

	18h (at harvest)		42h (18h imbibition+ 24h isolated radicle)		Increase in μm	% increase
	Length (μm)	SE	Length (μm)	SE		
Control	2995.2	64.37	7202.7	189.62	4207.5	140.5
Amanitin	2999.2	64.27	7636.9	199.95	4637.7	154.6
Cycloheximide	3068.1	72.77	3201.9	61.157	133.8	4.36

Supplemental Table S1: The effect of α -amanitin and cycloheximide on radicle growth. Seeds were imbibed as described in the Materials and Methods section. Radicles were dissected after 18h imbibition and further incubated. Mean values and standard error (SE) of 20 radicles are presented.

Tags	CAP				RAD				Common			
	8h	18h	30h	96h	8h	18h	30h	96h	8h	18h	30h	96h
Dormancy related	14	29	21	16	54	28	31	45	146	153	166	162
Germination related	6	6	3	6	10	3	3	3	28	30	33	32
ABA	17	40	34	23	43	24	26	32	125	124	132	137
Auxin	15	31	36	21	39	25	23	32	113	111	109	116
Brassinosteroid	1	1	4	3	12	7	6	8	22	26	23	21
Cytokinin	7	10	7	8	15	5	8	7	20	19	23	22
Ethylene	3	13	7	6	26	10	17	16	57	55	55	57
Gibberellin	5	10	12	7	10	2	7	9	35	35	33	35
Jasmonic acid	4	15	10	10	10	4	2	8	24	25	26	24
Seed storage proteins/Late Embryogenesis Abundant	7	15	13	17	25	13	11	17	46	52	56	49
Inhibition of protein degradation	1	5	4	3	5	2	2	2	10	10	13	15
Protein degradation	16	53	55	64	95	42	48	55	285	310	300	292
Heat Shock	11	24	25	23	44	24	22	35	121	122	127	128
Cell-wall modification	19	49	46	40	57	41	38	50	130	118	128	131
Cell cycle related	15	32	44	25	60	37	30	46	157	177	175	157
Cytoskeleton	12	29	34	29	62	29	32	41	103	106	110	105
Translation associated	7	31	23	23	77	46	49	72	395	403	398	379
DNA repair	6	20	24	25	54	27	23	29	56	62	70	62
Respiration	1	0	1	3	3	3	2	3	12	14	14	14
Electron Transport	1	2	2	2	3	0	3	4	18	18	17	16
Pentose phosphate pathway	1	2	1	3	3	1	2	1	11	11	12	11
Glycolysis and gluconeogenesis	7	13	13	7	15	4	6	13	63	73	73	70
Krebs cycle	8	7	6	5	4	2	0	3	23	27	30	28
Beta oxidation	3	1	2	3	2	1	1	0	11	12	13	14
Stress	29	95	95	83	116	60	60	69	333	328	329	343
Photosynthesis/chloroplast related	80	244	202	191	408	196	164	265	1002	1031	1100	1084
Unannotated	3	6	2	5	5	4	6	7	18	17	18	19
Unclassified	618	1759	1602	1577	2830	1364	1281	1729	6052	6046	6452	6286
Total genes in lists	917	2542	2328	2228	4087	2004	1903	2601	9416	9515	10035	9809
Total genes classified above	299	783	726	651	1257	640	622	872	3364	3469	3583	3523
Percentage classified	32.61	30.8	31.19	29.77	30.51	31.9	32.99	33.5	35.75	36.46	35.71	35.92

Supplemental Table S4. Proportional representation in functional categories of the GO-based seed-specific TAGGIT workflow (Carrera et al., 2007) of expressed (“present”) genes on +ABA-arrays.

