1e-121	Solyc02g080880.2.1	66.60	515	4.0e-190
Populus *trichocarpa*	POPTR_0006s02730.1	65.3	326	7.8e-109	POPTR_0011s04430.1	71.90	274	6.2e-116	POPTR_0004s00900.1	64.79	514	1.0e-186
Oryza *sativa*	OS11T0134700-01	56.5	329	6.2e-87	OS04T0636400-01	67.23	296	7.5e-114	OS01T0663400-01	60.99	523	1.4e-178
Brachypodium *distachyon*	BRADI2G50480.1	50.7	337	8.7e-77	BRADI5G23280.1	69.64	280	1.4e-115	BRADI2G16160.1	62.23	511	7.3e-183
Hordeum *vulgare*	MLOC_5735.2	52.9	331	7.9e-81	MLOC_73587.1	56.57	293	1.1e-113	MLOC_64394.1	54.33	508	7.2e-158
Zea *mays*	GRMZM2G022799_P01	51.2	336	1.1e-76	GRMZM2G168744_P01	68.93	280	4.3e-114	GRMZM2G065757_P01	60.74	517	6.2e-177
Amborella *trichopoda*	ERM98168	54.1	320	1.6e-85	ERN03432	56.57	274	1.4e-86	ERN00700	64.24	509	1.5e-183
Selaginella *moellendorffii*	EFJ20498	50.5	196	6.4e-68	EFJ33450	46.32	285	1.4e-70	EFJ06917	52.80	500	1.8e-146
Physcomitrella *patens*	PP1S165_65V6	55.0	169	7.1e-73	PP1S211_122V6.1	49.20	311	2.2e-78	PP1S93_73V6.2	55.29	510	3.6e-156
Chlamydomonas *reinhardtii*	EDP04316	39.5	253	3.1e-57	EDP02767	37.84	37	7.7	EDP04281	55.74	235	6.1e-74

Supplemental Table S7 (continued)

	RNS3 (222AA)				SCPL48 (510AA)			
	best blast hit	%ID	blast length	e-value	best blast hit	%ID	blast length	e-value
Arabidospis *lyrata*	fgenesh2_kg.1	96.40	222	2.4e-124	fgenesh2_kg.5	97.06	510	1.6e-276
Medicago *truncatula*	AES96753	65.91	220	1.7e-90	AES67523	66.47	501	1.1e-184
Solanum *lycopersicum*	Solyc05g007940.2.1	58.48	224	1.0e-74	Solyc06g017860.1.1	68.18	506	1.1e-187
Populus *trichocarpa*	POPTR_0008s08650.1	64.89	225	1.1e-84	POPTR_0004s22520.1	66.67	504	1.9e-185
Oryza *sativa*	OS08T0434100-01	56.68	217	5.3e-74	OS02T0114200-01	66.02	465	6.4e-172
Brachypodium *distachyon*	BRADI3G37130.2	58.05	205	2.4e-74	BRADI3G01320.1	66.11	478	2.5e-175
Hordeum *vulgare*	MLOC_19306.1	58.42	202	4.8e-74	MLOC_77869.2	65.68	472	3.5e-174
Zea *mays*	GRMZM2G161274_P02	56.16	219	2.9e-76	GRMZM2G020146_P01	63.47	501	1.5e-173
Amborella *trichopoda*	ERM94495	60.55	218	5.2e-78	ERN12871	65.73	496	1.5e-181
Selaginella *moellendorffii*	EFJ09665	50.22	225	7.2e-65	EFJ15031	59.57	465	6.8e-156
Physcomitrella *patens*	PP1S59_320V6.1	47.87	211	2.1e-57	PP1S149_206V6.1	59.53	467	6.9e-153
Chlamydomonas *reinhardtii*	EDP05112	38.24	204	7.8e-35	EDP01561	44.67	441	2.9e-106