Electronic Supplementary Material (ESI) for Photochemical & Photobiological Sciences.

Electronic Supplementary Information

UVR8-dependent reporters reveal spatial characteristics of signal spreading in plant tissues

Lucas Vanhaelewyn, Péter Bernula, Dominique Van Der Straeten, Filip Vandenbussche, András Viczián

Supplementary Figure. 1.

Venn diagram of *Arabidopsis* UV-B upregulated genes taken from lists as published in Favory *et al.,* 2009, Oravecz *et al.,* 2006 and Brown and Jenkins, 2008.

Supplementary Figure 2.

Schematic diagram of the performed irradiation and dissection protocols

Supplementary Figure 3.

The GFP signal is not altered by the applied UV-B irradiation.

Supplementary Figure. 4.

Venn diagram of *Arabidopsis* UV-B upregulated genes listed in Supplementary table 2, showing overlap with the stress UV-B dataset from Kilian *et al.,* 2007.

Supplementary Figure 5.

Reporters of transcriptional changes in different plant organs.

Supplementary Figure 6.

Accumulation of HY5-GFP and HYH-GFP in different organs of Arabidopsis seedlings under UV-B irradiation.

Supplementary Figure 7.

UV-B induction of *pHYH:HYH-GFP* in the hypocotyl cells of transgenic lines expressing YFP-UVR8 in different tissues.

Supplementary Figure 8.

UV-B induced accumulation of HY5-GFP in the hypocotyl cells of transgenic lines expressing YFP-UVR8 in different tissues.

Supplementary Figure 9.

Expression levels of YFP-UVR8 in different transgenic lines.

Supplementary table 1

Oligonucleotides used in qRT-PCR assays**.**

Supplementary table 2

UV-B upregulated genes identified in the examined transcriptome datasets.

Supplementary table 3

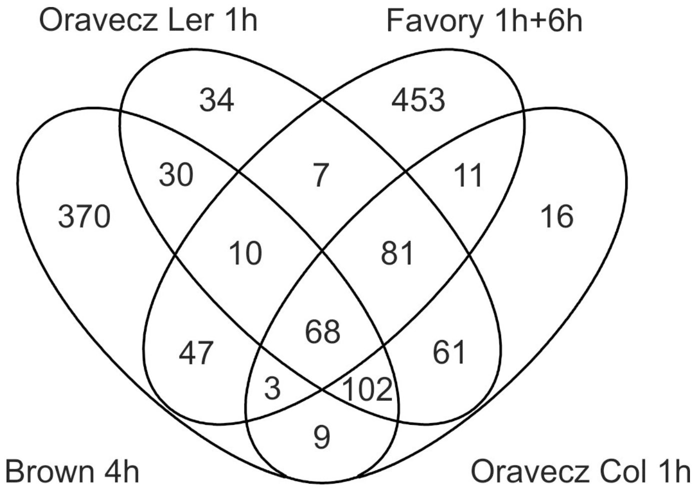
UV-B downregulated genes identified in the examined transcriptome datasets.

Supplementary table 4

GENE Ontology (GO) categories of the UVR8-dependent up-regulated genes shown in Supplementary table 2.

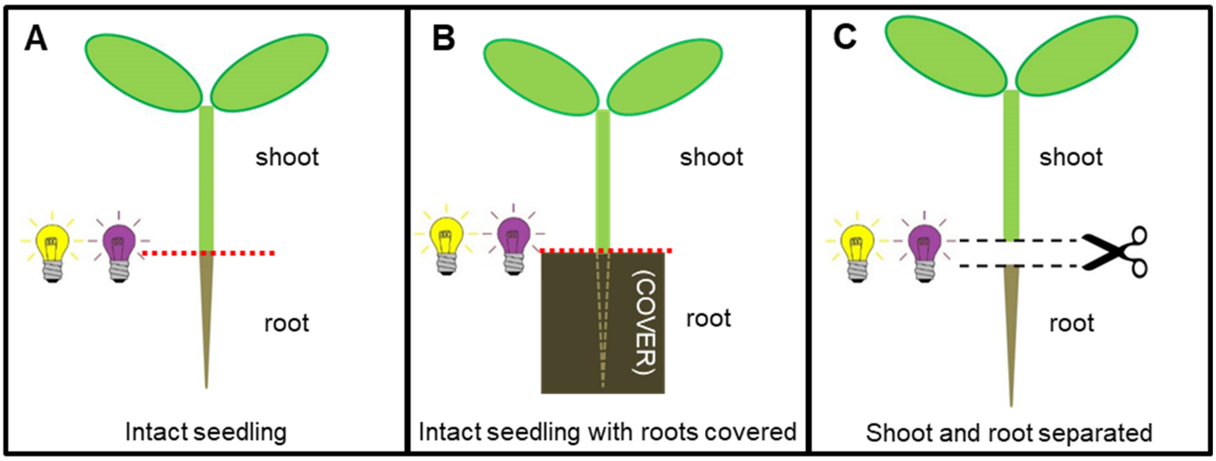
Supplementary table 5

GENE Ontology (GO) categories of the UVR8-dependent down-regulated genes shown in Supplementary table 3.

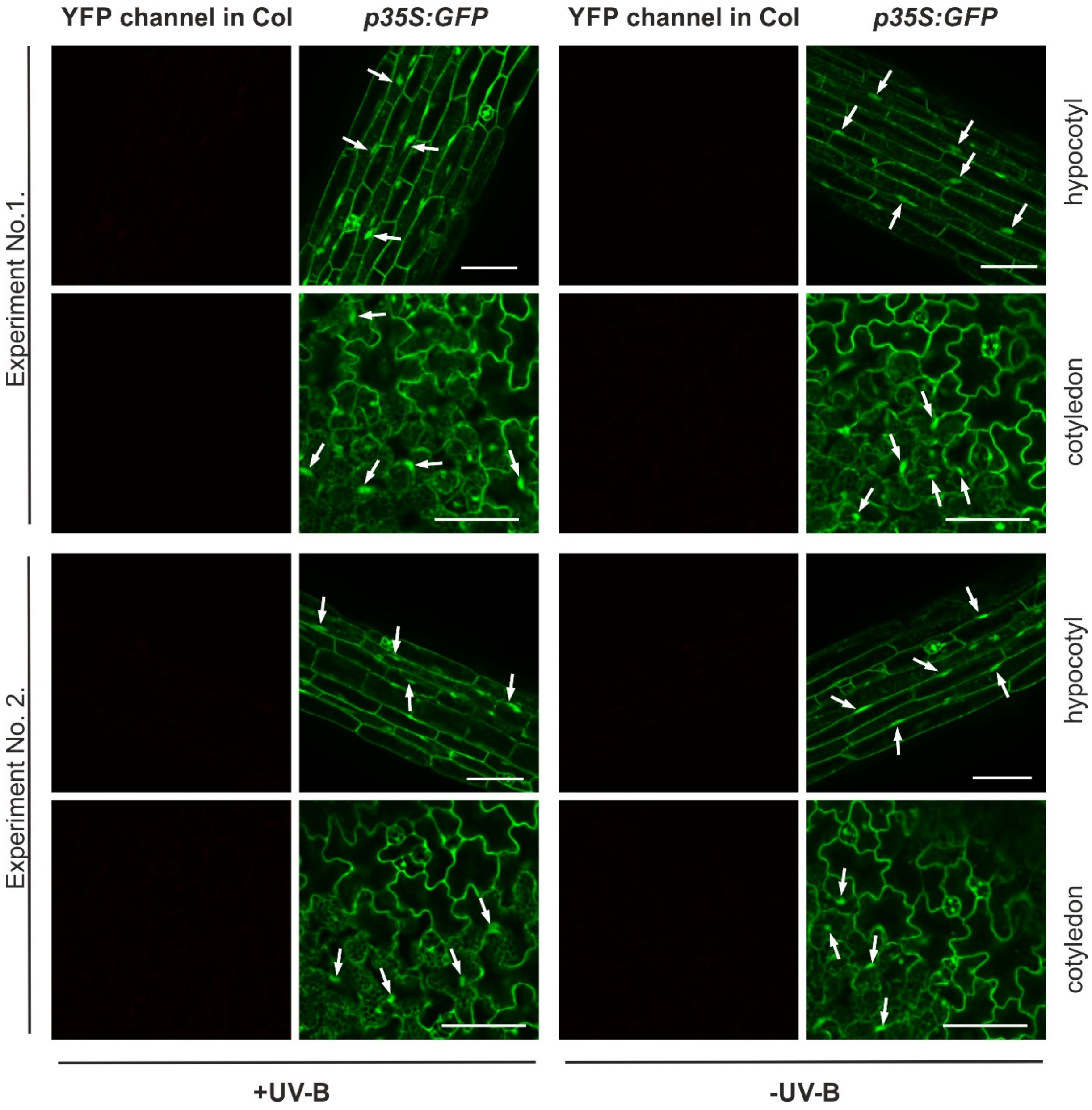


Supplementary Figure 1.

Venn diagram of Arabidopsis UV-B up-regulated genes taken from lists as published in Favory *et al*., 2009[1], Oravecz *et al*., 2006[2] and Brown and Jenkins, 2008[3]. Time point of harvesting after onset of UV-B treatment is indicated with the dataset name.

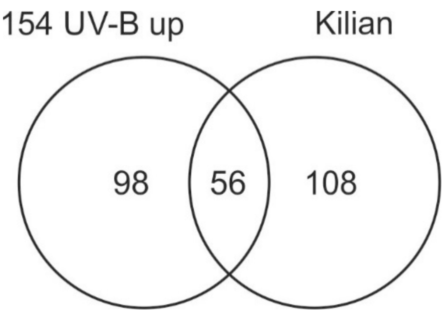


Supplementary Figure 2.
Schematic diagram of the performed irradiation and dissection protocols. **A.** Seedlings were irradiated with white light (WL) supplemented with UV-B (yellow and purple bulbs, respectively). **B.** Plants were irradiated with WL+UV-B while their roots were covered with aluminium foil whereas the shoots not. **C.** Plants having the roots and shoots separated before the irradiation treatment (Black dashed lines). Red dashed line (A, B) shows how roots (brown coloured plant parts) and shoots (green coloured plant parts) were separated after the irradiation, and subsequently collected and processed separately.