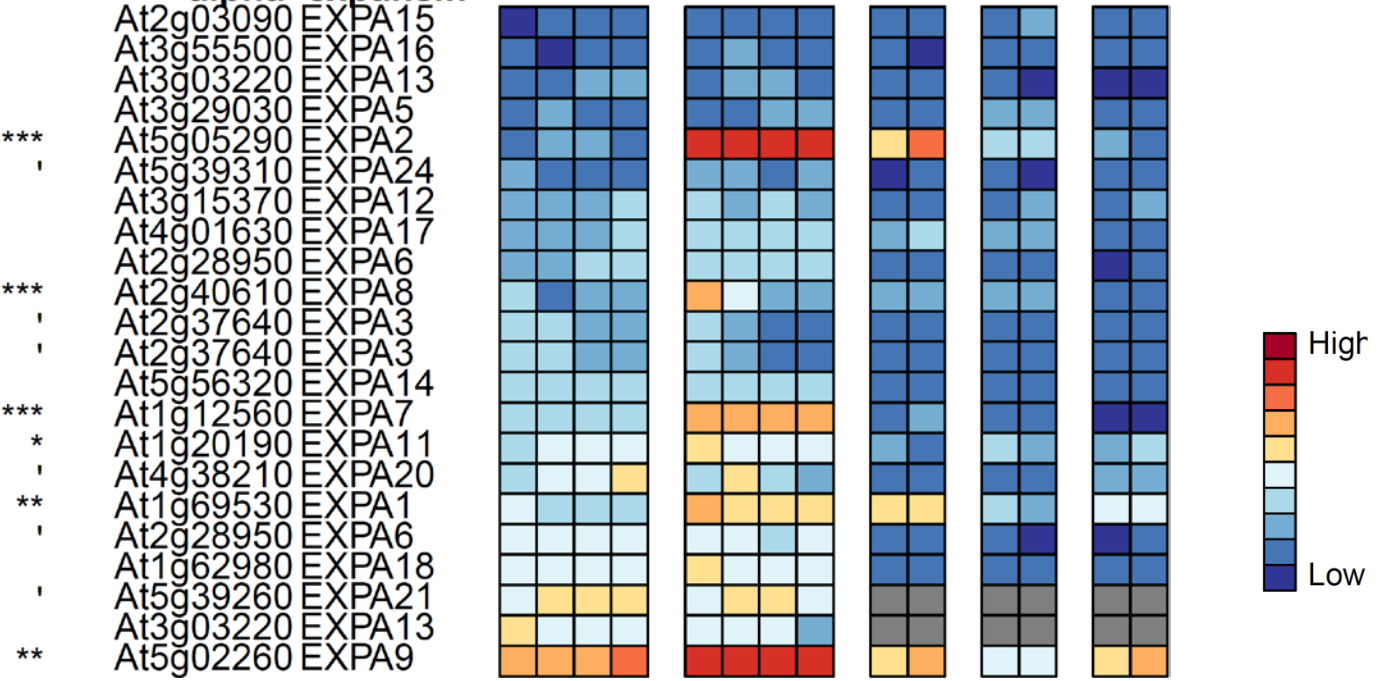
Tags	CAP				RAD			
	8h	18h	30h	96h	8h	18h	30h	96h
Dormancy related	0	5	3	2	7	3	1	6
Germination related	1	0	0	1	2	1	1	0
ABA	2	3	4	1	4	3	0	5
Auxin	2	5	5	0	8	5	3	2
Brassinosteroid	1	0	1	1	2	1	0	1
Cytokinin	2	1	0	0	2	0	1	0
Ethylene	0	0	0	0	5	1	0	0
Gibberellin	1	1	2	0	1	0	0	2
Jasmonic acid	0	3	0	2	2	0	0	2
Seed storage proteins/Late Embryogenesis Abundant	0	1	1	4	2	1	1	1
Inhibition of protein degradation	0	1	1	1	0	0	0	0
Protein degradation	5	8	8	11	14	3	3	5
Heat Shock	1	4	3	6	5	1	1	5
Cell-wall modification	1	8	4	7	7	7	3	10
Cell cycle related	1	4	7	1	5	1	5	2
Cytoskeleton	3	2	4	4	6	3	0	5
Translation associated	2	5	2	3	5	4	3	2
DNA repair	1	0	3	1	6	2	3	3
Respiration	0	0	0	1	0	0	0	1
Electron Transport	0	0	0	0	0	0	0	1
Pentose phosphate pathway	0	0	0	0	0	0	0	0
Glycolysis and gluconeogenesis	1	1	4	1	0	0	0	5
Krebs cycle	1	0	0	0	2	0	0	0
Beta oxidation	0	0	0	0	0	0	0	0
Stress	6	16	7	8	11	8	5	13
Photosynthesis/chloroplast related	12	27	23	25	45	19	9	31
Unannotated	0	2	0	2	0	0	0	1
Unclassified	111	201	203	239	372	166	106	219
Total genes in lists	154	298	285	321	513	229	145	322
Total genes classified above	43	97	82	82	141	63	39	103
Percentage classified	27.92	32.55	28.77	25.55	27.49	27.51	26.9	31.99

Supplemental Table S5. The numbers of genes, with expression on +ABA-arrays that is unique to each tissue/time combination, classified in functional categories of the GO-based seed-specific TAGGIT workflow (Carrera et al., 2007).

A

	+ABA				-ABA		
	RAD		CAP		CAP	NME	RAD
	8	96	8	96	8 18	8 18	8 18

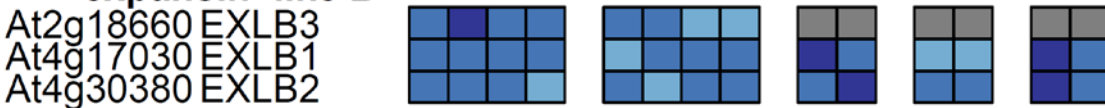
alpha-expansin



beta-expansin



expansin-like B

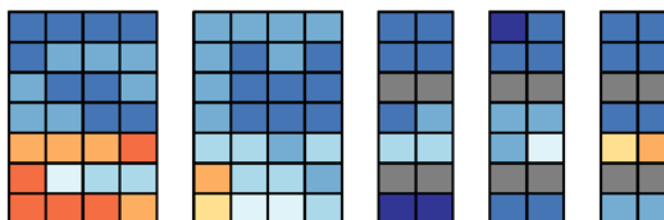


B

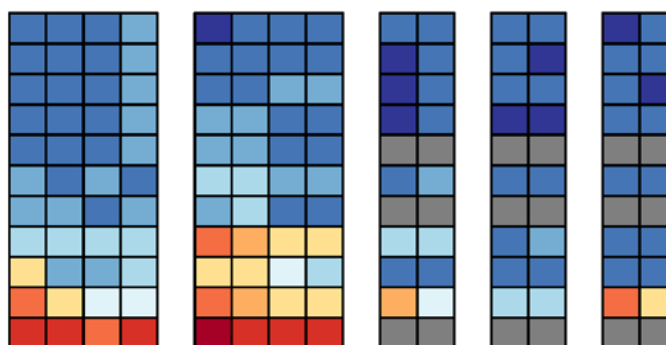
	+ABA				-ABA		
	RAD		CAP		CAP	NME	RAD
	8	96	8	96	8 18	8 18	8 18

