

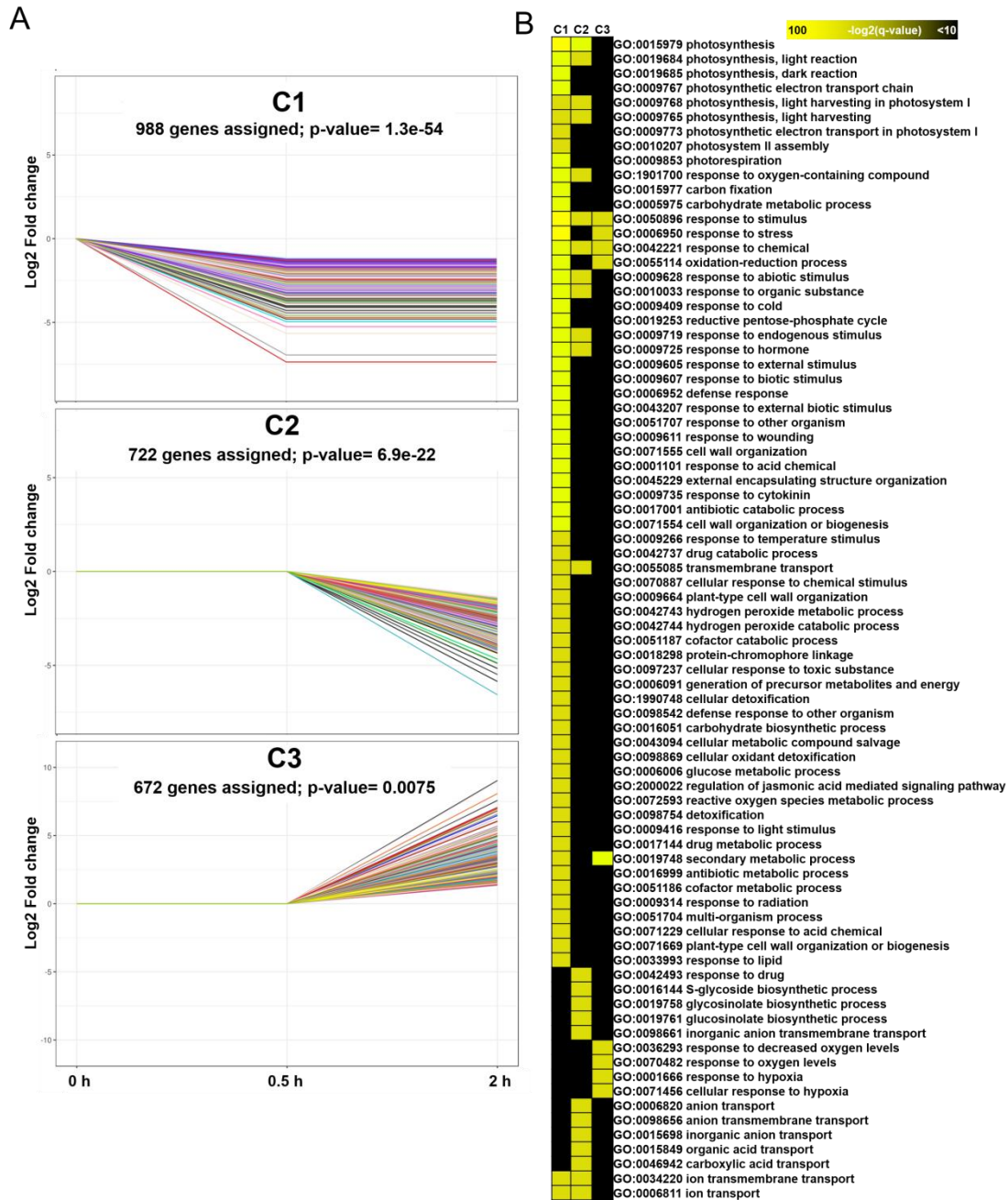


Fig. 1 Suppl. A - clustering ultraviolet-B-regulated genes ($P \leq 0.05$). C1 - cluster 1, C2 - cluster 2, C3 - cluster 3. B - gene ontology enrichment for the three clusters is shown as a heatmap ($P \leq 0.05$) (see Table 3 Suppl. for the detailed gene list).