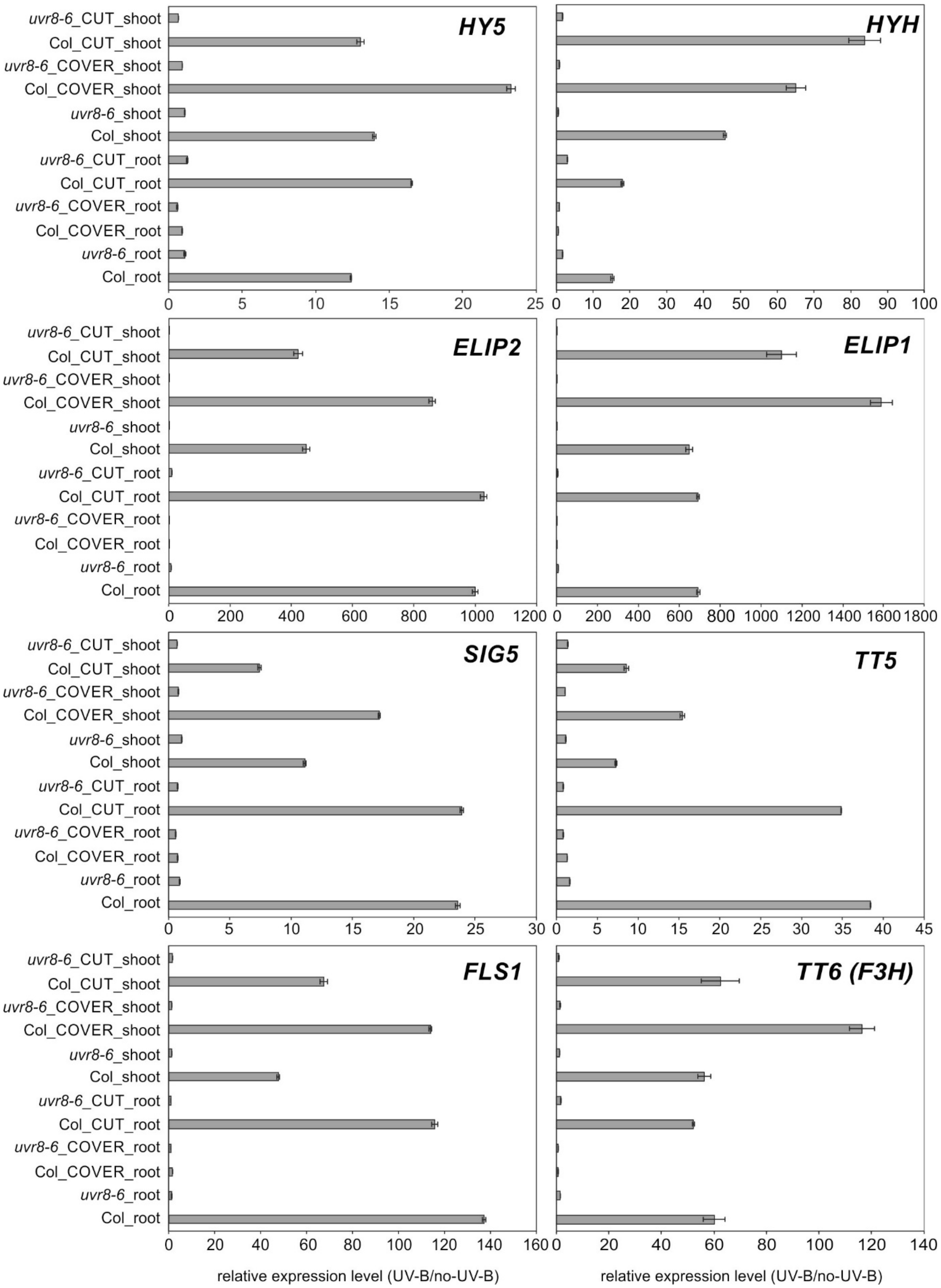
Supplementary Figure 3.

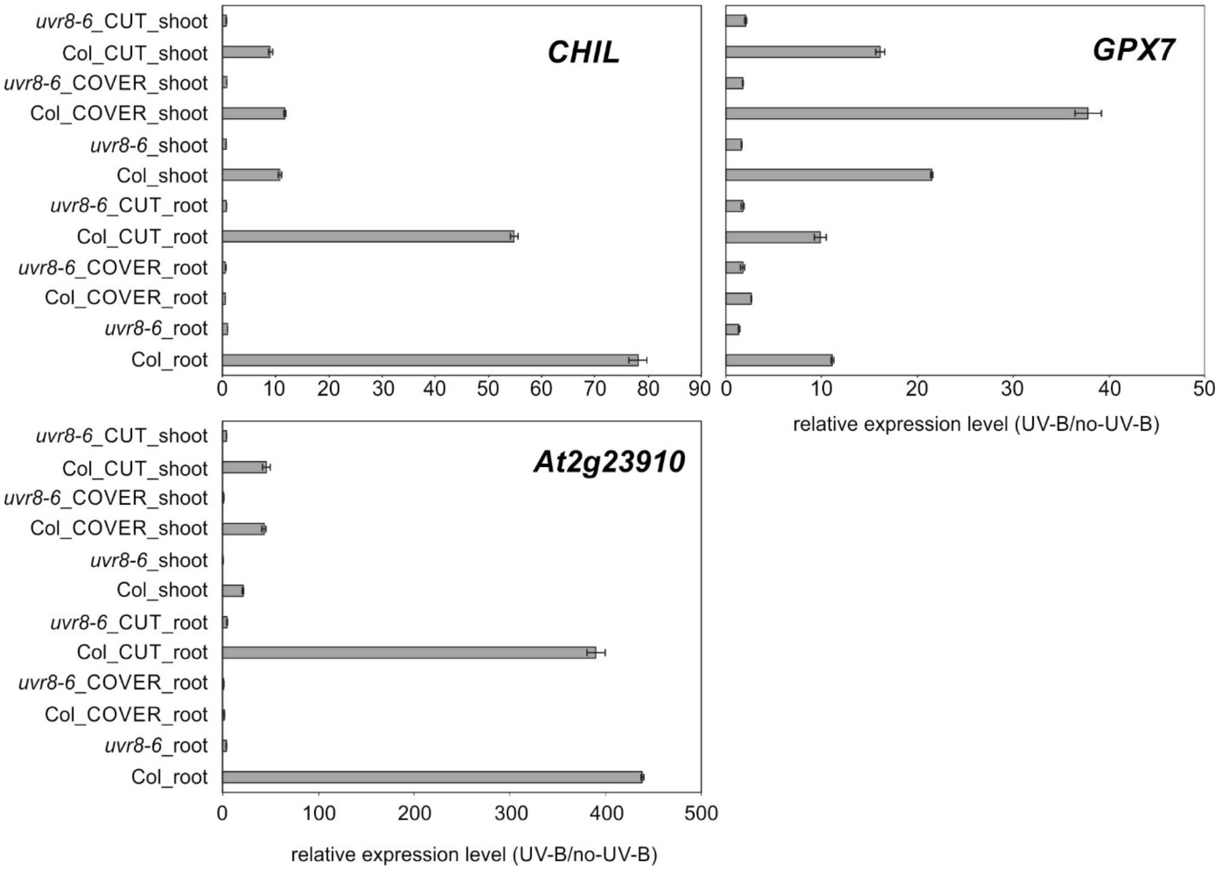
The GFP signal is not altered by the applied UV-B irradiation. *35S:GFP*/Col seedlings were grown and irradiated as those what were used for all of our CLSM assays (see Materials and methods). Epidermis of hypocotyls and cotyledons were monitored using CLSM, applying GFP- and YFP-specific excitation and detection settings. White arrows point at selected nuclei, scale bars represent 75 *µ*m.



Supplementary Figure 4.

Venn diagram of Arabidopsis UV-B up-regulated genes listed in Supplementary table 2, showing overlap with the stress UV-B dataset from Kilian *et al*., 2007[4].

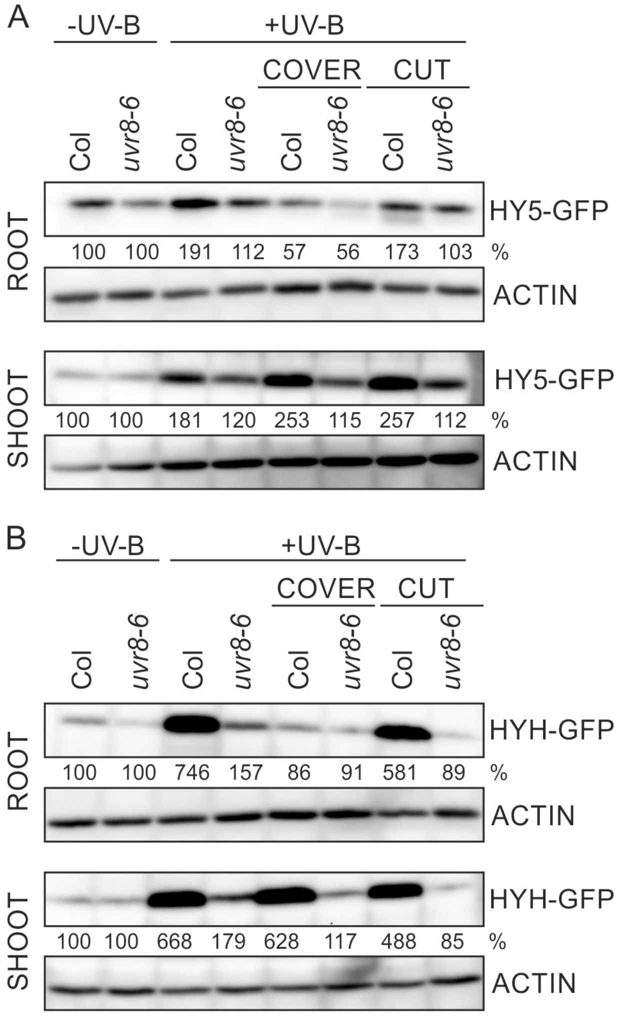

uvr8-6_CUT_shoot
Col_CUT_shoot
uvr8-6_COVER_shoot
Col_COVER_shoot
uvr8-6_shoot
Col_shoot
uvr8-6_CUT_root
Col_CUT_root
uvr8-6_COVER_root
Col_COVER_root
uvr8-6_root
Col_root
HY5
0 5 10 15 20 25
HYH
0 10 20 30 40 50 60 70 80 90 100
ELIP2
0 200 400 600 800 1000 1200
ELIP1
0 200 400 600 800 1000 1200 1400 1600 1800
SIG5
0 5 10 15 20 25 30
TT5
0 5 10 15 20 25 30 35 40 45
FLS1
0 20 40 60 80 100 120 140 160
TT6 (F3H)
0 20 40 60 80 100 120 140
relative expression level (UV-B/no-UV-B)
relative expression level (UV-B/no-UV-B)



Supplementary Figure 5.

