

DNA microarray analysis

UV-B regulated clones identified with DNA microarray analysis. RNA was isolated from leaves of *Arabidopsis thaliana* Columbia 0 plants irradiated with UV-B_{BE} = 0.137 W/m² for 3 hours. A positive value indicates induction (up-regulation) whereas a negative value indicates repression (down-regulation) of mRNA transcripts. Genes marked in red were used for northern blot analysis. The annotation is based on sequencing from Monsanto (in black) or in our department (in red).

Fold change	Genecode or SmartBlast Hit ID (gi)	Gene description
9.0	MEB5.2	Unknown protein
7.4	F24K9.8	Protein phosphatase 2C (PP2C)
7.0	T911.8	Unknown protein
6.2	T22E19.1	Putative zinc finger protein similar to zinc finger protein 6
5.8	MLD14.3	Cysteine proteinase
5.6	T10O8.120	Putative PyroA, pyridoxine biosynthesis
5.5	MPN9.19	Monosaccharide transport protein
5.0	F508.26	Unknown protein
4.6	T3F24.21	Unknown protein
4.5	T1J1.5	Putative WD-repeat membrane protein
4.4	F15H11.14	Putative auxin transport protein, REH1
4.4	F23F1.10	Omega-3 fatty acid desaturase, endoplasmic reticulum
4.2	F28A23.190	Probable caffeoyl-CoA O-methyltransferase
4.2	F25A4.18	Hypothetical protein
4.1	MRP15.17	Unknown protein
4.1	F5N5.2	Similar to aluminum-induced protein
4.0	T8P19.70	Acetolactate synthase, chloroplast precursor
3.7	T1B3.18	Hypothetical protein
3.6	9294409	Polygalacturonase inhibitor-like protein
3.6	MXK3.30	MADS box transcription factor
3.6	T15C9.10	Phosphoribosylformylglycinamide cyclo-ligase
3.5	F16M14.16	Probable ethylene-inducible protein (similar to SOR1 singlet oxygen resistance protein from <i>Cercospora nicotianae</i>)
3.5	MAH20.20	Flavonol synthase
3.5	MCB17.5	Putative 40S ribosomal protein S10
3.5	T4D2.40	RNA helicase-like protein
3.4	F16P17.17	Unknown protein
3.2	MUJ8.3	Glutathione reductase
3.2	T5J17	GTP-binding protein GB3
3.2	T21P5.13	RGA1-like protein
3.1	MAC9.6	Putative protein Mt N19
3.1	M4E13.70	β-galactosidase-like protein
3.1	MIL23.12	Unknown protein
3.1	MLP3.21	Unknown protein
3.0	T6H20.230	Chloroplast import-associated channel protein
2.9	12229666	4-Coumarate-CoA ligase 3

2.9	2281113	(AC002333) Putative endochitinase
2.8	7469320	Similar to fibrillin <i>Synechocystis</i> (strain PCC 6803)
2.7	11278888	Similar to transcription regulator, from <i>Chlamydia muridarum</i> (strain Nigg)
2.7	7518564	Similar to hypothetical protein PH0283 from <i>Pyrococcus horikoshii</i>
2.7	4587572	(AC006550) Similar to lysosomal trafficking regulator from <i>Mus musculus</i> . Contains 2 WD40, G-beta repeats.
2.7	F18F4.120	DAG-like protein DAG precursor
2.6	F15A17.270	Polyubiquitin (UBQ3)
2.6	9964117	(AF287697) Half-molecule ABC transporter ATM1
2.6	11358588	Nucleoid DNA-binding cnd41-like protein
2.5	1403138	(X98190) Peroxidase ATP2a
2.5	T23J18.30	Pseudogene putative RNA polymerase II subunit Rpb 10
2.4	1703091	Acyl carrier protein, mitochondrial precursor (NADH-ubiquinone oxidoreductase 9.6 kDa SUBUNIT)
2.3	F309.7	Putative Ser/Thr protein kinase
2.3	417527	Pathogenesis-related protein 1 precursor (PR-1)
2.2	7433013	Catalase
2.2	7484929	DNA-binding protein F4I18.20
2.2	4432856	(AC006300) Putative dioxygenase
2.2	12328547	(AP002913) Nucleoid DNA-binding protein cnd41-like protein
2.2	6498419	(AP000815) Similar to Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (AL035356)
2.1	4432856	(AC006300) Putative dioxygenase
2.1	5360792	(AB027252) f-AtMBP
2.1	1169278	Dehydrin ERD14
2.1	6755622	Alpha-spectrin 1, erythroid
2.1	5091620	(AC007454) Contains similarity to FAB1 protein from <i>Saccharomyces cerevisiae</i>
-2.1	8927661	(AC034256) Lhcb6 protein
-2.1	9998817	(AJ278970) LPG2 protein
-2.1	115385	Chlorophyll a-b binding protein 4 precursor (LHCI type IIICAB-4)
-2.1	112739	2S seed storage protein 2 precursor (2S albumin storage protein)
-2.2	4176420	(AB008097) Cytochrome P450
-2.2	7443228	Chlorophyll a/b-binding protein F24G24.140
-2.3	683723	(X02608) FLP
-2.3	F5024.300	Monogalactosyldiacylglycerol synthase
-2.3	MGD8.26	Putative S-adenosylmethionine synthetase
-2.4	9294537	(AB024034) DnaJ-like protein

-2.5	9294650	(AP000600) Lipase/acylhydrolase; myrosinase-associated protein
-2.6	11292138	Hypothetical protein
-2.7	F7H2.16	Chlorophyll binding protein (Lhcb6)
-2.8	F5D21.10	Unknown protein
-3.0	4836947	(AC006085) Putative photosystem II 5 KD protein