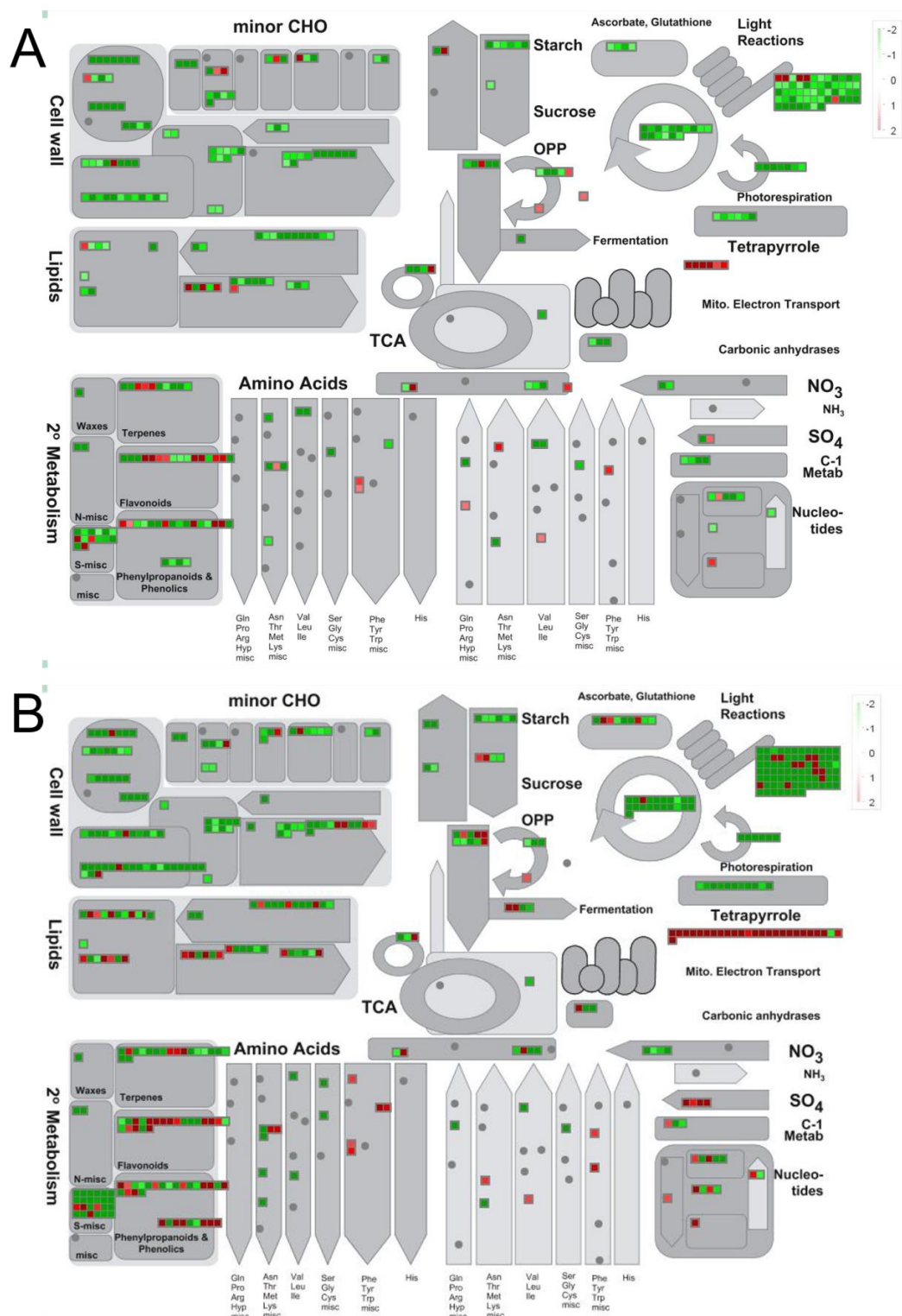


Fig. 2 Suppl. The MapMan (<http://mapman.gabipd.org>) analysis illustrates metabolism-associated differentially expressed genes (DEGs) in *Arabidopsis thaliana* roots. Five-day-old seedlings were subjected to 2.6 kJ m⁻² of ultraviolet-B radiation for 3 min, and then the seedlings were transferred to normal growth conditions for 0.5 h (A) and 2 h (B). Log₂ fold change > 1, false discovery rate ≤ 0.01. See Table 4 Suppl. for the detailed gene list of DEGs involved in the biosynthesis and metabolism of cell wall and lipids, and Table 5 Suppl. for the detailed gene list of DEGs involved in photosynthesis and mitochondrial electron transport. 2° - secondary metabolites, CHO - carbohydrate metabolism, OPP - oxidative pentose phosphate pathway, TCA - tricarboxylic acid cycle.