Reporters of transcriptional changes in different plant organs.

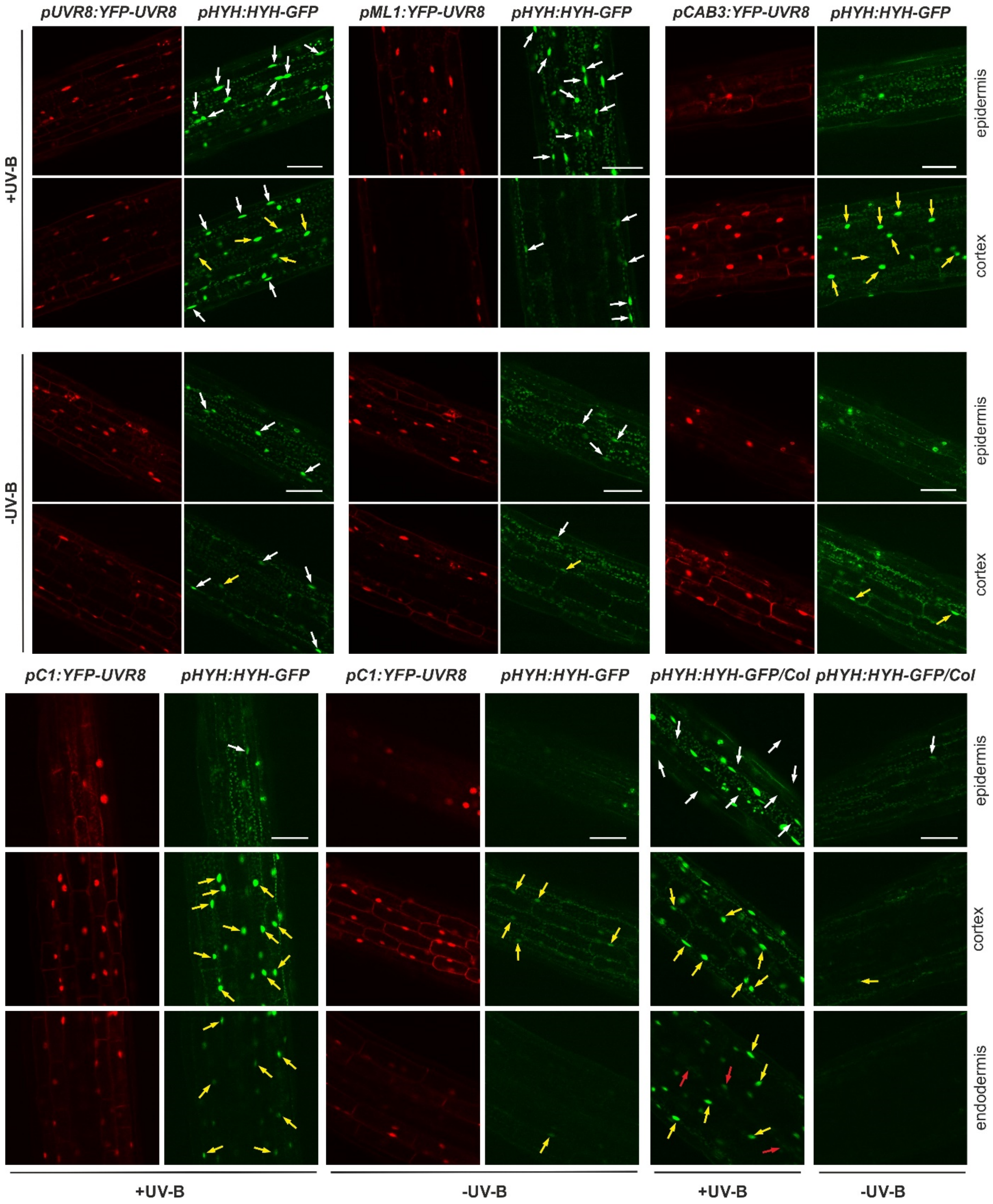
Repetition of the experiment shown in Figure 3. See detailed legend there.

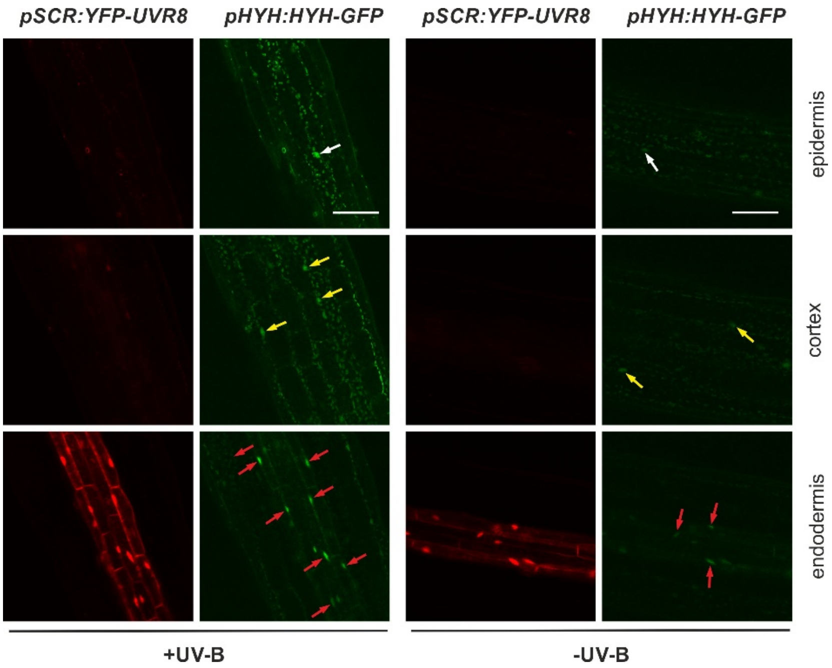


Supplementary Figure 6.

Accumulation of HY5-GFP and HYH-GFP in different organs of Arabidopsis seedlings under UV-B irradiation.

Repetition of the experiment shown in Figure 4. See detailed legend there.


pUVR8:YFP-UVR8
pHYH:HYH-GFP
pML1:YFP-UVR8
pHYH:HYH-GFP
pCAB3:YFP-UVR8
pHYH:HYH-GFP
+UV-B
-UV-B
epidermis
cortex
epidermis
cortex
pC1:YFP-UVR8
pHYH:HYH-GFP
pC1:YFP-UVR8
pHYH:HYH-GFP
pHYH:HYH-GFP/Col
pHYH:HYH-GFP/Col
epidermis
cortex
endodermis
+UV-B
-UV-B
+UV-B
-UV-B

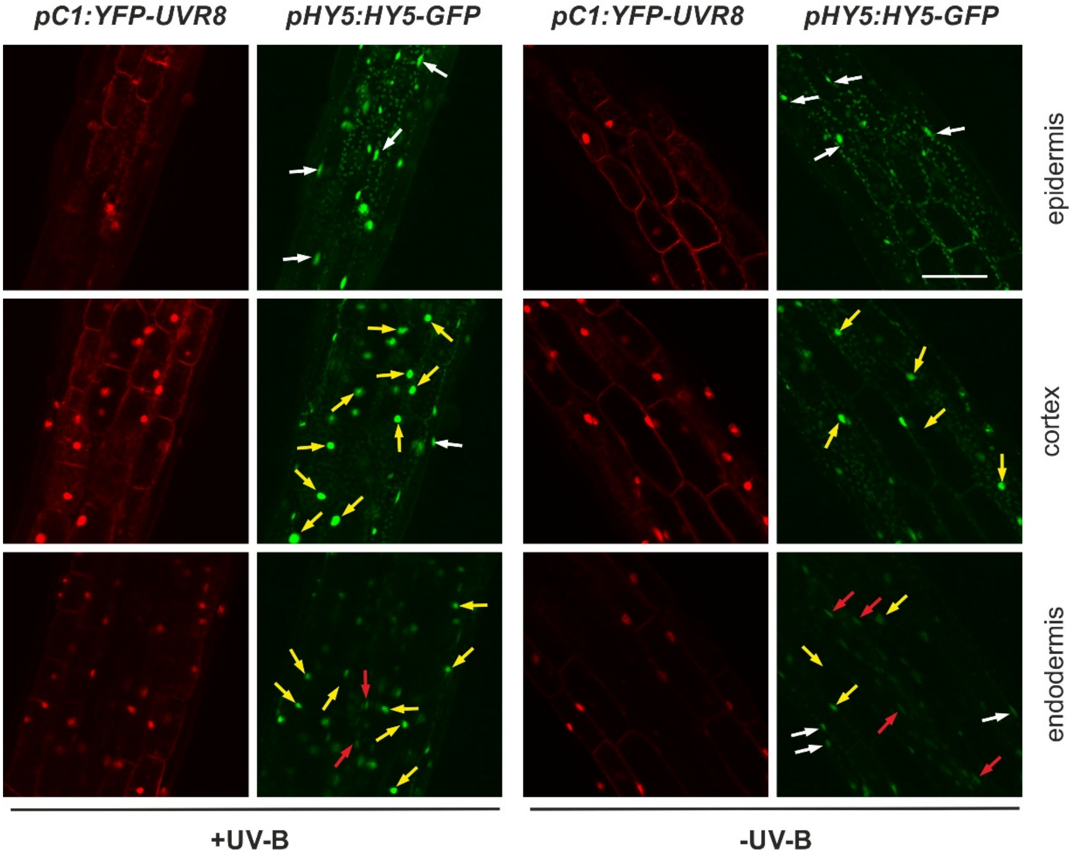


Supplementary Figure 7.