XTH Group 1

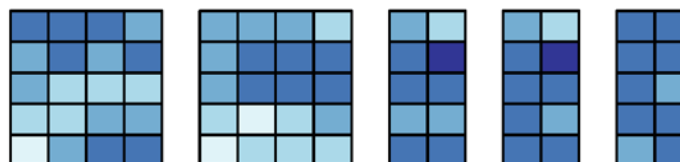
At3g48580 XTH11
 At3g25050 XTH3
 At4g13080 XTH1
 At2g14620 XTH10
 ** At1g11545 XTH8
 ** At4g03210 XTH9
 At5g13870 XTH5

**XTH Group 2**

At5g57550 XTH25
 At2g18800 XTH21
 At4g28850 XTH26
 At4g25820 XTH14
 At4g25810 XTH23
 ** At5g48070 XTH20
 At5g57530 XTH12
 *** At4g30270 XTH24
 ** At4g14130 XTH15
 At3g23730 XTH16
 At5g57560 XTH22

**XTH Group 3**

* At3g44990 XTH31
 * At1g32170 XTH30
 * At2g36870 XTH32
 * At1g14720 XTH28
 * At2g01850 XTH27



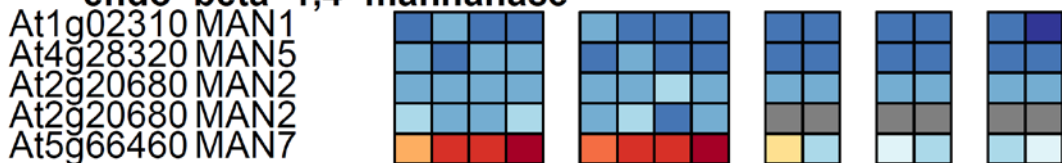
C

	+ABA				-ABA		
	RAD		CAP		CAP	NME	RAD
	8	96	8	96	8 18	8 18	8 18

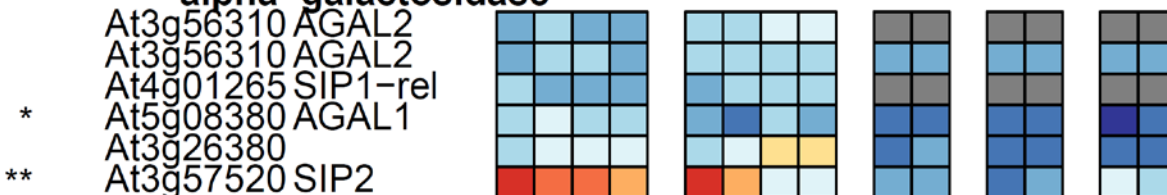
beta-1,4-mannan synthase



endo-beta-1,4-mannanase



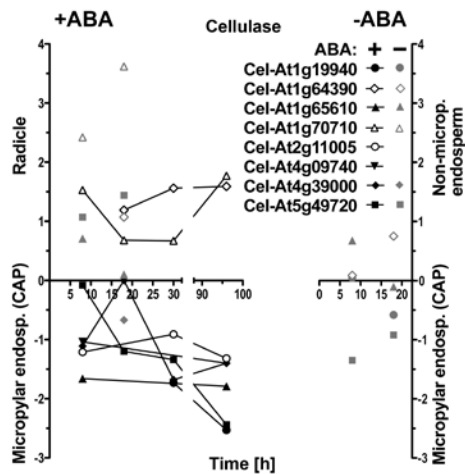
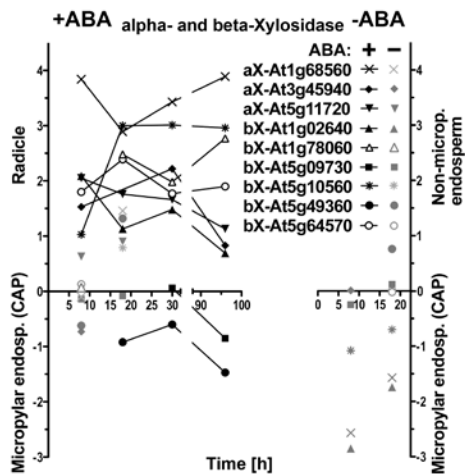
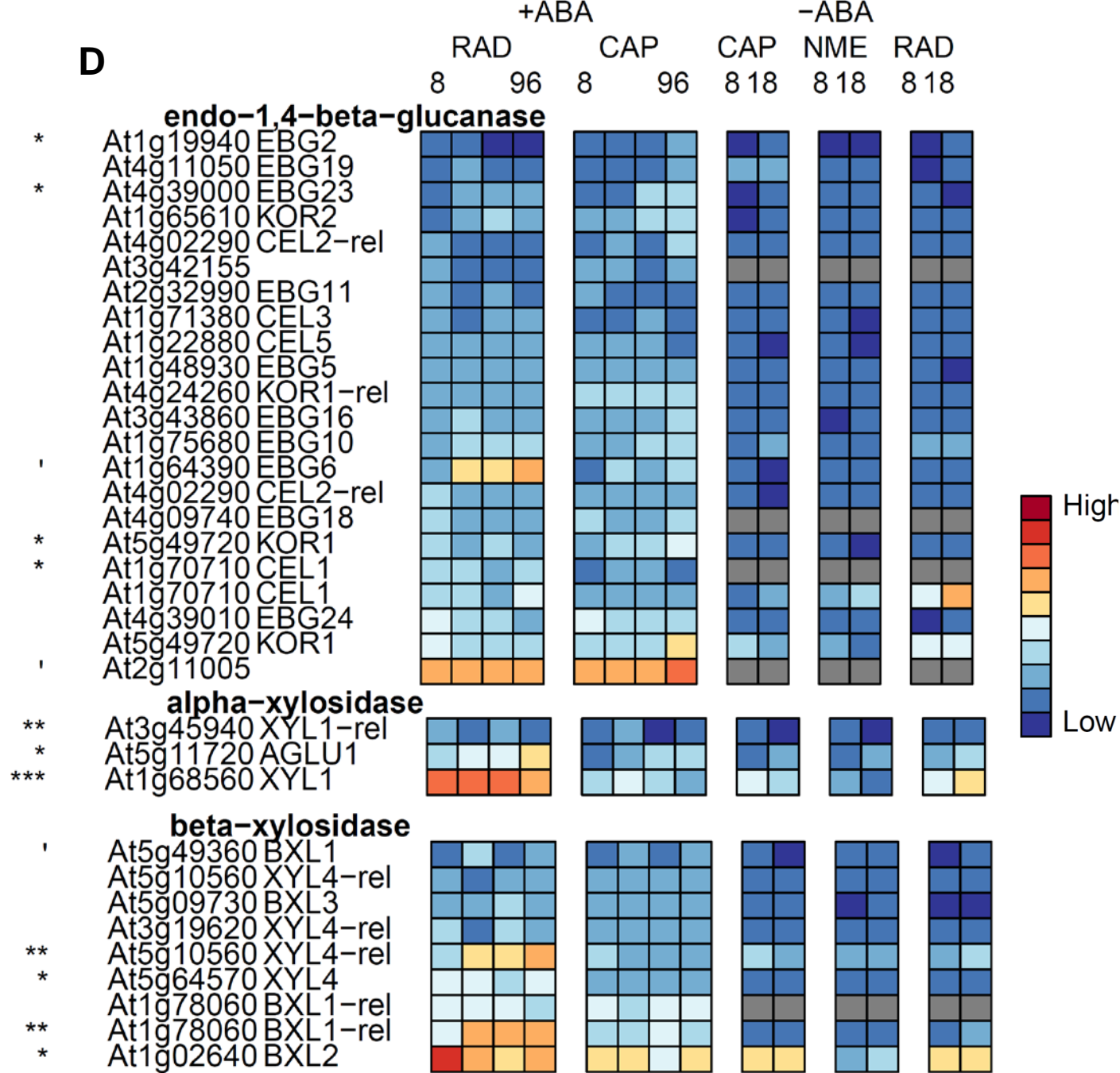
alpha-galactosidase