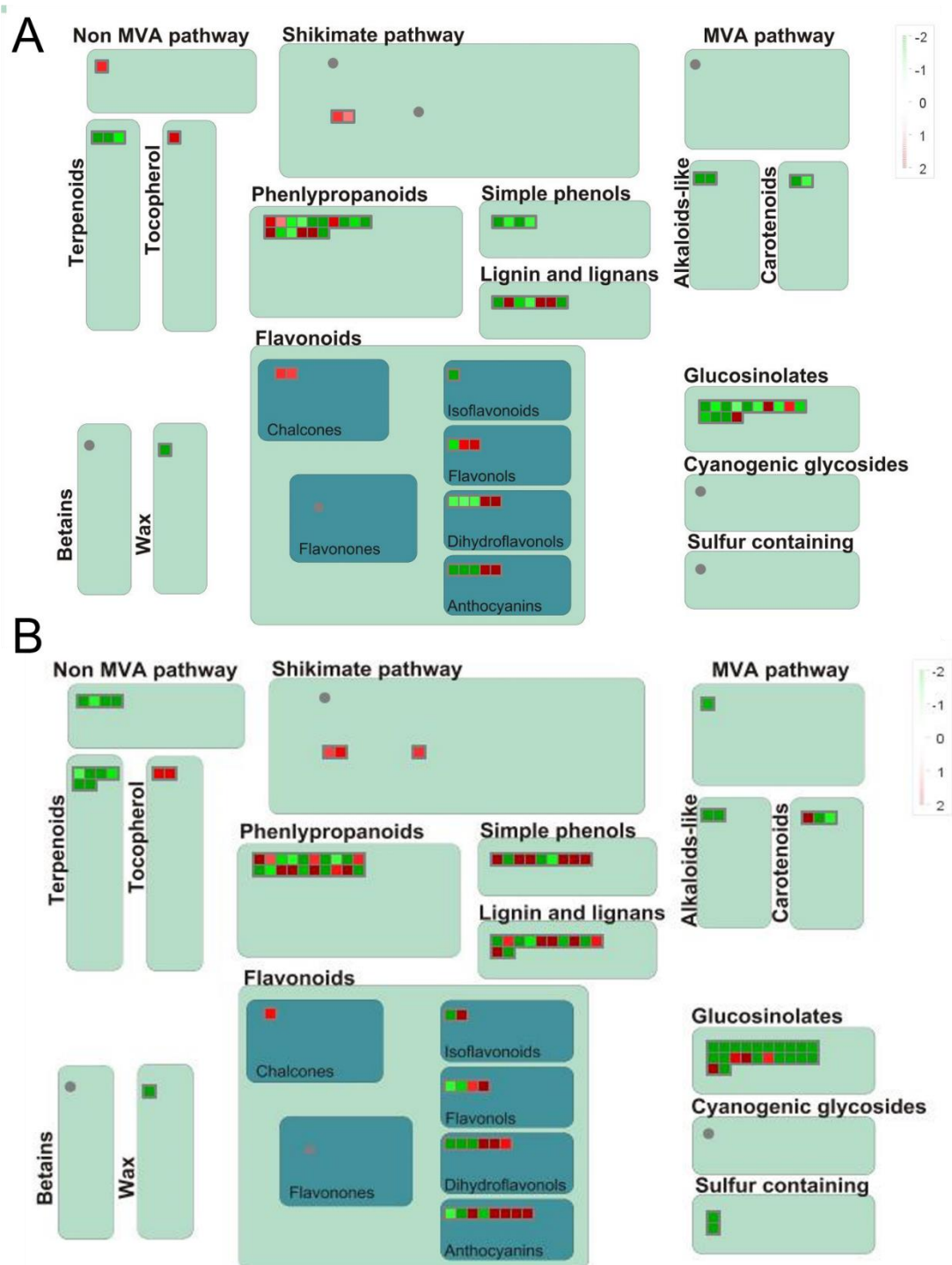


Fig. 3 Suppl. The *MapMan* (<http://mapman.gabipd.org>) analysis illustrates secondary metabolism-related differentially expressed genes (DEGs) in *Arabidopsis thaliana* roots. Five-day-old seedlings were subjected to 2.6 kJ m⁻² of ultraviolet-B radiation for 3 min, and then the seedlings were transferred to normal growth conditions for 0.5 h (A) and 2 h (B). Log₂ fold change > 1, false discovery rate ≤ 0.01. See Table 4 Suppl. for the detailed gene list of DEGs involved in the biosynthesis and metabolism of glucosinolates and terpenoids. MVA - mevalonic acid.

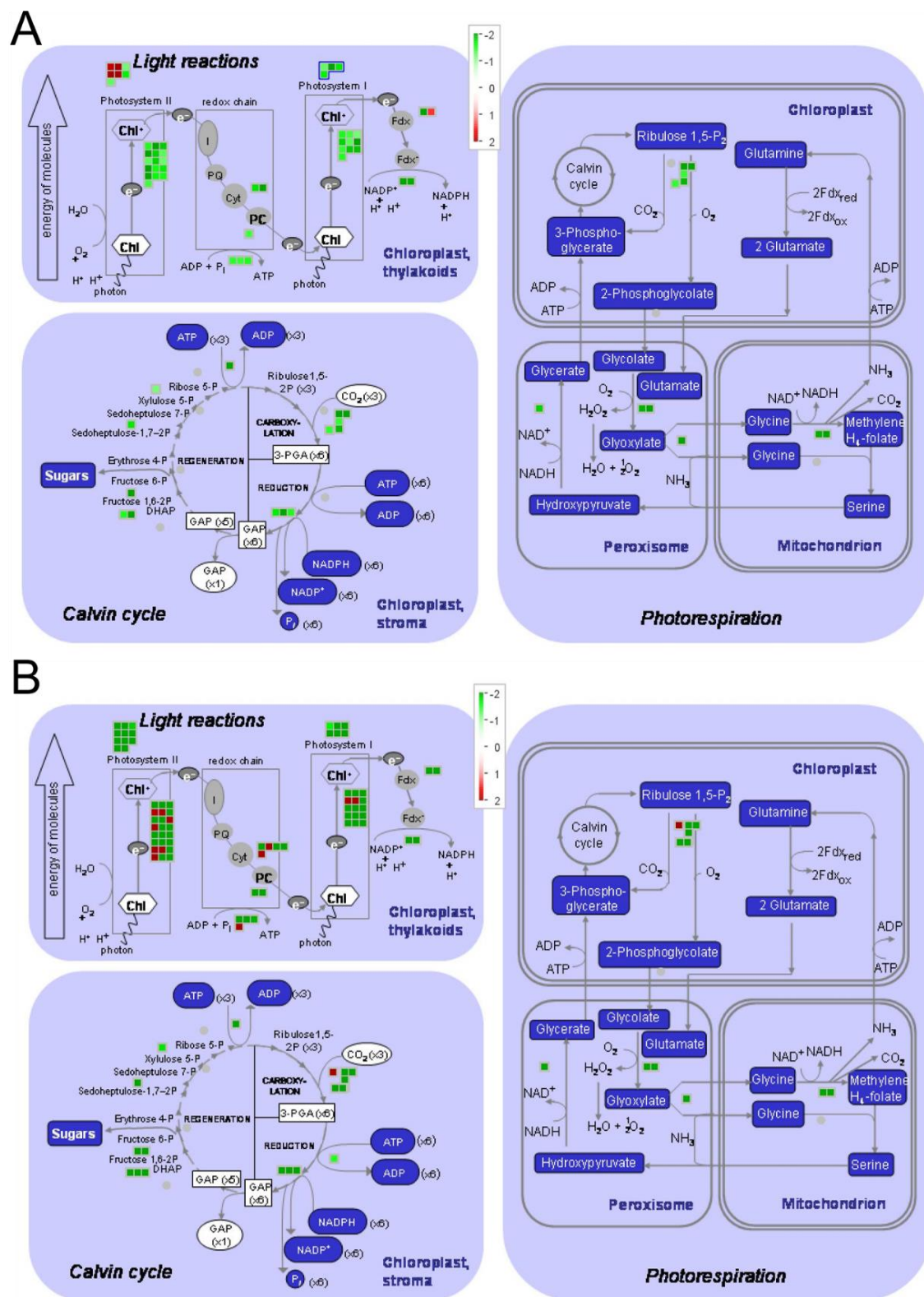


Fig. 4 Suppl. The MapMan (<http://mapman.gabipd.org>) analysis illustrates photosynthesis-associated differentially expressed genes (DEGs) in *Arabidopsis thaliana* roots. Five-day-old seedlings were subjected to 2.6 kJ m^{-2} of UV-B radiation for 3 min, and then the seedlings were transferred to normal growth conditions for 0.5 h (A) and 2 h (B). Log₂ fold change > 1, false discovery rate ≤ 0.01 . See Table 5 Suppl. for the detailed gene list of DEGs involved in photosynthesis and mitochondrial electron transport.