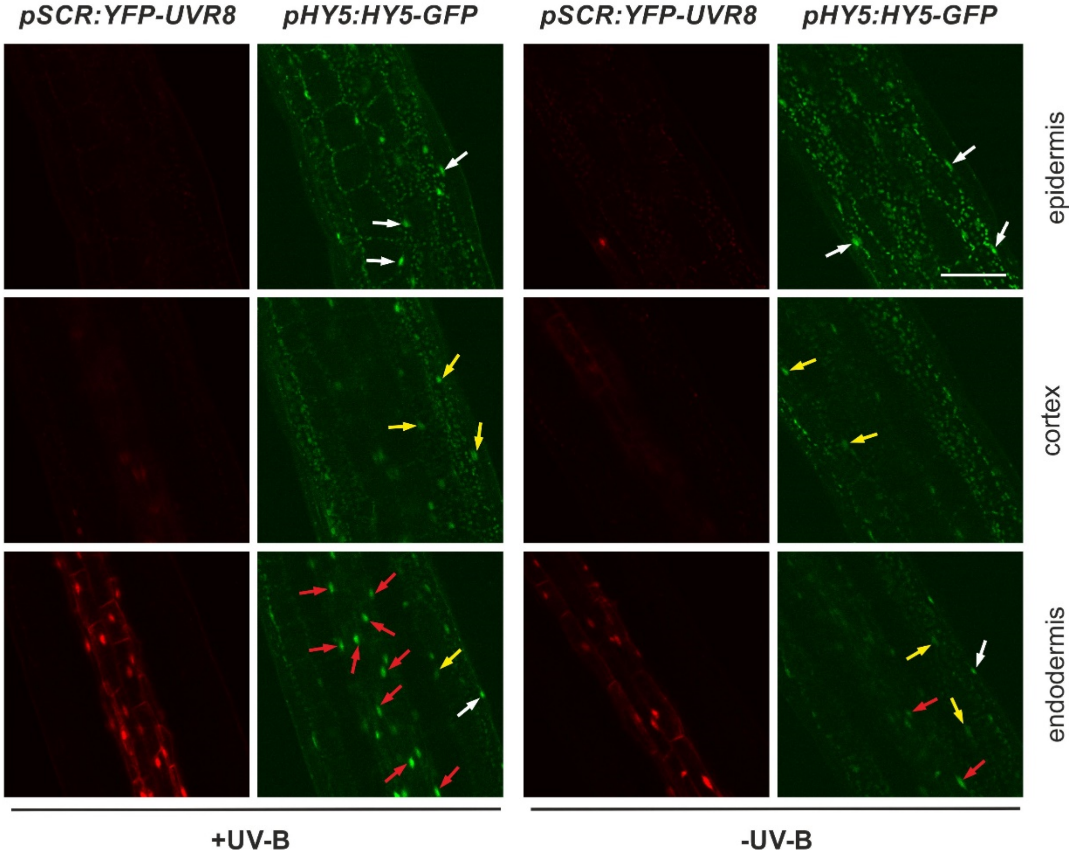
UV-B induction of *pHYH:HYH-GFP* in the hypocotyl cells of transgenic lines expressing YFP-UVR8 in different tissues.

Repetition of the experiment shown in Figure 5. See detailed legend there.

A


pC1:YFP-UVR8
pHY5:HY5-GFP
pC1:YFP-UVR8
pHY5:HY5-GFP
epidermis
cortex
endodermis
+UV-B
-UV-B

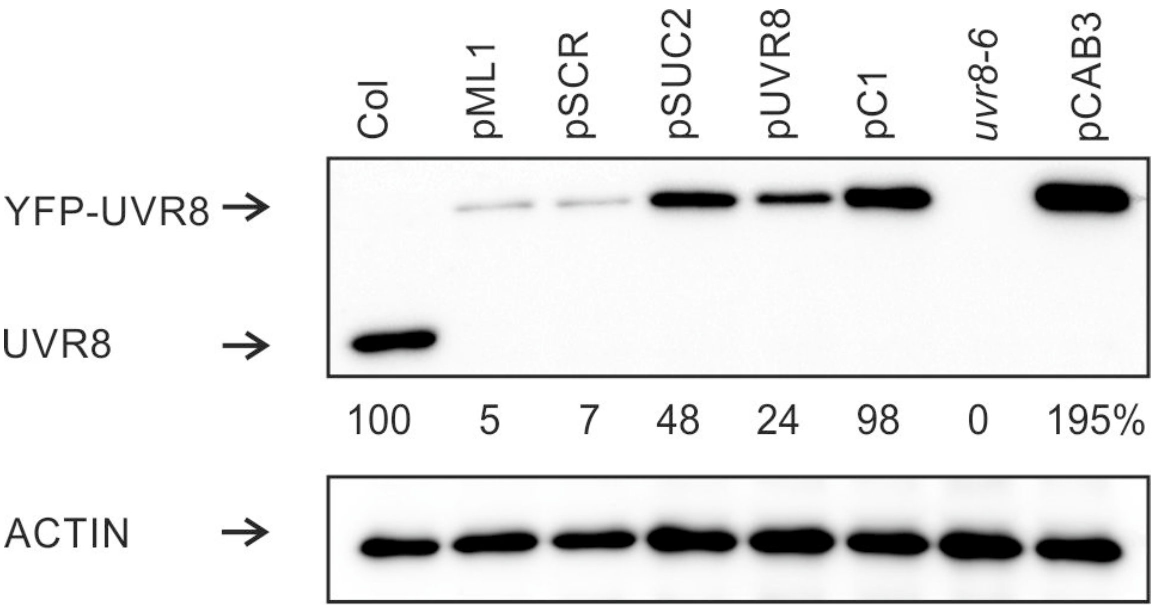
B


pSCR:YFP-UVR8
pHY5:HY5-GFP
pSCR:YFP-UVR8
pHY5:HY5-GFP
epidermis
cortex
endodermis
+UV-B
-UV-B

Supplementary Figure 8.

UV-B induction of *pHY5:HY5-GFP* in the hypocotyl cells of transgenic lines expressing YFP-UVR8 in different tissues.

Repetition of the experiment shown in Figure 6. See detailed legend there.



Supplementary Figure 9.

Expression levels of YFP-UVR8 in different transgenic lines.

Repetition of the experiment shown in Figure 7B. See detailed legend there.

References

1. J. J. Favory, A. Stec, H. Gruber, L. Rizzini, A. Oravecz, M. Funk, A. Albert, C. Cloix, G. I. Jenkins, E. J. Oakeley, H. K. Seidlitz, F. Nagy and R. Ulm, *The EMBO journal*, 2009, **28**, 591-601.
2. A. Oravecz, A. Baumann, Z. Mate, A. Brzezinska, J. Molinier, E. J. Oakeley, E. Adam, E. Schafer, F. Nagy and R. Ulm, *The Plant cell*, 2006, **18**, 1975-1990.
3. B. A. Brown and G. I. Jenkins, *Plant physiology*, 2008, **146**, 576-588.
4. J. Kilian, D. Whitehead, J. Horak, D. Wanke, S. Weinl, O. Batistic, C. D'Angelo, E. Bornberg-Bauer, J. Kudla and K. Harter, *The Plant Journal*, 2007, **50**, 347-363.

Supplementary table 1.
Oligonucleotides used in qRT-PCR assays

Locus Identifier	Gene name	Primer name	Sequence 5'-3'
AT3G55120	*CHALCONE ISOMERASE, TRANSPARENT TESTA 5*	TT5 Fwd	AATCTATCCCGTTCTTCCGTG
		TT5 Rev	CACAATTCTCCGTCACTTTCTC
AT5G11260	*ELONGATED HYPOCOTYL 5*	HY5 Fwd	CTACTCTTCAGAACGAGAACC
		HY5 Rew	CATCAGCATTAGAACCACCA
AT3G22840	*EARLY LIGHT-INDUCABLE PROTEIN 1*	ELIP1 Fwd	TACAACAGCGATCTTGACAC
		ELIP1 Rev	CATGATACCTTTGGACTTGGA
AT4G14690	*EARLY LIGHT-INDUCIBLE PROTEIN 2*	ELIP2 Fwd	CAGTTAGCAAGCCTAAGGTG
		ELIP2 Rew	AATCCAACCATTGCTAGTCTC
AT3G17609	*HY5-HOMOLOG*	HYH Fwd	GCCTCAAGAGATTATTCAGCA
		HYH Rev	CTTGATTCCAAATCACTCAC
AT5G62700 AT5G62690	*TUBULIN 2/3*	TUB Fwd	CCAGCTTTGGTGATTTGAAC
		TUB Rev	CAAGCTTTCGGAGGTCAGAG
AT2G23910		AT2G23910 Fw	GCTTCCACTTATGTTGGTTTCTG
		AT2G23910 Rev	TCTCTTCAAGCACACTCTCC
AT5G05270	*CHALCONE ISOMERASE LIKE*	CHIL Fwd	CTCCGTTATCACTTACCATTTCTC
		CHIL Rev	ATTCTCCACCTTCAGTTTCTCC
AT3G51240	*FLAVANONE 3-HYDROXYLASE, TRANSPARENT TESTA 6*	F3H Fwd	CATCGTCTCTAGTCACCTCCA
		F3H Rev	CCAACCTTCCGGCTTATCTG
AT5G08640	*FLAVONOL SYNTHASE 1*	FLS1 Fwd	AATACAGGGAGGTGAATGAAGAG
		FLS1 Rev	TCACGCTTTAACCCTAATCCA
AT5G24120	*SIGMA FACTOR 5*	SIG5 Fwd	ACTTTACGAGATACTTCACACCC
		SIG5 Rev	AATACAACGATTGCGATTCACTG
AT4G31870	*GLUTATHIONE PEROXIDASE 7*	GPX7 Fw	GGTTCAAAGCAGAGTTCCCT
		GPX7 Rev	GATGATATCACCAAGGAAACCAC

Supplementary table 2.
UV-B upregulated genes identified in the examined transcriptome datasets