beta-mannosidase



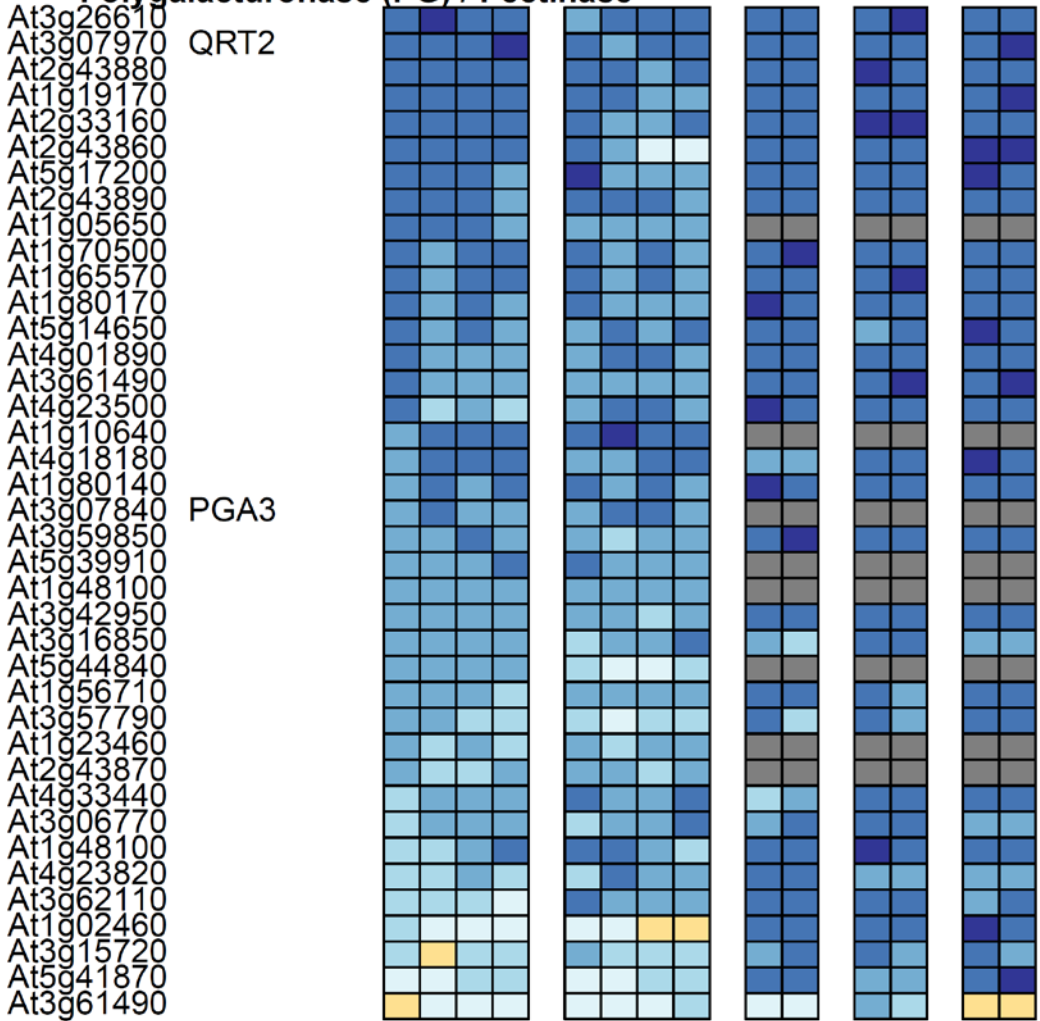
D



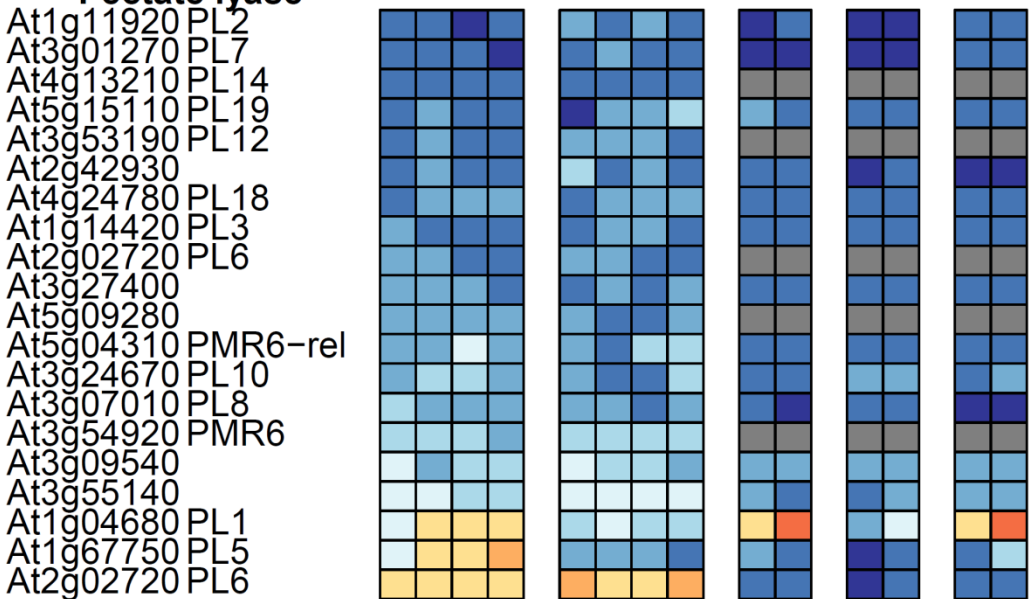
E

+ABA -ABA
 RAD CAP CAP NME RAD
 8 96 8 96 8 18 8 18 8 18