Table 1 Suppl. Cell cycle- and stem cell-associated gene expressions. Five-day-old *Arabidopsis thaliana* Col-0 seedlings were subjected to 2.6 kJ m⁻² of ultraviolet-B radiation for 3 min, and then the seedlings were transferred to normal growth conditions for 0.5 and 2 h. FC - fold change, FDR - false discovery rate.

Gene ID	0.5 h log ₂ FC	FDR	2 h log ₂ FC	FDR	annotation
AT1G70210	-	-	-1.8959585	5.21E-05	<i>CYCD1;1</i>
AT2G45080	-	-	-1.806905	0.000435	<i>CYCP3;1</i>
AT1G18670	-	-	-1.9409305	2.93E-05	<i>IBS1</i>
AT1G46480	-2.081473	0.001762	-3.1054488	1.81E-05	<i>WOX4</i>

Table 2 Suppl. Cell death- and senescence-associated gene expressions. Five-day-old *Arabidopsis thaliana* Col-0 seedlings were subjected to 2.6 kJ m⁻² of UV-B radiation for 3 min, and then the seedlings were transferred to normal growth conditions for 0.5 h and 2 h. FC - fold change.

Gene ID	0.5 h log ₂ FC	2 h log ₂ FC	annotation
AT1G42990	1.489499	2.281369	<i>bZIP60</i>
At3g60140	-	3.030978	<i>DIN2</i>
At1G77450	1.432402	-	<i>ANAC032</i>
At2g47190	-	2.684974	<i>MYB2</i>
At4g37990	-	2.633183	<i>ELI3-2</i>
At1g29860	-	3.404071	<i>WRKY71</i>
At3g21520	-	2.224826	<i>At3g21520</i>
At3g18250	1.614153	3.182206	<i>At3g18250</i>
At5g40690	-	2.927578	<i>At5g40690</i>
At1g74590	-	1.578883	<i>GSTU10</i>
At4g33040	1.607422	-	<i>GRXC10</i>
At1g62300	1.39906	1.492612	<i>WRKY6</i>
At4g03320	-	2.158381	<i>tic20-IV</i>
At2g15480	-	2.251661	<i>UGT73B5</i>
At5g02780	-	1.955724	<i>GSTL1</i>
At3g01970	-	1.973306	<i>WRKY45</i>
At1g68620	-	1.702593	<i>hydrolase</i>

Table 3 Suppl. Clustering differentially expressed genes (DEGs) and *gene ontology* categories in the three clusters. The *green* background represents downregulated genes, the *red* background represents upregulated genes by ultraviolet-B radiation. *Q*-value - adjusted *P*-value.

Cluster 1

id	gene number	Q-value	id	gene number	Q-value
GO:0015979 photosynthesis	66	1.64E-30	GO:0070887 cellular response to chemical stimulus	99	8.30E-06
GO:0050896 response to stimulus	386	5.55E-21	GO:0009664 plant-type cell wall organization	23	8.30E-06
GO:0006950 response to stress	246	1.85E-17	GO:0042743 hydrogen peroxide metabolic process	19	8.45E-06
GO:0019684 photosynthesis, light reaction	34	3.02E-15	GO:0051187 cofactor catabolic process	20	8.45E-06
GO:0042221 response to chemical	210	3.21E-13	GO:0018298 protein-chromophore linkage	12	8.52E-06
GO:0055114 oxidation-reduction process	138	4.22E-12	GO:0042744 hydrogen peroxide catabolic process	17	8.81E-06
GO:0009628 response to abiotic stimulus	154	4.87E-12	GO:0009765 photosynthesis, light harvesting	11	8.81E-06
GO:0010033 response to organic substance	154	2.30E-11	GO:0097237 cellular response to toxic substance	25	1.80E-05
GO:0009409 response to cold	52	8.03E-11	GO:0006091 generation of precursor metabolites and energy	45	1.93E-05
GO:0019253 reductive pentose-phosphate cycle	12	1.85E-10	GO:1990748 cellular detoxification	24	2.03E-05
GO:0019685 photosynthesis, dark reaction	12	1.85E-10	GO:0098542 defense response to other organism	72	3.20E-05
GO:0009767 photosynthetic electron transport chain	18	3.96E-10	GO:0016051 carbohydrate biosynthetic process	35	4.68E-05
GO:0009719 response to endogenous stimulus	132	1.58E-09	GO:0043094 cellular metabolic compound salvage	16	6.27E-05
GO:0009725 response to hormone	130	1.72E-09	GO:0009768 photosynthesis, light harvesting in photosystem I	8	6.38E-05
GO:0009605 response to external stimulus	122	1.91E-09	GO:0009773 photosynthetic electron transport in photosystem I	7	7.75E-05
GO:1901700 response to oxygen-containing compound	125	3.63E-09	GO:0098869 cellular oxidant detoxification	22	7.88E-05
GO:0015977 carbon fixation	12	4.14E-09	GO:0006006 glucose metabolic process	11	8.62E-05
GO:0009607 response to biotic stimulus	97	1.60E-08	GO:2000022 regulation of jasmonic acid mediated signaling pathway	10	8.64E-05
GO:0006952 defense response	109	1.69E-08	GO:0072593 reactive oxygen species metabolic process	22	0.000139499
GO:0043207 response to external biotic stimulus	96	1.74E-08	GO:0098754 detoxification	26	0.000139499
GO:0051707 response to other organism	96	1.74E-08	GO:0009416 response to light stimulus	55	0.000171295
GO:0009611 response to wounding	30	2.57E-08	GO:0017144 drug metabolic process	59	0.000175774
GO:0071555 cell wall organization	57	2.62E-08	GO:0019748 secondary metabolic process	35	0.000245853
GO:0001101 response to acid chemical	96	1.93E-07	GO:0006811 ion transport	67	0.000245857
GO:0045229 external encapsulating structure organization	57	2.28E-07	GO:0016999 antibiotic metabolic process	25	0.000314652
GO:0005975 carbohydrate metabolic process	88	2.99E-07	GO:0051186 cofactor metabolic process	48	0.000343292