Locus Identifier	UVR8 dependent	differential in root	differential in leaf	Gene Model Name	Primary Gene Symbol
AT1G01520	yes		Y	AT1G01520.1	ALTERED SEED GERMINATION 4 (ASG4)
AT1G05575	ND	Y		AT1G05575.1	
AT1G05680	ND	Y	Y	AT1G05680.1	URIDINE DIPHOSPHATE GLYCOSYLTRANSFERASE 74E2 (UGT74E2)
AT1G06000	yes	Y	Y	AT1G06000.1	(UGT89C1)
AT1G06180	yes		Y	AT1G06180.1	MYB DOMAIN PROTEIN 13 (MYB13)
AT1G10170	ND	Y		AT1G10170.1	NF-X-LIKE 1 (NFXL1)
AT1G10370	yes	Y	Y	AT1G10370.1	EARLY-RESPONSIVE TO DEHYDRATION 9 (ERD9)
AT1G12370	yes	Y		AT1G12370.2	PHOTOLYASE 1 (PHR1)
AT1G17170	ND	Y		AT1G17170.1	GLUTATHIONE S-TRANSFERASE TAU 24 (GSTU24)
AT1G17180	ND	Y		AT1G17180.1	GLUTATHIONE S-TRANSFERASE TAU 25 (GSTU25)
AT1G18570	ND	Y		AT1G18570.1	MYB DOMAIN PROTEIN 51 (MYB51)
AT1G18900	yes	Y		AT1G18900.3	
AT1G19020	ND	Y		AT1G19020.1	
AT1G23010	yes	Y	Y	AT1G23010.1	LOW PHOSPHATE ROOT1 (LPR1)
AT1G23550	yes	Y	Y	AT1G23550.1	SIMILAR TO RCD ONE 2 (SRO2)
AT1G27730	yes		Y	AT1G27730.1	SALT TOLERANCE ZINC FINGER (STZ)
AT1G30370	ND	Y		AT1G30370.1	DAD1-LIKE ACYLHYDROLASE (DLAH)
AT1G32870	yes	Y	Y	AT1G32870.1	NAC DOMAIN PROTEIN 13 (NAC13)
AT1G33600	ND	Y		AT1G33600.1	
AT1G35210	ND	Y		AT1G35210.1	
AT1G42990	ND	Y		AT1G42990.1	BASIC REGION/LEUCINE ZIPPER MOTIF 60 (BZIP60)
AT1G48320	yes		Y	AT1G48320.1	DHNA-COA THIOESTERASE 1 (DHNAT1)
AT1G51920	ND	Y		AT1G51920.1	
AT1G55450	ND	Y		AT1G55450.2	
AT1G59590	ND	Y		AT1G59590.1	(ZCF37)
AT1G61370	yes	Y		AT1G61370.1	
AT1G65060	yes	Y	Y	AT1G65060.1	4-COUMARATE:COA LIGASE 3 (4CL3)
AT1G65560	yes		Y	AT1G65560.1	
AT1G67810	ND	Y	Y	AT1G67810.1	SULFUR E2 (SUFE2)
AT1G67970	ND	Y		AT1G67970.1	HEAT SHOCK TRANSCRIPTION FACTOR A8 (HSFA8)
AT1G68620	yes	Y		AT1G68620.1	

AT1G70000	yes	Y	Y	AT1G70000.1	(MYBD)
AT1G76600	ND	Y		AT1G76600.1	
AT1G78600	yes	Y		AT1G78600.2	LIGHT-REGULATED ZINC FINGER PROTEIN 1 (LZF1)
AT1G79270	yes		Y	AT1G79270.1	EVOLUTIONARILY CONSERVED C-TERMINAL REGION 8 (ECT8)
AT2G03760	ND	Y	Y	AT2G03760.1	SULPHOTRANSFERASE 12 (SOT12)
AT2G04040	ND	Y		AT2G04040.1	DETOXIFICATION 1 (DTX1)
AT2G15480	ND	Y	Y	AT2G15480.1	UDP-GLUCOSYL TRANSFERASE 73B5 (UGT73B5)
AT2G15490	ND	Y		AT2G15490.1	UDP-GLYCOSYLTRANSFERASE 73B4 (UGT73B4)
AT2G16890	no	Y	Y	AT2G16890.2	
AT2G18690	yes			AT2G18690.1	
AT2G21640	ND	Y	Y	AT2G21640.1	
AT2G21970	yes	Y		AT2G21970.1	STRESS ENHANCED PROTEIN 2 (SEP2)
AT2G22590	yes	Y	Y	AT2G22590.1	
AT2G23270	ND	Y		AT2G23270.1	
AT2G23910	yes	Y	Y	AT2G23910.1	
AT2G25530	yes		Y	AT2G25530.1	
AT2G27420	yes		Y	AT2G27420.1	
AT2G27820	yes	Y		AT2G27820.1	PREPHENATE DEHYDRATASE 1 (PD1)
AT2G30040	yes		Y	AT2G30040.1	MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 14 (MAPKKK14)
AT2G30250	ND	Y	Y	AT2G30250.1	WRKY DNA-BINDING PROTEIN 25 (WRKY25)
AT2G30490	yes		Y	AT2G30490.1	CINNAMATE-4-HYDROXYLASE (C4H)
AT2G32020	ND	Y	Y	AT2G32020.1	
AT2G32030	ND	Y		AT2G32030.1	
AT2G35480	ND	Y		AT2G35480.1	
AT2G36750	ND		Y	AT2G36750.1	UDP-GLUCOSYL TRANSFERASE 73C1 (UGT73C1)
AT2G37040	yes		Y	AT2G37040.1	PHE AMMONIA LYASE 1 (pal1)
AT2G37430	ND	Y		AT2G37430.1	ZINC FINGER OF ARABIDOPSIS THALIANA 11 (ZAT11)
AT2G37970	yes		Y	AT2G37970.1	(SOUL-1)
AT2G41040	yes		Y	AT2G41040.1	
AT2G41100	ND	Y		AT2G41100.1	TOUCH 3 (TCH3)
AT2G41730	ND	Y	Y	AT2G41730.1	
AT2G46270	yes		Y	AT2G46270.1	G-BOX BINDING FACTOR 3 (GBF3)
AT2G46310	ND	Y		AT2G46310.1	CYTOKININ RESPONSE FACTOR 5 (CRF5)
AT2G46420	yes	Y		AT2G46420.1	
AT2G47000	ND		Y	AT2G47000.1	ATP-BINDING CASSETTE B4 (ABCB4)

AT2G47460	yes	Y	Y	AT2G47460.1	MYB DOMAIN PROTEIN 12 (MYB12)
AT2G47520	ND	Y		AT2G47520.1	ETHYLENE RESPONSE FACTOR 71 (ERF71)
AT3G01830	ND	Y		AT3G01830.1	
AT3G01970	no	Y		AT3G01970.1	WRKY DNA-BINDING PROTEIN 45 (WRKY45)
AT3G05360	yes	Y	Y	AT3G05360.1	RECEPTOR LIKE PROTEIN 30 (RLP30)
AT3G09520	yes	Y		AT3G09520.1	EXOCYST SUBUNIT EXO70 FAMILY PROTEIN H4 (EXO70H4)
AT3G16175	yes		Y	AT3G16175.1	
AT3G17609	yes	Y	Y	AT3G17609.2	HY5-HOMOLOG (HYH)
AT3G19450	yes		Y	AT3G19450.1	(ATCAD4)
AT3G21560	yes	Y	Y	AT3G21560.1	UDP-GLUCOSYL TRANSFERASE 84A2 (UGT84A2)
AT3G22160	ND	Y	Y	AT3G22160.1	JASMONATE-ASSOCIATED VQ MOTIF GENE 1 (JAV1)
AT3G22370	ND	Y	Y	AT3G22370.1	ALTERNATIVE OXIDASE 1A (AOX1A)
AT3G22840	yes	Y	Y	AT3G22840.1	EARLY LIGHT-INDUCABLE PROTEIN (ELIP1)
AT3G25250	ND		Y	AT3G25250.1	AGC2 KINASE 1 (AGC2-1)
AT3G27170	yes		Y	AT3G27170.1	CHLORIDE CHANNEL B (CLC-B)
AT3G28210	ND			AT3G28210.1	(PMZ)
AT3G30460	yes		Y	AT3G30460.1	
AT3G44450	yes	Y		AT3G44450.1	BLUE-LIGHT INHIBITOR OF CRYPTOCHROMES 2 (BIC2)
AT3G44720	yes	Y		AT3G44720.1	AROGENATE DEHYDRATASE 4 (ADT4)
AT3G47780	yes	Y		AT3G47780.1	ATP-BINDING CASSETTE A7 (ABCA7)
AT3G48850	ND	Y		AT3G48850.1	PHOSPHATE TRANSPORTER 3;2 (PHT3;2)
AT3G50930	ND	Y		AT3G50930.1	CYTOCHROME BC1 SYNTHESIS (BCS1)
AT3G51240	yes	Y	Y	AT3G51240.1	FLAVANONE 3-HYDROXYLASE (F3H)
AT3G52450	yes		Y	AT3G52450.1	PLANT U-BOX 22 (PUB22)
AT3G52740	yes	Y		AT3G52740.1	BLUE-LIGHT INHIBITOR OF CRYPTOCHROMES 1 (BIC1)
AT3G53260	yes	Y	Y	AT3G53260.1	PHENYLALANINE AMMONIA-LYASE 2 (PAL2)
AT3G53810	ND	Y		AT3G53810.1	L-TYPE LECTIN RECEPTOR KINASE IV.2 (LECRK-IV.2)
AT3G54420	yes	Y		AT3G54420.1	HOMOLOG OF CARROT EP3-3 CHITINASE (EP3)
AT3G55120	yes	Y	Y	AT3G55120.1	TRANSPARENT TESTA 5 (TT5)
AT3G56290	yes	Y		AT3G56290.1	
AT3G61630	ND	Y	Y	AT3G61630.1	CYTOKININ RESPONSE FACTOR 6 (CRF6)
AT3G63380	ND	Y		AT3G63380.1	AUTO-INHIBITED CA2+ ATPASE 12 (ACA12)
AT4G01870	ND	Y		AT4G01870.1	
AT4G03320	ND	Y	Y	AT4G03320.1	TRANSLOCON AT THE INNER ENVELOPE MEMBRANE OF CHLOROPLASTS 20-IV (tic20-IV)
AT4G05020	ND	Y		AT4G05020.2	NAD(P)H DEHYDROGENASE B2 (NDB2)