Polygalacturonase (PG) / Pectinase



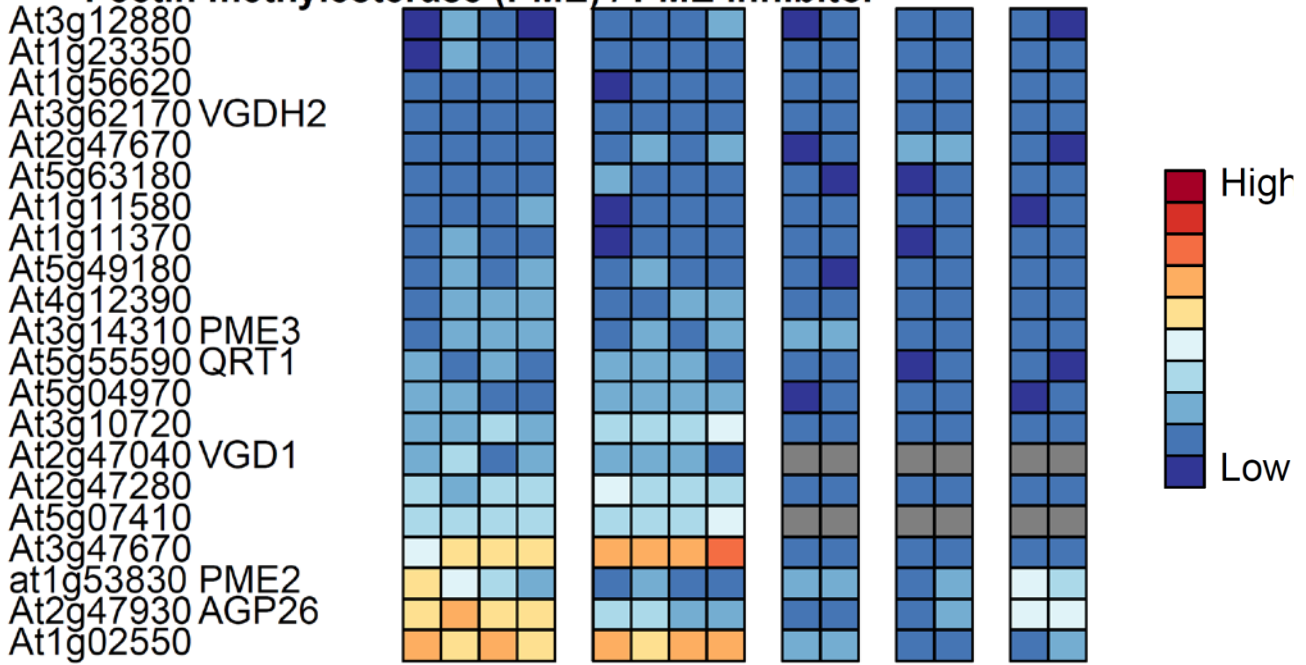
Pectate lyase

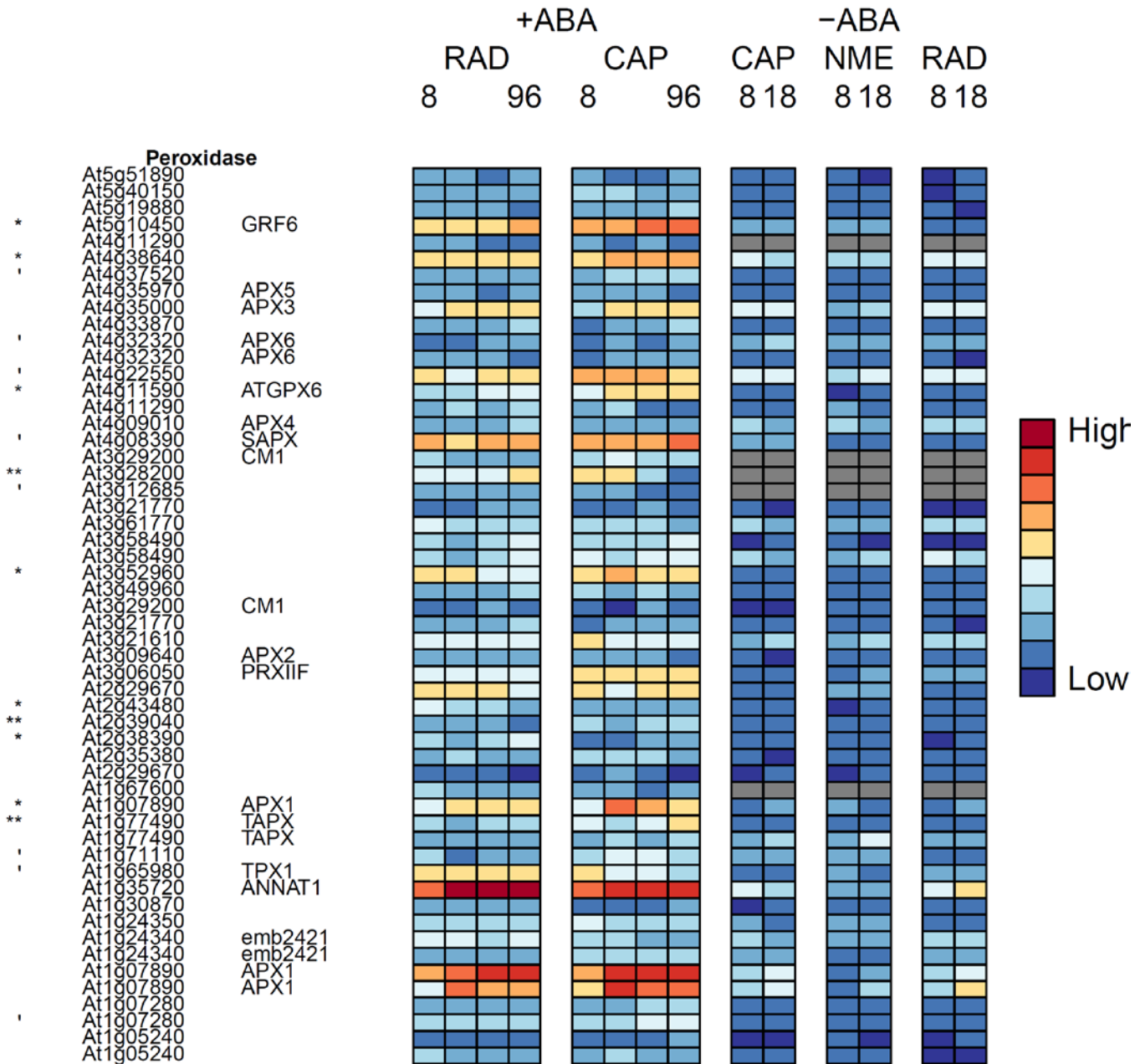