id	gene number	Q-value	id	gene number	Q-value
GO:0009735 response to cytokinin	32	3.92E-07	GO:0009314 response to radiation	55	0.000343292
GO:0009853 photorespiration	15	5.63E-07	GO:0051704 multi-organism process	107	0.000431087
GO:0017001 antibiotic catabolic process	20	8.31E-07	GO:0034220 ion transmembrane transport	50	0.000521851
GO:0071554 cell wall organization or biogenesis	63	8.78E-07	GO:0071229 cellular response to acid chemical	45	0.000544085
GO:0009266 response to temperature stimulus	55	1.15E-06	GO:0010207 photosystem II assembly	7	0.000598559
GO:0042737 drug catabolic process	31	2.10E-06	GO:0071669 plant-type cell wall organization or biogenesis	28	0.000751003
GO:0055085 transmembrane transport	90	8.30E-06	GO:0033993 response to lipid	58	0.000885508

Cluster 2

GO:0015979 photosynthesis	31	7.66E-08	GO:0042493 response to drug	41	0.000159043
GO:0050896 response to stimulus	248	1.15E-06	GO:0009725 response to hormone	86	0.000200455
GO:0042221 response to chemical	143	1.23E-06	GO:0034220 ion transmembrane transport	42	0.000234629
GO:0006820 anion transport	34	1.86E-06	GO:0009719 response to endogenous stimulus	86	0.000361996
GO:0006811 ion transport	60	4.92E-06	GO:0015698 inorganic anion transport	16	0.000361996
GO:0019684 photosynthesis, light reaction	19	4.92E-06	GO:0015849 organic acid transport	16	0.000461537
GO:0009768 photosynthesis, light harvesting in photosystem I	8	3.24E-05	GO:0046942 carboxylic acid transport	16	0.000461537
GO:0055085 transmembrane transport	70	4.56E-05	GO:0016144 S-glycoside biosynthetic process	10	0.000490078
GO:0010033 response to organic substance	100	8.67E-05	GO:0019758 glucosinolate biosynthetic process	10	0.000490078
GO:0009628 response to abiotic stimulus	98	0.000104049	GO:0019761 glucosinolate biosynthetic process	10	0.000490078
GO:0098656 anion transmembrane transport	21	0.000106611	GO:1901700 response to oxygen-containing compound	81	0.000528029
GO:0009765 photosynthesis, light harvesting	9	0.000153387	GO:0098661 inorganic anion transmembrane transport	10	0.000942265

Cluster 3

GO:0019748 secondary metabolic process	34	6.83E-07	GO:0036293 response to decreased oxygen levels	11	0.000261687
GO:0050896 response to stimulus	223	1.23E-05	GO:0070482 response to oxygen levels	11	0.000267615
GO:0009636 response to toxic substance	28	8.37E-05	GO:0055114 oxidation-reduction process	79	0.000267615
GO:0044550 secondary metabolite biosynthetic process	18	0.000142073	GO:0009407 toxin catabolic process	9	0.000420506
GO:0042221 response to chemical	122	0.000251654	GO:0001666 response to hypoxia	10	0.000596616
GO:0006950 response to stress	135	0.000261687	GO:0071456 cellular response to hypoxia	7	0.000865942

Table 4 Suppl. Differentially expressed genes involved in the biosynthesis and metabolism of cell wall, lipids, glucosinolates, and terpenoids. *Arabidopsis thaliana* Col-0 seedlings were subjected to 2.6 kJ m⁻² of ultraviolet-B radiation for 3 min, and then the seedlings were transferred to normal growth conditions for 0.5 h and 2 h. FC - fold change, HRGP - hydroxyproline-rich glycoprotein, AGPs - arabinogalactan proteins, LRR - leucine-rich repeat, PME - pectin methyl esterases, TAG - triacylglycerols, FA - fatty acid.

		id	0.5 h/0 h log ₂ FC	2 h/0 h log ₂ FC
Cell wall	cell wall proteins, HRGP	at3g54590	-2.3204281	-2.7493317
		at4g08410	-3.1582146	-3.4471586
		at4g08400	-2.059378	-2.5656147
		at1g26240	-3.822138	2.8586931
		at2g43150	-2.8506532	-2.9554813
		at1g21310	-1.9902403	-2.3128648
		at1g76930	-2.2266283	-2.361234
	cell wall proteins, AGPs	at1g35230	1.4185833	-
		at4g16980	-	-2.1962712
		at2g20520	-	-1.9190106
		at5g53250	-	-1.3671583
		at3g11700	-	-1.4176238
		at4g37450	-1.3188659	-2.2954361
		at5g44130	-2.8731081	-2.3968544
	cell wall proteins, LRR	at4g40090	-1.3240207	-1.5785434
		at1g26250	-4.80842	-3.0231287
		at2g46630	-	-1.7645087
		at4g13340	-2.7774153	-3.612536
		at2g15880	-3.9316342	-2.5841475
		at3g22800	-2.5324168	-2.0772662
		at1g12040	-2.4457607	-2.5822916
	cell wall proteins, proline rich proteins	at2g21140	-2.264178	-4.4583497
		at4g38770	-3.7272084	-5.3191147
		at3g62680	-1.3948995	-2.5424037
		at1g54970	-2.5046413	-3.503002
	pectin esterases, PME	at1g53830	-1.4550455	-
		at3g49220	-	-1.7523342
		at5g04960	-	-2.7805586
		at5g19730	-	-1.9124206
		at1g02810	-1.4372346	-3.296232
		at3g10710	-1.2581284	-2.1265929
		at2g43050	-2.137511	-1.5751618
	pectin esterases, acetyl esterase	at3g09405	2.4055593	5.3430276
		at5g23870	-	-1.9145523
		at4g19420	-2.2111564	-2.9848702
	pectin esterases, misc	at2g45220	-2.1128685	-2.1894445
		at4g02330	-	-1.4826165
		at4g33220	-2.0044744	-2.3925028
	cell wall modification	at5g57540	-1.7076644	-3.2124486
		at2g36870	-	-2.6003363
		at2g18660	-	4.150959
		at4g28250	-	-2.4216468
		at1g14720	-	-1.6884775
		at4g25810	-	-2.4143205
		at1g62980	-	-1.3904278
		at5g57560	-	-2.6772473
		at3g44990	-	-2.5646167
		at4g03210	-	-2.1978927
		at3g45960	-	-2.4515166
		at5g57530	-	-2.7562933
		at4g18990	-	3.416187
		at4g37800	-3.553003	-5.6986084
		at2g37640	-1.7256963	-2.6526709
		at1g10550	-2.1714447	-2.290024