AT4G10040	yes	Y		AT4G10040.1	CYTOCHROME C-2 (CYTC-2)
AT4G13180	ND		Y	AT4G13180.1	
AT4G14365	ND	Y	Y	AT4G14365.1	XB3 ORTHOLOG 4 IN ARABIDOPSIS THALIANA (XBAT34)
AT4G14690	yes	Y	Y	AT4G14690.1	EARLY LIGHT-INDUCIBLE PROTEIN 2 (ELIP2)
AT4G15480	yes	Y	Y	AT4G15480.1	(UGT84A1)
AT4G17260	ND	Y		AT4G17260.1	
AT4G20830	ND	Y		AT4G20830.1	(ATBBE19)
AT4G20860	ND		Y	AT4G20860.1	(ATBBE22)
AT4G22530	ND	Y		AT4G22530.1	
AT4G23190	ND	Y		AT4G23190.1	CYSTEINE-RICH RLK (RECEPTOR-LIKE PROTEIN KINASE) 11 (CRK11)
AT4G27030	yes	Y		AT4G27030.1	FATTY ACID DESATURASE A (FADA)
AT4G27657	yes		Y	AT4G27657.1	
AT4G27940	yes	Y		AT4G27940.1	MANGANESE TRACKING FACTOR FOR MITOCHONDRIAL SOD2 (MTM1)
AT4G31870	yes		Y	AT4G31870.1	GLUTATHIONE PEROXIDASE 7 (GPX7)
AT4G36500	ND	Y		AT4G36500.1	
AT4G37150	yes		Y	AT4G37150.1	METHYL ESTERASE 9 (MES9)
AT4G37290	ND	Y		AT4G37290.1	
AT4G37370	ND	Y	Y	AT4G37370.1	CYTOCHROME P450, FAMILY 81, SUBFAMILY D, POLYPEPTIDE 8 (CYP81D8)
AT5G01540	ND	Y		AT5G01540.1	L-TYPE LECTIN RECEPTOR KINASE-VI.2 (LECRK-VI.2)
AT5G02270	yes		Y	AT5G02270.2	ATP-BINDING CASSETTE I20 (ABCI20)
AT5G04000	yes		Y	AT5G04000.2	
AT5G04340	ND		Y	AT5G04340.1	ZINC FINGER OF ARABIDOPSIS THALIANA 6 (ZAT6)
AT5G05270	yes	Y	Y	AT5G05270.1	CHALCONE ISOMERASE LIKE (CHIL)
AT5G05410	yes		Y	AT5G05410.1	DRE-BINDING PROTEIN 2A (DREB2A)
AT5G08640	yes	Y	Y	AT5G08640.1	FLAVONOL SYNTHASE 1 (FLS1)
AT5G11260	yes		Y	AT5G11260.1	ELONGATED HYPOCOTYL 5 (HY5)
AT5G14730	ND	Y		AT5G14730.1	
AT5G17050	yes	Y		AT5G17050.1	UDP-GLUCOSYL TRANSFERASE 78D2 (UGT78D2)
AT5G17220	yes		Y	AT5G17220.1	GLUTATHIONE S-TRANSFERASE PHI 12 (GSTF12)
AT5G17780	yes	Y		AT5G17780.2	
AT5G18470	yes	Y		AT5G18470.1	
AT5G19850	yes	Y		AT5G19850.1	
AT5G20230	ND	Y		AT5G20230.1	BLUE-COPPER-BINDING PROTEIN (BCB)
AT5G23730	yes	Y	Y	AT5G23730.1	REPRESSOR OF UV-B PHOTOMORPHOGENESIS 2 (RUP2)
AT5G24120	yes	Y	Y	AT5G24120.1	SIGMA FACTOR E (SIGE)

AT5G24850	yes	Y		AT5G24850.1	CRYPTOCHROME 3 (CRY3)
AT5G39050	ND	Y		AT5G39050.1	PHENOLIC GLUCOSIDE MALONYLTRANSFERASE 1 (PMAT1)
AT5G39670	ND	Y	Y	AT5G39670.1	
AT5G40690	ND	Y		AT5G40690.1	
AT5G42760	yes		Y	AT5G42760.2	
AT5G43450	ND	Y	Y	AT5G43450.1	
AT5G44110	yes	Y	Y	AT5G44110.1	ATP-BINDING CASSETTE A21 (ABCI21)
AT5G49330	yes		Y	AT5G49330.1	MYB DOMAIN PROTEIN 111 (MYB111)
AT5G52250	yes		Y	AT5G52250.1	REPRESSOR OF UV-B PHOTOMORPHOGENESIS 1 (RUP1)
AT5G52750	ND	Y		AT5G52750.1	
AT5G53970	yes	Y		AT5G53970.1	TYROSINE AMINOTRANSFERASE 7 (TAT7)
AT5G54490	ND	Y		AT5G54490.1	PINOID-BINDING PROTEIN 1 (PBP1)
AT5G57220	ND	Y		AT5G57220.1	CYTOCHROME P450, FAMILY 81, SUBFAMILY F, POLYPEPTIDE 2 (CYP81F2)
AT5G59450	yes	Y		AT5G59450.1	
AT5G59820	yes		Y	AT5G59820.1	RESPONSIVE TO HIGH LIGHT 41 (RHL41)
AT5G60540	yes		Y	AT5G60540.1	PYRIDOXINE BIOSYNTHESIS 2 (PDX2)
AT5G62210	yes	Y	Y	AT5G62210.1	
AT5G62480	ND	Y		AT5G62480.1	GLUTATHIONE S-TRANSFERASE TAU 9 (GSTU9)
ND: no data available as yet.					
in red: from Brown 2005					

Supplementary table 3.

UV-B downregulated genes identified in the examined transcriptome datasets

Locus Identifier	UVR8 dependent	differential in root	differential in leaf	Gene Model Name	Primary Gene Symbol
AT1G01070	No	Y		AT1G01070.1	USUALLY MULTIPLE ACIDS MOVE IN AND OUT TRANSPORTERS 28 (UMAMIT28)
AT1G01240	Yes	Y		AT1G01240.1	
AT1G02660	Yes	Y		AT1G02660.1	
AT1G06090	No		Y	AT1G06090.1	
AT1G06350	No	Y		AT1G06350.1	DELTA 9 DESATURASE 4 (ADS4)
AT1G06360	No	Y	Y	AT1G06360.1	
AT1G09390	Yes	Y		AT1G09390.1	
AT1G11850	Yes	Y		AT1G11850.2	
AT1G12110	Yes	Y		AT1G12110.1	NRT1/ PTR FAMILY 6.3 (NPF6.3)
AT1G12330	No	Y		AT1G12330.1	
AT1G13250	Yes	Y		AT1G13250.1	GALACTURONOSYLTRANSFERASE-LIKE 3 (GATL3)
AT1G13300	No	Y		AT1G13300.1	HYPERSENSITIVITY TO LOW PI-ELICITED PRIMARY ROOT SHORTENING 1 (HRS1)
AT1G13420	Yes	Y		AT1G13420.1	SULFOTRANSFERASE 4B (ST4B)
AT1G13700	No	Y		AT1G13700.1	6-PHOSPHOGLUCONOLACTONASE 1 (PGL1)
AT1G15210	Yes	Y		AT1G15210.1	ATP-BINDING CASSETTE G35 (ABCG35)
AT1G15380	Yes	Y		AT1G15380.1	GLYOXYLASE I 4 (GLYI4)
AT1G19330	Yes	Y		AT1G19330.3	
AT1G19530	Yes	Y		AT1G19530.1	
AT1G20160	Yes	Y		AT1G20160.1	(ATSBT5.2)
AT1G22500	Yes	Y		AT1G22500.1	ARABIDOPSIS TOXICOS EN LEVADURA 15 (ATL15)
AT1G25230	Yes	Y		AT1G25230.1	
AT1G28330	Yes	Y		AT1G28330.5	DORMANCY-ASSOCIATED PROTEIN-LIKE 1 (DYL1)
AT1G29090	Yes	Y		AT1G29090.1	
AT1G32450	Yes	Y		AT1G32450.1	NRT1/ PTR FAMILY 7.3 (NPF7.3)
AT1G33055	Yes	Y		AT1G33055.1	
AT1G34510	Yes	Y		AT1G34510.1	
AT1G44800	Yes	Y		AT1G44800.1	SILIQUES ARE RED 1 (SIAR1)
AT1G49470	Yes	Y		AT1G49470.1	
AT1G52400	No	Y		AT1G52400.1	BETA GLUCOSIDASE 18 (BGLU18)

AT1G56220	Yes	Y		AT1G56220.3	
AT1G62280	Yes	Y		AT1G62280.1	SLAC1 HOMOLOGUE 1 (SLAH1)
AT1G62980	No	Y		AT1G62980.1	EXPANSIN A18 (EXPA18)
AT1G63880	Yes	Y		AT1G63880.1	
AT1G68710	Yes	Y		AT1G68710.1	
AT1G69690	Yes	Y		AT1G69690.1	TEOSINTE BRANCHED1/CYCLOIDEA/PCF 15 (TCP15)
AT1G70850	No	Y		AT1G70850.1	MLP-LIKE PROTEIN 34 (MLP34)
AT1G70880	No	Y		AT1G70880.1	
AT1G74670	Yes	Y		AT1G74670.1	GA-STIMULATED ARABIDOPSIS 6 (GASA6)
AT1G75500	Yes	Y		AT1G75500.1	WALLS ARE THIN 1 (WAT1)
AT1G75900	Yes	Y		AT1G75900.1	
AT1G76410	Yes	Y		AT1G76410.1	(ATL8)
AT1G77210	Yes	Y		AT1G77210.1	SUGAR TRANSPORT PROTEIN 14 (STP14)
AT1G78000	Yes	Y		AT1G78000.1	SULFATE TRANSPORTER 1;2 (SULTR1;2)
AT1G78490	Yes	Y		AT1G78490.1	CYTOCHROME P450, FAMILY 708, SUBFAMILY A, POLYPEPTIDE 3 (CYP708A3)
AT1G80050	No	Y		AT1G80050.1	ADENINE PHOSPHORIBOSYL TRANSFERASE 2 (APT2)
AT1G80280	Yes		Y	AT1G80280.1	
AT1G80440	Yes	Y		AT1G80440.1	KISS ME DEADLY 1 (KMD1)
AT2G13610	Yes	Y		AT2G13610.1	ATP-BINDING CASSETTE G5 (ABCG5)
AT2G16980	No	Y		AT2G16980.2	
AT2G22500	Yes	Y		AT2G22500.1	UNCOUPLING PROTEIN 5 (UCP5)
AT2G23620	No	Y		AT2G23620.1	METHYL ESTERASE 1 (MES1)
AT2G24762	No	Y		AT2G24762.1	GLUTAMINE DUMPER 4 (GDU4)
AT2G25900	Yes	Y		AT2G25900.1	(ATCTH)
AT2G26710	Yes	Y		AT2G26710.1	PHYB ACTIVATION TAGGED SUPPRESSOR 1 (BAS1)
AT2G28160	Yes		Y	AT2G28160.1	FER-LIKE REGULATOR OF IRON UPTAKE (FRU)
AT2G28410	Yes		Y	AT2G28410.1	
AT2G28780	Yes	Y		AT2G28780.1	
AT2G29750	No	Y		AT2G29750.1	UDP-GLUCOSYL TRANSFERASE 71C1 (UGT71C1)
AT2G36050	Yes		Y	AT2G36050.1	OVATE FAMILY PROTEIN 15 (OFP15)
AT2G37130	Yes	Y		AT2G37130.1	
AT2G38940	No	Y	Y	AT2G38940.1	PHOSPHATE TRANSPORTER 1;4 (PHT1;4)
AT2G39530	Yes	Y		AT2G39530.1	CASP-LIKE PROTEIN 4D1 (CASPL4D1)