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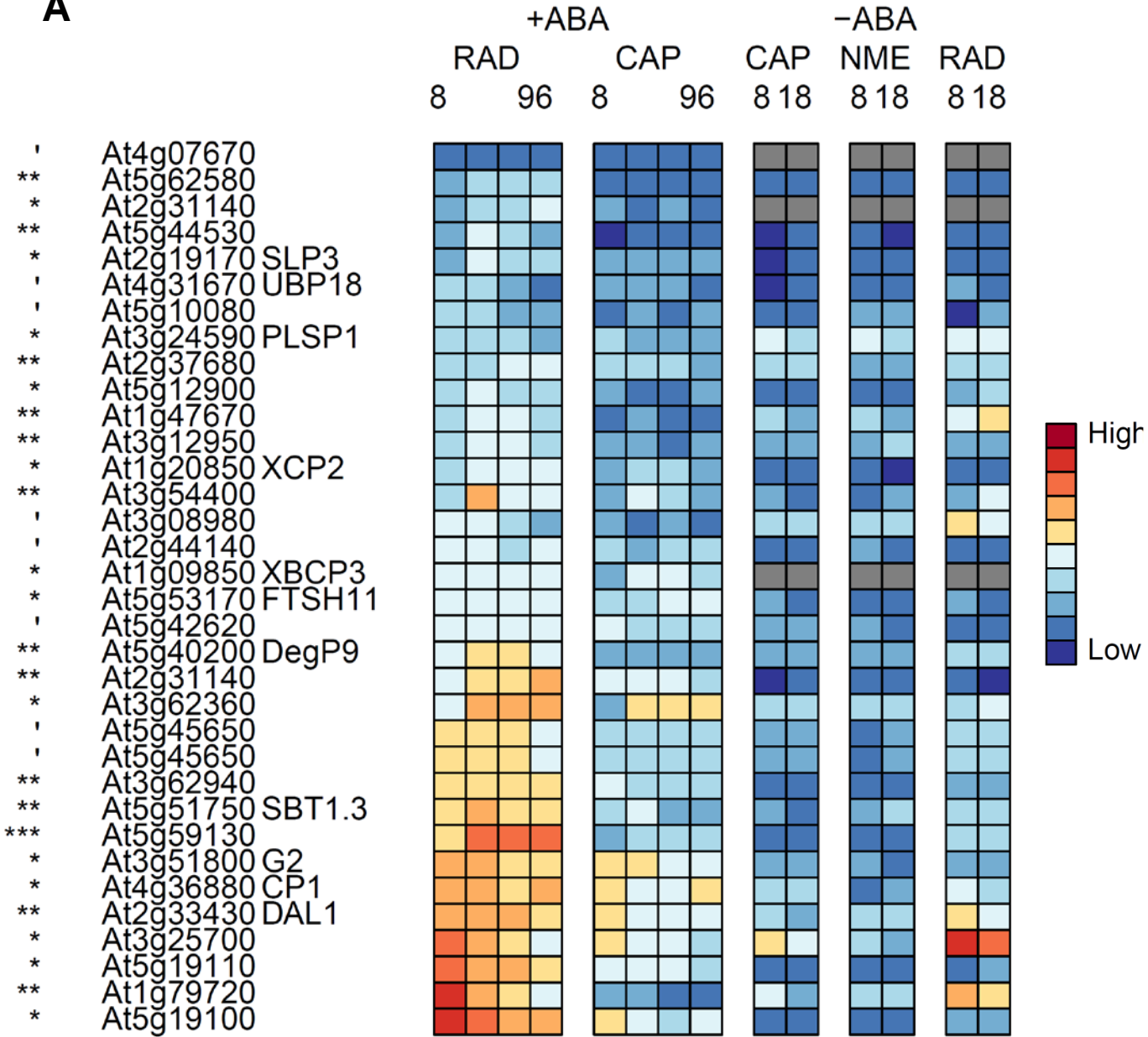
	+ABA				-ABA		
	RAD		CAP		CAP	NME	RAD
	8	96	8	96	8 18	8 18	8 18