	id	0.5 h/0 h log2 FC	2 h/0 h log2 FC
	at3g29030	-2.8996863	-3.385122
	at3g45970	-1.3942853	-3.6135986
	at1g32170	-1.8517832	-
	at4g38400	-1.5705711	-2.2215183
	at4g01630	-1.9832588	-
	at4g14130	-1.5535307	-
	at4g28850	-2.8259723	-3.728546
	at1g65310	-1.2507527	-1.3679723
cell wall hemicellulose synthesis	at2g15370	-1.3539146	-1.6448382
	at2g28110	-1.5074604	-
cell wall.cellulose synthesis	at4g07960	-1.8000576	-2.9852986
	at3g28180	-	-1.4505665
	at5g22740	-	-2.0075326
	at1g23480	-1.39527	-
	at5g09870	-1.1990116	-1.9679866
	at5g16910	-1.5064669	-1.9880654
	at4g15290	-4.612082	-3.9547858
	at1g02730	-	-1.3587577
	at3g29810	-	-1.3976165
	at2g32620	-1.754619	-
	at4g39350	-1.2641138	-2.071338
	at2g32610	-1.8289467	-
cell wall.pectin synthesis	at1g56550	-1.3583914	-
	at5g33290	-1.3155562	-
cell wall.precursor synthesis	at1g12780	-1.3071299	-
	at1g63180	-2.5463276	-
	at4g30440	-	-2.0390162
	at4g20460	-1.3320618	-
cell wall.degradation, mannan-xylose-arabinose-fucose	at2g32990	-	-2.632557
	at5g49360	-1.591757	-1.5257767
	at3g10740	-1.6118058	-
	at1g67830	-	-2.0221696
	at1g78060	-	-1.6067927
	at4g30270	-	-1.5397258
	at2g28100	-1.5220562	-
	at1g02640	-1.7867166	-1.6121831
	at5g64570	-1.1820127	-
	at3g52840	-2.7447705	-2.7125876
cell wall.degradation, pectate lyases, and polygalacturonases	at5g14650	-2.321785	-3.7982285
	at4g22080	-	-1.8941739
	at1g17150	-	3.7123752
	at1g02460	-	1.9160066
	at1g70500	-	1.6602348
	at3g07970	-	1.4638039
	at1g70370	-	-2.5702302
	at5g63180	-3.5743377	-3.4865878
	at1g65570	-2.68724	-1.5349661
	at2g41850	-2.6685848	-
	at5g06870	-3.141299	-3.8453472
	at3g27400	-2.2071176	-2.4944978
Lipid metabolism	phospholipid synthesis	at5g06090	1.4701706
		at1g73600	-3.2284663
		at3g11430	2.2393343
		at2g38110	1.4005938
		at1g02390	-1.6617974
		at1g06520	-2.648386
		at4g01950	-1.6259023
		at4g15130	2.1111093
		at5g57190	2.5955298
		at2g18730	-1.1511959

	id	0.5 h/0 h log2 FC	2 h/0 h log2 FC
glycolipid synthesis, sulfolipid synthase exotics (steroids, squalene etc)	at3g23510	-1.615391	-1.5526195
	at4g25970	-1.1589534	-
	at5g01220	-1.164011	-1.506484
	at3g06460	-1.6176536	-
	at1g27480	-2.223567	-4.9694276
	at1g13430	-	1.6814398
	at3g45070	-	-2.7161784
	at1g13420	-	-1.3889475
	at2g03770	-	5.5367665
	at3g58490	-	1.4743773
	at3g44830	-	3.416187
	at5g56100	-3.695994	-2.9248104
	at1g06360	-2.831261	-4.485988
	at1g06350	-	-3.846037
	at1g06120	-1.5835662	-
	at4g14070	-2.872902	-3.4565985
	at5g16370	-1.4355943	-
	at1g77590	-	1.4605918
	at1g04220	-	1.6572304
	at4g34510	-	3.1933897
TAG synthesis FA desaturation, desaturase	at5g16230	-	-1.6340839
	at2g47240	-1.298137	-
	at1g07720	-2.8440738	-3.6493104
	at5g04530	-3.5183866	-5.5050926
	at2g28630	-3.4173222	-3.6561136
	at4g34250	-3.4489253	-2.532059
	at2g15090	-2.9189088	-4.0624394
	at4g24510	-2.931688	-3.1408324
	at4g25050	-1.7135395	-3.1697521
	at4g24230	-1.4020026	-
lipid degradation, lipases, triacylglycerol lipase	at4g10955	5.7506094	5.090182
	at2g30550	-	1.7512985
	at1g45201	-2.3834095	-2.8336287
	at4g16820	3.4245603	5.425762
	at1g02660	-1.6416214	-2.4298406
	at1g30370	1.8385651	1.6102424
lipid degradation, lysophospholipases	at4g38690	-2.0556164	-
	at1g47480	-1.3819231	-
	at1g66970	-3.182494	-3.6827712
	at4g26690	-1.9668796	-2.528711
	at1g66980	-3.1151183	-3.4228091
	at1g68620	-	1.702593
Lipid degradation	at5g41080	-	-1.5845605
	at3g03520	-1.4870119	-2.2853136
	at3g03530	1.4711449	-
	at1g35250	-1.2956789	-1.8195516
	at4g14440	-	1.7920003
	at2g03550	-	-3.2020674
	at3g44540	-	2.078074
Glucosinolates.synthesis	at4g33790	-3.5212946	-3.0695403
	at5g22500	-1.6197114	-1.4183154
	at3g19710	-2.0267432	-4.5739756
	at5g23020	-1.5605596	-4.0757675
	at5g23010	-2.7520516	-4.2454815
	at3g58990	-1.203438	-3.45139
	at1g16410	-2.320543	-3.9344063
	at2g22330	-1.4042937	-