AT2G42320	Yes	Y		AT2G42320.1	
AT2G42840	Yes	Y	Y	AT2G42840.1	PROTODERMAL FACTOR 1 (PDF1)
AT2G42870	Yes	Y		AT2G42870.1	PHY RAPIDLY REGULATED 1 (PAR1)
AT2G43050	Yes	Y		AT2G43050.1	(ATPMEPCRD)
AT2G44130	Yes	Y		AT2G44130.1	KISS ME DEADLY 3 (KMD3)
AT2G44740	Yes		Y	AT2G44740.1	CYCLIN P4;1 (CYCP4;1)
AT2G45220	Yes	Y		AT2G45220.1	PECTIN METHYLESTERASE 17 (PME17)
AT3G01260	Yes	Y		AT3G01260.1	
AT3G01490	Yes	Y		AT3G01490.1	
AT3G02550	Yes	Y		AT3G02550.1	LOB DOMAIN-CONTAINING PROTEIN 41 (LBD41)
AT3G02850	Yes	Y		AT3G02850.1	STELAR K+ OUTWARD RECTIFIER (SKOR)
AT3G03870	Yes	Y		AT3G03870.2	
AT3G04290	Yes	Y	Y	AT3G04290.1	LI-TOLERANT LIPASE 1 (LTL1)
AT3G10020	Yes	Y		AT3G10020.1	
AT3G10190	No	Y		AT3G10190.1	CALMODULIN-LIKE 36 (CML36)
AT3G14060	No	Y		AT3G14060.1	
AT3G14210	Yes	Y		AT3G14210.1	EPITHIOSPECIFIER MODIFIER 1 (ESM1)
AT3G14760	Yes		Y	AT3G14760.1	
AT3G15530	Yes	Y		AT3G15530.1	
AT3G20015	No	Y		AT3G20015.1	
AT3G20470	Yes	Y		AT3G20470.1	GLYCINE-RICH PROTEIN 5 (GRP5)
AT3G21090	Yes	Y		AT3G21090.1	ATP-BINDING CASSETTE G15 (ABCG15)
AT3G21770	Yes	Y		AT3G21770.1	
AT3G23080	Yes	Y		AT3G23080.1	
AT3G23430	Yes	Y	Y	AT3G23430.1	PHOSPHATE 1 (PHO1)
AT3G23800	No	Y		AT3G23800.1	SELENIUM-BINDING PROTEIN 3 (SBP3)
AT3G24300	No	Y		AT3G24300.1	AMMONIUM TRANSPORTER 1;3 (AMT1;3)
AT3G25190	Yes	Y		AT3G25190.1	VACUOLAR IRON TRANSPORTER-LIKE 5 (VTL5)
AT3G28180	Yes	Y		AT3G28180.1	CELLULOSE-SYNTHASE-LIKE C4 (CSLC04)
AT3G48970	Yes	Y		AT3G48970.1	
AT3G50740	Yes	Y		AT3G50740.1	UDP-GLUCOSYL TRANSFERASE 72E1 (UGT72E1)
AT3G51330	No	Y		AT3G51330.1	
AT3G53250	Yes		Y	AT3G53250.1	SMALL AUXIN UPREGULATED RNA 57 (SAUR57)

AT3G54580	No	Y		AT3G54580.1	
AT3G58120	Yes		Y	AT3G58120.1	(BZIP61)
AT3G61160	No	Y		AT3G61160.2	
AT4G00700	No	Y		AT4G00700.1	
AT4G04955	No		Y	AT4G04955.1	ALLANTOINASE (ALN)
AT4G07820	Yes	Y		AT4G07820.1	
AT4G08300	Yes	Y		AT4G08300.1	USUALLY MULTIPLE ACIDS MOVE IN AND OUT TRANSPORTERS 17 (UMAMIT17)
AT4G11320	No	Y	Y	AT4G11320.1	CYSTEINE PROTEASE 2 (CP2)
AT4G13840	Yes	Y		AT4G13840.1	ECERIFERUM 26 (CER26)
AT4G14130	Yes	Y		AT4G14130.1	XYLOGLUCAN ENDOTRANSGLUCOSYLASE/HYDROLASE 15 (XTH15)
AT4G15340	No	Y		AT4G15340.1	PENTACYCLIC TRITERPENE SYNTHASE 1 (PEN1)
AT4G15390	Yes	Y		AT4G15390.1	
AT4G18510	Yes	Y		AT4G18510.1	CLAVATA3/ESR-RELATED 2 (CLE2)
AT4G18970	Yes	Y	Y	AT4G18970.2	
AT4G21680	No	Y		AT4G21680.1	NRT1/ PTR FAMILY 7.2 (NPF7.2)
AT4G22610	No	Y		AT4G22610.1	
AT4G23700	Yes	Y		AT4G23700.1	CATION/H+ EXCHANGER 17 (CHX17)
AT4G23870	Yes	Y		AT4G23870.1	
AT4G27440	Yes	Y		AT4G27440.1	PROTOCHLOROPHYLLIDE OXIDOREDUCTASE B (PORB)
AT4G27450	Yes	Y		AT4G27450.1	
AT4G28240	Yes	Y		AT4G28240.1	
AT4G31910	Yes	Y		AT4G31910.1	BR-RELATED ACYLTRANSFERASE1 (BAT1)
AT4G33960	No	Y		AT4G33960.1	
AT4G36670	No	Y		AT4G36670.1	POLYOL/MONOSACCHARIDE TRANSPORTER 6 (PMT6)
AT4G39675	Yes	Y		AT4G39675.1	
AT5G04950	Yes	Y		AT5G04950.1	NICOTIANAMINE SYNTHASE 1 (NAS1)
AT5G07580	Yes	Y		AT5G07580.1	(ERF106)
AT5G08520	Yes	Y		AT5G08520.1	(MYBS2)
AT5G10430	Yes		Y	AT5G10430.1	ARABINOGALACTAN PROTEIN 4 (AGP4)
AT5G10580	Yes	Y		AT5G10580.1	
AT5G14920	Yes	Y		AT5G14920.1	A-STIMULATED IN ARABIDOPSIS 14 (GASA14)
AT5G16000	Yes		Y	AT5G16000.1	NSP-INTERACTING KINASE 1 (NIK1)
AT5G18860	No	Y		AT5G18860.1	NUCLEOSIDE HYDROLASE 3 (NSH3)

AT5G22500	Yes	Y		AT5G22500.1	FATTY ACID REDUCTASE 1 (FAR1)
AT5G22940	No		Y	AT5G22940.1	FRA8 HOMOLOG (F8H)
AT5G23660	Yes	Y		AT5G23660.1	(SWEET12)
AT5G25240	No	Y		AT5G25240.1	
AT5G40780	Yes	Y		AT5G40780.1	LYSINE HISTIDINE TRANSPORTER 1 (LHT1)
AT5G43180	Yes	Y		AT5G43180.1	
AT5G43520	Yes	Y		AT5G43520.1	
AT5G44680	Yes	Y		AT5G44680.1	
AT5G44920	Yes	Y		AT5G44920.1	TIR-KASH PROTEIN (TIK)
AT5G45500	Yes	Y		AT5G45500.1	
AT5G45670	Yes	Y	Y	AT5G45670.1	
AT5G47450	Yes	Y		AT5G47450.1	TONOPLAST INTRINSIC PROTEIN 2;3 (TIP2;3)
AT5G47500	Yes		Y	AT5G47500.1	PECTIN METHYLESTERASE 5 (PME5)
AT5G52790	No	Y		AT5G52790.1	
AT5G53250	No	Y		AT5G53250.1	ARABINOGALACTAN PROTEIN 22 (AGP22)
AT5G56100	No	Y		AT5G56100.1	
AT5G57340	Yes	Y		AT5G57340.2	
AT5G57530	No	Y		AT5G57530.1	XYLOGLUCAN ENDOTRANSGLUCOSYLASE/HYDROLASE 12 (XTH12)
AT5G59080	Yes	Y		AT5G59080.1	
AT5G59780	Yes	Y		AT5G59780.3	MYB DOMAIN PROTEIN 59 (MYB59)
AT5G60660	Yes	Y	Y	AT5G60660.1	PLASMA MEMBRANE INTRINSIC PROTEIN 2;4 (PIP2;4)
AT5G61250	Yes	Y		AT5G61250.2	GLUCURONIDASE 1 (GUS1)
AT5G63180	Yes	Y		AT5G63180.1	
AT5G63600	Yes	Y		AT5G63600.2	FLAVONOL SYNTHASE 5 (FLS5)
AT5G64410	Yes	Y		AT5G64410.1	OLIGOPEPTIDE TRANSPORTER 4 (OPT4)
AT5G65390	No		Y	AT5G65390.1	ARABINOGALACTAN PROTEIN 7 (AGP7)
Genes, showing induction in the shoot only are marked with green background ('shoot specific').					
Genes, induced both in the shoot and in the root are marked with yellow backgound ('universal').					
Genes marked with yellow background and red text are 'universal'and their induction depends on UVR8.					