Pectin methylesterase (PME) / PME inhibitor



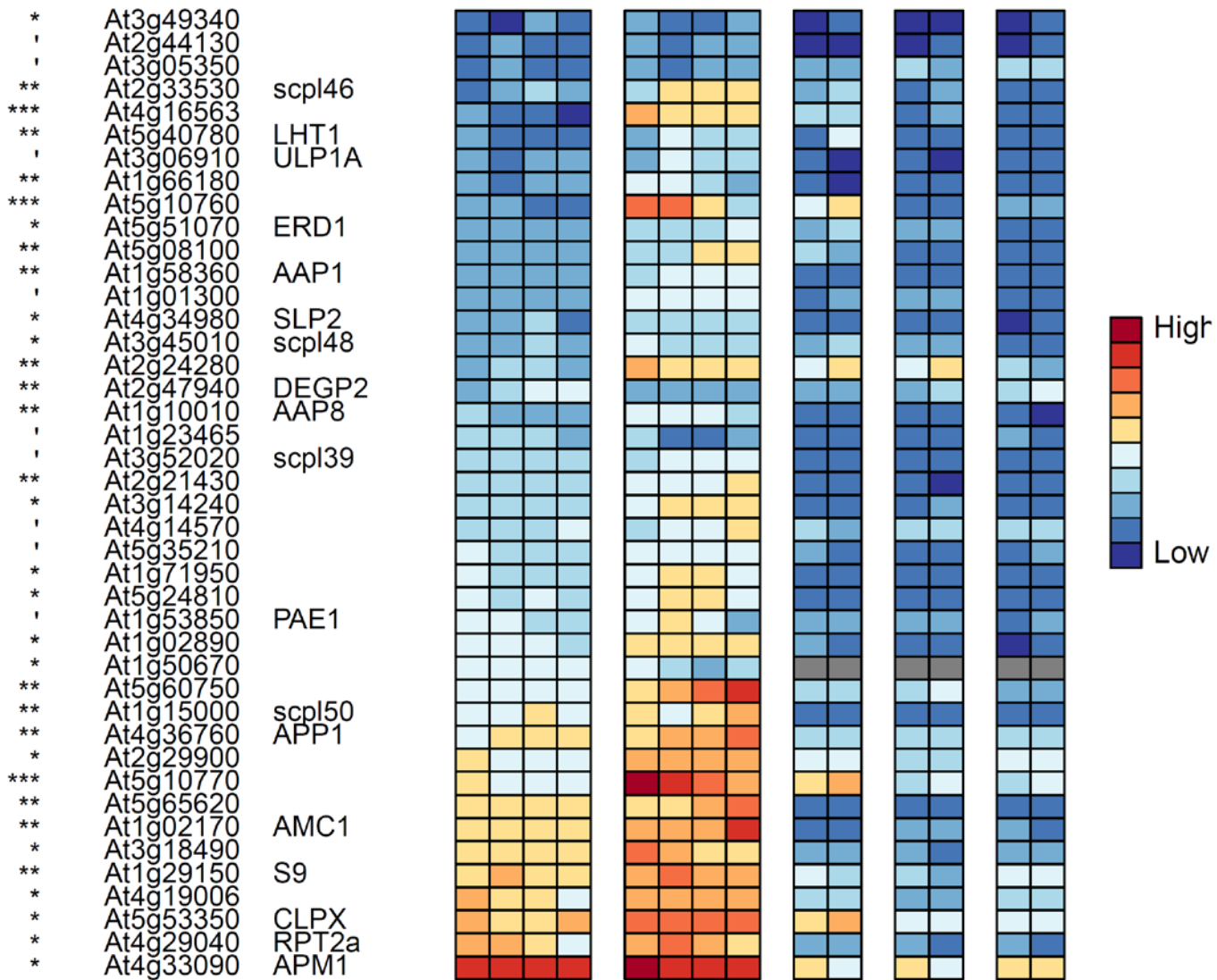


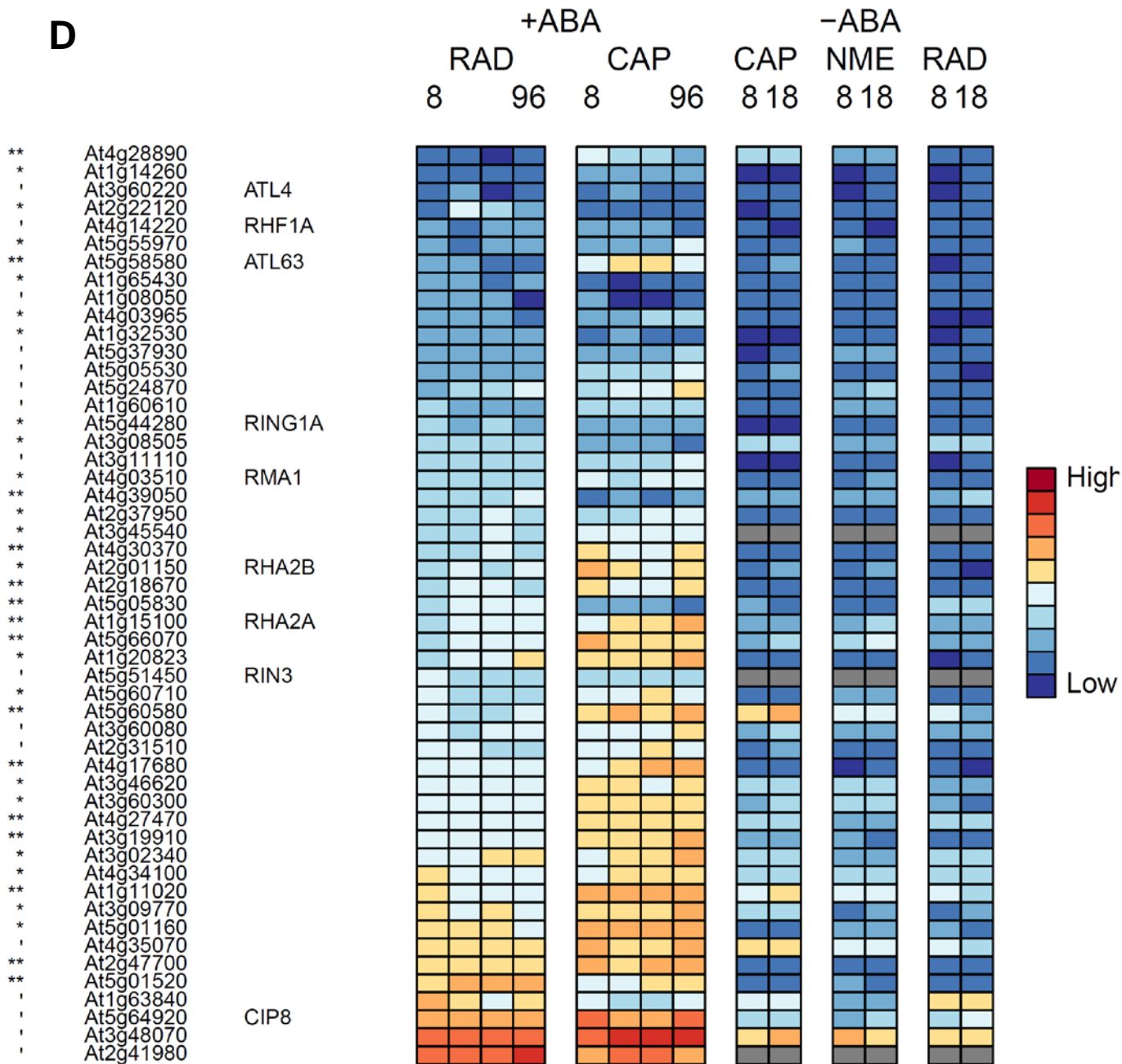
Supplemental Figure. S1: Heat maps showing the expression levels of genes encoding cell wall modification proteins. **A**, Expansins, **B**, XTHs, **C**, Mannans, **D**, Cellulases, **E**, Hydrolytic enzymes and **F**, peroxidases. ‘, *, **, *** indicate that transcript numbers are significantly different between the tissues on +ABA-arrays at $P < 0.1$, < 0.05 , < 0.01 , < 0.001 respectively. Genes not present in the data sets are coloured grey.

A

B

+ABA -ABA
RAD CAP CAP NME RAD
8 96 8 96 8 18 8 18 8 18





Supplemental Figure. S2: Heat maps showing the expression levels of genes encoding proteins associated with posttranslational modification.

A, Genes in the TAGGIT protein degradation category that are up-regulated in the RAD. **B,** Genes in the TAGGIT protein degradation category that are up-regulated in the CAP. **C,** Genes encoding F box proteins that are significantly differentially expressed between the RAD and CAP. **D,** Genes encoding RING finger E3 ligase proteins that are significantly differentially expressed between the RAD and CAP. .', *, **, *** indicate that transcript numbers are significantly different between the tissues on +ABA-arrays at $P < 0.1$, < 0.05 , < 0.01 , < 0.001 respectively. Genes not present in the data sets are coloured grey.