	id	0.5 h/0 h log2 FC	2 h/0 h log2 FC
		0.5 h/0 h log ₂ FC	2 h/0 h log ₂ FC
Secondary metabolism, isoprenoids, terpenoids	at5g57220	3.216872	4.496544
	at5g60890	-1.4754952	-
	at1g18570	1.5339658	1.5127577
	id	0.5 h/0 h log ₂ FC	2 h/0 h log ₂ FC
	at1g54010	-1.7743998	-2.0531497
	at1g47600	-1.8355955	-
	at5g26000	-3.0453742	-7.863354
	at5g25980	-3.0507236	-6.5849805
	at5g22300	2.484657	3.8303678
	at2g43100	-	-3.436901
	at1g16400	-	-4.3360415
	at4g13770	-	-4.940894
	at2g31790	-	-3.0459068
	at1g74090	-	-1.9559413
	at1g65860	-	-4.674168
	at1g62560	-	-2.0345945
	at1g74100	-	1.6953199
	at5g61420	-	-2.696464
	at3g14210	-	-4.8769608
	at4g12030	-	-3.6994874
	at1g78970	-2.2437341	-2.3089921
	at5g48010	-2.9566853	-3.535414
	at5g42600	-1.6244817	-2.0729625
	at4g15340	-	-1.3595387
	at4g20230	-	-2.6416292
	at1g78950	-	-1.6759322

Table 5 Suppl. Differentially expressed genes involved in photosynthesis and mitochondrial electron transport. *Arabidopsis thaliana* Col-0 seedlings were subjected to 2.6 kJ m⁻² of ultraviolet-B radiation for 3 min, and then the seedlings were transferred to normal growth conditions for 0.5 h and 2 h. FC - fold change, LHC - light-harvesting complex, PS - photosystem, ATP - adenosine triphosphate, NADH - nicotinamide adenine dinucleotide, GAP - glyceraldehyde-3-phosphate, FBPase – fructose-1,6-bisphosphatase, RPE - ribulose-5-phosphate epimerase, PRK - phosphoribulokinase.

		id	0.5 h/0 h log ₂ FC	2 h/0 h log ₂ FC
Photosynthesis	light reactions, photosystem II, LHC II	at3g27690	1.8763764	-
		at2g05100	3.1977382	-
		at4g10340	-1.2000487	-4.4158325
		at1g29920	2.8608253	-2.7820992
		at2g05070	2.3141744	-2.7534819
		at3g08940	-	-2.4359987
		at5g54270	-	-2.0146093
		at2g34420	-	-1.8296537
		at2g34430	-	-3.9485705
		at1g29910	-	-5.491672
		at1g15820	-	-2.6557035
		at1g29930	-1.6619109	-4.7989273
		at5g01530	-1.2620002	-3.3192167
	light reactions, photosystem II, PS II polypeptide subunits	at3g50820	-1.5077208	-2.8601515
		at2g39470	-2.204047	-4.101241
		at4g21280	-1.8371494	-5.424377
		atcg00680	-2.320543	1.9361768
		atcg00270	-	4.0048814
		atcg00580	-	2.3824353
		atcg00700	-	2.9256563
		atcg00280	-1.8045826	2.8397286
		at4g05180	-1.2975839	-4.126419
		at1g06680	-1.2982153	-3.4261785
		at1g51400	-	-2.33287
		atcg00020	-	6.844727
		atcg00550	-	5.1185718
		at3g21055	-1.7930832	-5.5251613
		at2g06520	-1.2223674	-2.954734
	light reactions, photosystem I, LHC I	at1g14150	-2.2712007	-4.0489645
		at2g30570	-1.5553817	-3.7367327
		at1g67740	-	-3.0884988
		at3g01440	-	-4.235773
		at1g44575	-	-3.464988
		at1g03600	-1.6899108	-3.8356276
		at3g55330	-1.9887574	-3.5442665
		at5g51545	-1.589208	-
		at5g66570	-1.5486174	-3.9043756
		at1g79040	-1.3990164	-3.1607811
		at1g61520	-1.2643255	-3.5744169
		at3g47470	-	-1.6475455
		at3g54890	-	-3.966105
		at1g19150	-2.0328617	-5.4534335
		at3g61470	-1.692147	-5.0953507
	light reactions, photosystem I, PS I polypeptide subunits	at1g45474	-1.6615142	-3.404439
		at1g31330	-1.531521	-3.3583066
		at5g64040	-1.3986472	-3.8849478
		at4g28750	-	-3.8371253
		atcg00340	-	3.9156067
		atcg00350	-	3.975031
		at1g30380	-	-3.070793
		at1g52230	-	-4.219814
		at2g46820	-1.1920578	-3.233876
		at2g20260	-1.7933549	-4.064017
		at1g03130	-1.2975179	-5.330215