Supplementary table 4.

GENE Ontology (GO) categories of the UVR8-dependent up-regulated genes shown in Supplementary table 2.

Biological process - Upregulated - UVR8 dependent	**pValue**
response to UV	2.47E-19
response to UV-B	1.02E-17
response to light stimulus	2.17E-16
response to radiation	3.97E-16
aromatic compound biosynthetic process	1.88E-15
phenylpropanoid metabolic process	2.04E-15
cellular aromatic compound metabolic process	2.60E-15
phenylpropanoid biosynthetic process	5.49E-15
response to abiotic stimulus	2.34E-14
secondary metabolic process	2.81E-13
cellular amino acid derivative biosynthetic process	1.41E-12
cellular amino acid derivative metabolic process	1.57E-12
response to stimulus	5.11E-12
small molecule biosynthetic process	9.20E-12
flavonoid biosynthetic process	4.45E-11
cellular amino acid and derivative metabolic process	4.65E-11
flavonoid metabolic process	9.51E-11
small molecule metabolic process	4.51E-09
response to red light	8.38E-09
response to far red light	9.77E-08
response to red or far red light	2.90E-07
response to stress	7.89E-06
response to wounding	3.44E-05
response to chitin	2.02E-04
L-phenylalanine biosynthetic process	2.11E-04
flavone biosynthetic process	2.11E-04
flavone metabolic process	2.11E-04
flavonol metabolic process	2.11E-04
flavonol biosynthetic process	2.11E-04

cellular metabolic process	2.51E-04
cellular biosynthetic process	2.63E-04
L-phenylalanine metabolic process	3.37E-04
aromatic amino acid family biosynthetic process, prephenate pathway	3.37E-04
cellular process	3.49E-04
biosynthetic process	5.71E-04
response to oxidative stress	6.19E-04
regulation of photomorphogenesis	6.77E-04
regulation of cellular biosynthetic process	9.61E-04
regulation of biosynthetic process	9.61E-04
regulation of nitrogen compound metabolic process	9.88E-04
response to light intensity	1.15E-03
pigment biosynthetic process	1.24E-03
response to carbohydrate stimulus	1.49E-03
regulation of transcription, DNA-dependent	1.74E-03
regulation of RNA metabolic process	1.79E-03
regulation of cellular metabolic process	1.87E-03
pigment metabolic process	2.15E-03
regulation of transcription	2.19E-03
metabolic process	2.52E-03
heterocycle metabolic process	2.54E-03
regulation of macromolecule biosynthetic process	2.65E-03
photosynthetic acclimation	2.78E-03
multicellular organism growth	2.78E-03
regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	2.98E-03
response to salt stress	3.25E-03
response to gibberellin stimulus	3.31E-03
regulation of metabolic process	4.01E-03
regulation of primary metabolic process	4.34E-03
response to osmotic stress	4.46E-03
regulation of gene expression	5.17E-03
chorismate metabolic process	5.27E-03
aromatic amino acid family biosynthetic process	5.27E-03

positive regulation of anthocyanin metabolic process	5.55E-03
red or far-red light signaling pathway	5.81E-03
cellular response to red or far red light	5.81E-03
regulation of macromolecule metabolic process	6.27E-03
lignin metabolic process	6.67E-03
response to abscisic acid stimulus	6.94E-03
response to chemical stimulus	6.98E-03
toxin catabolic process	7.27E-03
toxin metabolic process	7.27E-03
aromatic amino acid family metabolic process	7.58E-03
cellular response to light stimulus	7.58E-03
cellular response to radiation	7.58E-03
response to organic substance	7.76E-03
immune system process	7.95E-03
pyrimidine dimer repair	8.32E-03
photoreactive repair	8.32E-03
UV protection	8.32E-03
photoprotection	8.32E-03
phosphatidylglycerol metabolic process	8.32E-03
defense response	8.41E-03
response to blue light	8.55E-03
regulation of response to stimulus	9.55E-03
respiratory burst involved in defense response	1.11E-02
response to low fluence blue light stimulus by blue low-fluence system	1.11E-02
protein autoubiquitination	1.11E-02
vitamin biosynthetic process	1.14E-02
cellular response to abiotic stimulus	1.18E-02
dicarboxylic acid metabolic process	1.21E-02
vitamin metabolic process	1.33E-02
pyridoxine metabolic process	1.38E-02
tyrosine biosynthetic process	1.38E-02
pyridoxine biosynthetic process	1.38E-02
respiratory burst	1.38E-02

somatic embryogenesis	1.38E-02
cellular response to stimulus	1.56E-02
regulation of cellular process	1.57E-02
vitamin B6 metabolic process	1.66E-02
tyrosine metabolic process	1.66E-02
vitamin B6 biosynthetic process	1.66E-02
cellular response to stress	1.85E-02
response to low light intensity stimulus	1.93E-02
primary metabolic process	3.06E-02
immune response	4.01E-02
regulation of biological process	4.02E-02
regulation of anthocyanin metabolic process	4.09E-02
multicellular organismal process	4.90E-02
organic acid biosynthetic process	5.39E-02
carboxylic acid biosynthetic process	5.39E-02
cellular amino acid biosynthetic process	5.94E-02
response to hormone stimulus	6.17E-02
immune effector process	6.20E-02
DNA repair	6.85E-02
regulation of post-embryonic development	7.08E-02
amine biosynthetic process	7.24E-02
response to DNA damage stimulus	7.55E-02
regulation of secondary metabolic process	8.02E-02
response to endogenous stimulus	8.21E-02
cellular nitrogen compound biosynthetic process	8.80E-02
oxoacid metabolic process	9.37E-02
carboxylic acid metabolic process	9.37E-02
organic acid metabolic process	9.41E-02
cellular ketone metabolic process	9.79E-02
biological regulation	1.08E-01
glycerophospholipid metabolic process	1.13E-01
water-soluble vitamin biosynthetic process	1.18E-01
positive regulation of biological process	1.23E-01

water-soluble vitamin metabolic process	1.30E-01
regulation of multicellular organismal process	1.33E-01
glycerolipid metabolic process	1.35E-01
multicellular organismal development	1.74E-01
regulation of developmental process	1.76E-01
growth	1.82E-01
positive regulation of cellular metabolic process	1.95E-01
positive regulation of metabolic process	2.02E-01
cellular amino acid metabolic process	2.03E-01
DNA metabolic process	2.14E-01
phospholipid metabolic process	2.20E-01
cellular nitrogen compound metabolic process	2.30E-01
cellular amine metabolic process	2.31E-01
organophosphate metabolic process	2.33E-01
protein ubiquitination	2.35E-01
developmental process	2.40E-01
signaling pathway	2.50E-01
protein modification by small protein conjugation	2.56E-01
nitrogen compound metabolic process	2.59E-01
amine metabolic process	2.71E-01
embryonic development ending in seed dormancy	2.77E-01
protein modification by small protein conjugation or removal	2.91E-01
cellular lipid metabolic process	3.10E-01
positive regulation of cellular process	3.18E-01
embryonic development	3.35E-01
seed development	3.45E-01
fruit development	3.66E-01
cellular catabolic process	4.19E-01
nucleic acid metabolic process	4.34E-01
post-embryonic development	4.48E-01
reproductive process	4.67E-01
lipid metabolic process	4.80E-01
reproduction	4.82E-01

signaling	5.46E-01
anatomical structure development	5.47E-01
catabolic process	5.51E-01
post-translational protein modification	5.91E-01
nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	5.98E-01
reproductive structure development	6.11E-01
reproductive developmental process	6.76E-01
protein modification process	6.78E-01
macromolecule modification	7.46E-01
macromolecule metabolic process	9.52E-01
cellular macromolecule metabolic process	9.55E-01
protein metabolic process	9.82E-01
cellular protein metabolic process	9.87E-01
biological_process	1

Supplementary table 5.
GENE Ontology (GO) categories of the UVR8-dependent down-regulated genes shown in Supplementary table 3.

Biological process - Downregulated - UVR8 dependent	**pValue**
anaerobic respiration	4.90E-06
inorganic anion transport	4.19E-05
response to chemical stimulus	1.04E-04
anion transport	1.43E-04
response to fructose stimulus	4.24E-04
ion transport	4.33E-04
response to stimulus	4.81E-04
nitrate transport	6.78E-04
transport	7.42E-04
establishment of localization	8.05E-04
response to hormone stimulus	8.76E-04
localization	1.13E-03
energy derivation by oxidation of organic compounds	1.64E-03
cellular respiration	1.64E-03
response to endogenous stimulus	1.66E-03
response to organic substance	2.52E-03
response to nitrate	2.79E-03
response to glucose stimulus	3.38E-03
response to hexose stimulus	3.69E-03
response to monosaccharide stimulus	3.69E-03
regulation of tryptophan metabolic process	3.95E-03
positive regulation of cellular amino acid metabolic process	3.95E-03
positive regulation of tryptophan metabolic process	3.95E-03
regulation of iron ion transport	3.95E-03
positive regulation of cellular amine metabolic process	3.95E-03
regulation of metal ion transport	1.18E-02
regulation of cellular amino acid metabolic process	1.96E-02
regulation of cellular amine metabolic process	2.34E-02
response to carbohydrate stimulus	3.30E-02

generation of precursor metabolites and energy	4.42E-02
regulation of ion transport	4.63E-02
regulation of cellular ketone metabolic process	9.06E-02
response to inorganic substance	9.27E-02
regulation of transport	9.42E-02
regulation of localization	1.12E-01
positive regulation of nitrogen compound metabolic process	2.24E-01
regulation of nitrogen compound metabolic process	2.64E-01
positive regulation of cellular metabolic process	2.66E-01
positive regulation of metabolic process	2.74E-01
regulation of primary metabolic process	2.98E-01
regulation of cellular metabolic process	3.34E-01
positive regulation of cellular process	4.19E-01
regulation of metabolic process	4.32E-01
regulation of cellular process	5.04E-01
biological regulation	5.21E-01
positive regulation of biological process	5.79E-01
regulation of biological process	6.72E-01
metabolic process	9.36E-01
cellular process	9.62E-01
cellular metabolic process	9.90E-01
biological_process	1