	id	0.5 h/0 h log2 FC	2 h/0 h log2 FC
light reactions, cytochrome b6/f	at1g55670	-2.1725857	-5.2608857
	at1g08380	-1.4359654	-4.346929
	at3g16140	-1.8351303	-4.7271743
	at4g02770	-1.8720931	-3.6094217
	at4g12800	-1.4984682	-4.9025683
	at4g03280	-1.727897	-4.161792
	atcg00600	-	4.7340627
	at5g36120	-	-3.7536495
	atcg00720	-	2.5520976
	at2g26500	-2.0028405	-4.5218797
light reactions, ATP synthase	at4g32260	-1.4590739	-2.288466
	atcg00130	-	2.255831
	at4g09650	-	-1.9475765
	atcg00480	-1.4125648	-
light reactions, other electron carriers	at4g04640	-1.5034834	-3.4515657
	at1g20340	-1.3753052	-3.0488403
	at3g16250	-2.846135	-4.4583497
	at1g10960	1.4341776	-
light reactions, NADH	at1g20020	-3.2768877	-5.385827
	at1g76100	-	-2.9385843
	at1g60950	-	-1.9903321
	at5g66190	-1.9686861	-3.6369524
	atcg00420	-2.212397	-3.564786
	at1g74880	-1.950276	-3.6619084
	at1g70760	-2.123813	-4.0996943
	at5g58260	-2.7753048	-5.3148165
	at4g37925	-	-4.0540257
	atcg00430	-2.303677	-2.0519679
light reactions, state transition	at4g02630	-1.9190158	-2.960414
	at4g01330	-1.2262666	-
light reactions, cyclic electron flow, chlororespiration	at3g15840	-2.565512	-3.7694151
Calvin cycle, Rubisco large subunit	atcg00490	-	4.379878
Calvin cycle	at3g62410	-3.707302	-4.0210743
Calvin cycle, Rubisco small subunit	at2g47400	-1.8020762	-2.969566
	at5g38420	-3.098216	-7.8313236
	at5g38410	-1.4373697	-6.7950773
	at1g67090	-1.9104104	-5.477185
Calvin cycle, GAP	at5g38430	-2.7029116	-6.9786515
	at1g42970	-1.6804978	-4.9528155
	at3g26650	-2.184404	-5.3650236
	at1g12900	-1.5130042	-5.37792
Calvin cycle, aldolase	at4g38970	-1.5020701	-5.46999
	at2g21330	-	-6.5689263
Calvin cycle, FBPase	at4g26530	-3.4605267	-7.718547
	at3g54050	-2.2203217	-5.902322
	at5g64380	-	-2.3457503
Calvin cycle, seduheptulose biphosphatase	at3g55800	-1.6999073	-4.7058425
Calvin cycle, RPE	at5g61410	-1.1649035	-1.7295403
Calvin cycle, PRK	at1g32060	-2.4385726	-5.679783
Calvin cycle, Rubisco interacting	at2g39730	-1.4400653	-4.637211
	at1g73110	-	-2.0600207
Calvin cycle, phosphoglycerate kinase	at3g12780	-	-1.4799821
tetrapyrrole synthesis, glu-tRNA reductase	at1g58290	-1.3757048	-1.663282
tetrapyrrole synthesis, magnesium	at5g45930	-1.776968	-2.9391172
chelatase	at4g18480	-	-1.9173021
tetrapyrrole synthesis, magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase	at1g08520	-1.4995074	-1.973168
	at3g56940	-	-3.1705444

	id	0.5 h/0 h log2 FC	2 h/0 h log2 FC
Mitochondrial electron transport	tetrapyrrole synthesis, magnesium protoporphyrin IX methyltransferase	at4g25080	-1.425735
	tetrapyrrole synthesis, protochlorophyllide reductase	at1g03630	-1.7130002
	tetrapyrrole synthesis, divinyl chlorophyllide-a 8-vinyl-reductase	at4g27440	-2.4189405
	tetrapyrrole synthesis, chlorophyll synthase	at5g18660	-
	tetrapyrrole synthesis, regulation photorespiration, glycolate oxydase	at3g51820	-
	photorespiration, aminotransferases peroxisomal	at3g59400	-
	photorespiration, glycine cleavage.H protein	at3g14415	-1.9332889
	photorespiration, hydroxypyruvate reductase	at3g14420	-2.0025163
	photorespiration, glycerate kinase	at2g13360	-3.0523167
	ATP synthesis, NADH-DH.type II, internal matrix	at2g35370	-1.9560177
	ATP synthesis, NADH-DH.type II, external	at1g32470	-2.0091004
		at1g68010	-1.8129948
		at1g80380	-1.5695202
		at1g07180	4.0419564
		at2g29990	-
		at2g20800	5.190813
		at4g05020	-
		at4g21490	3.2333
	ATP synthesis, alternative oxidase	at3g22370	2.3352885
		at3g22360	-
		at1g32350	-
	ATP synthesis, cytochrome c	at4g10040	1.4030855
		atmg00110	-
	ATP synthesis, cytochrome c oxidase	at4g39740	1.7083158
		at2g07687	-
		atmg00160	-
		atmg01360	-
	ATP synthesis, cytochrome c reductase	at2g07727	-
	ATP synthesis, NADH-DH, complex I	atmg00650	-
	ATP synthesis, NADH-DH, localization not clear	atmg01320	-
		atmg01120	-
		atmg00070	-
		atmg00510	-
		atmg00580	-
		atmg00513	-
		atmg00270	-
		atmg00060	-
		atmg00285	-
	ATP synthesis, uncoupling protein	at4g24570	-
	ATP synthesis, F1-ATPase	at5g12420	-
		atmg00640	-