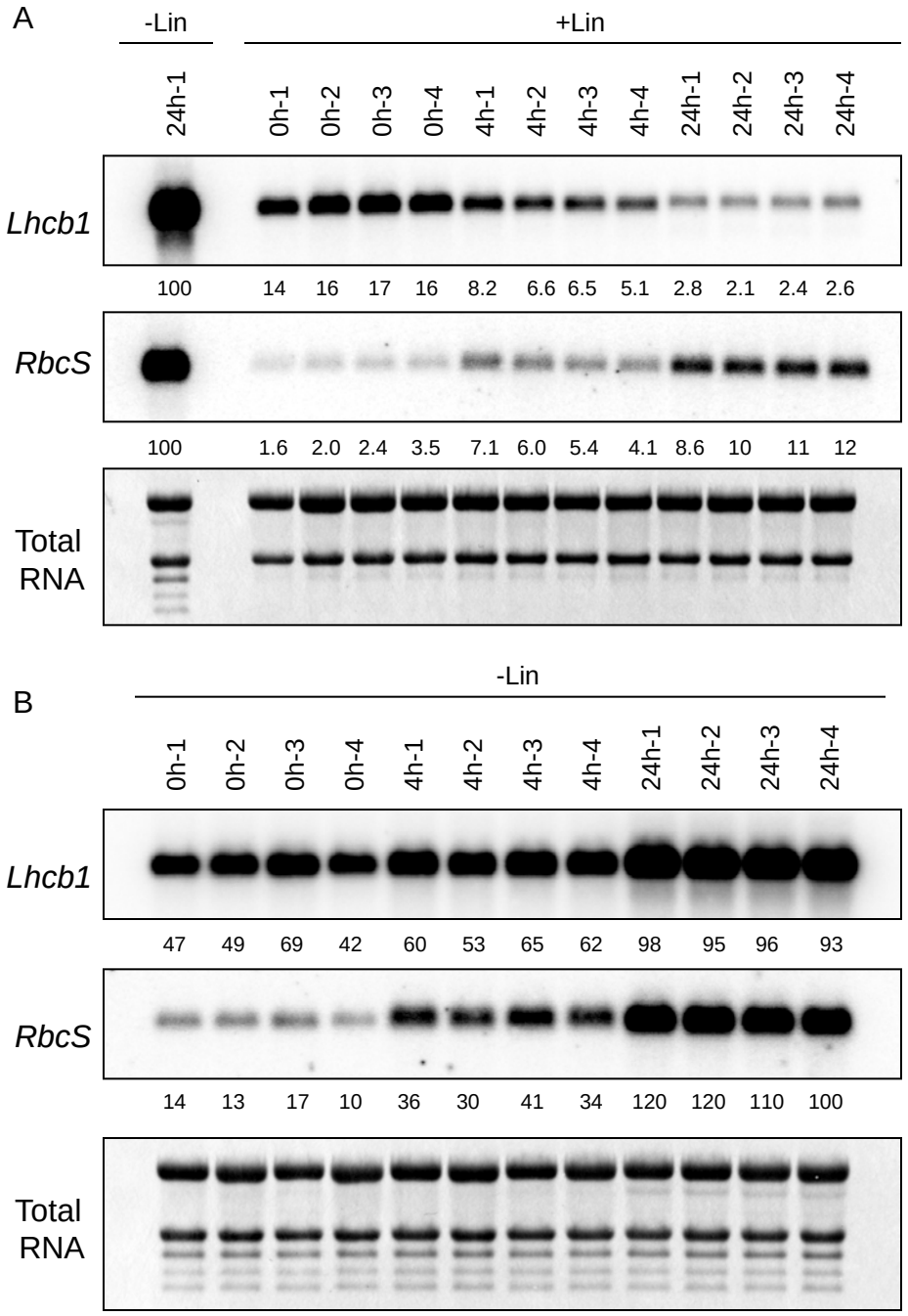
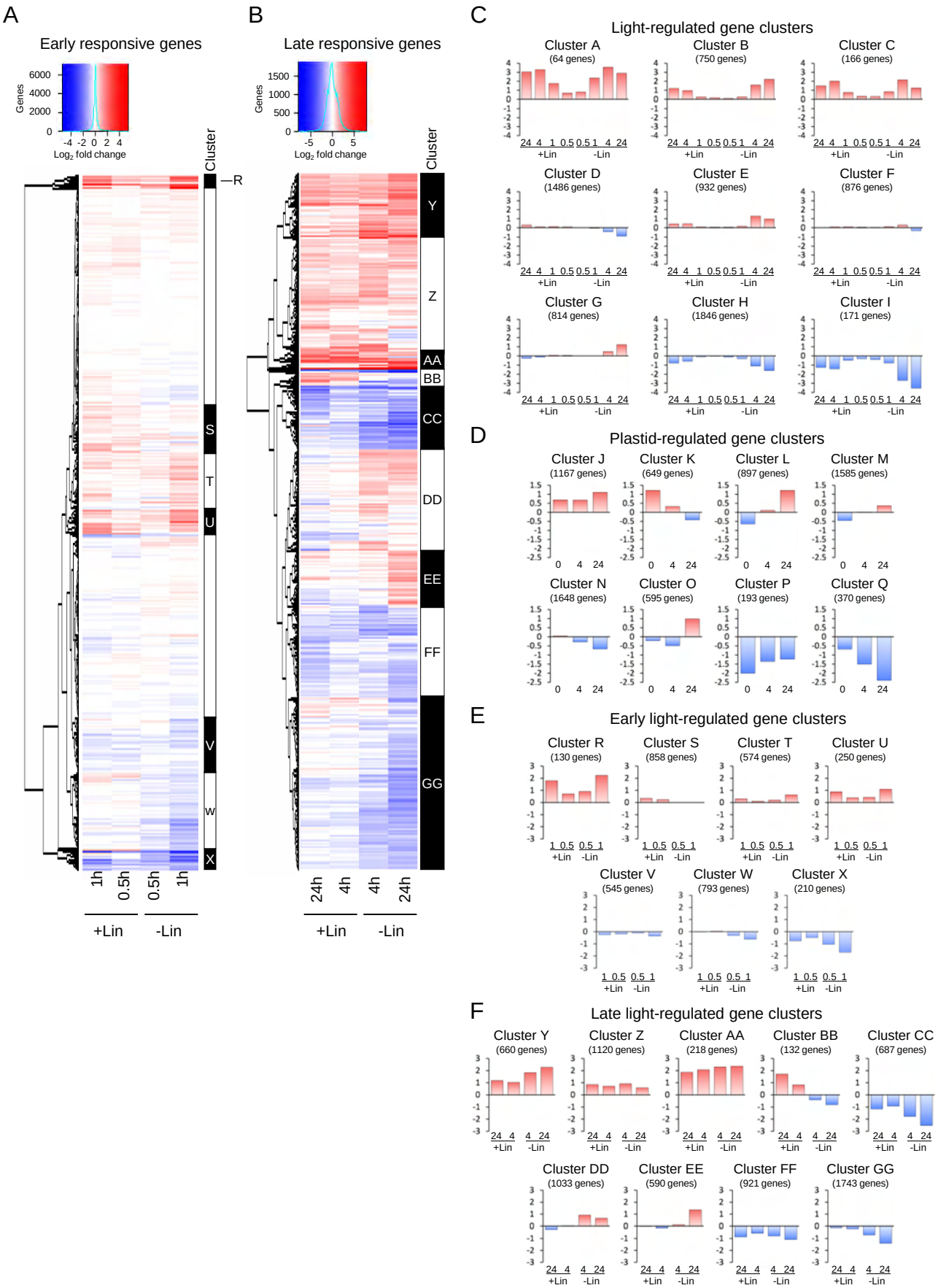


Supplemental Figure S1. Expression of *Lhcb1* and *RbcS* following a fluence-rate shift.
A, Expression of *Lhcb1* and *RbcS* in lincomycin-treated seedlings after a fluence-rate shift. Seedlings were grown in the presence of lincomycin (+Lin) or in the absence of lincomycin (-Lin) as described in Fig. 1. RNA was extracted and both Lhcb1 and RbcS mRNA levels were quantified with RNA blot hybridizations that utilized 2.5 µg of total RNA. Four biological replicates from each time point were quantified and normalized to total RNA stained with methylene blue. Numbers below each lane indicate the amount of hybridized RNA as a percentage of hybridized RNA in untreated seedlings after 24 h in 60 µmol m^{-2} s^{-1} BR light.
B, Expression of *Lhcb1* and *RbcS* in seedlings not treated with lincomycin following a fluence-rate shift. Seedlings were grown in the absence of lincomycin (-Lin) and the levels of Lhcb1 mRNA were quantified as in A.

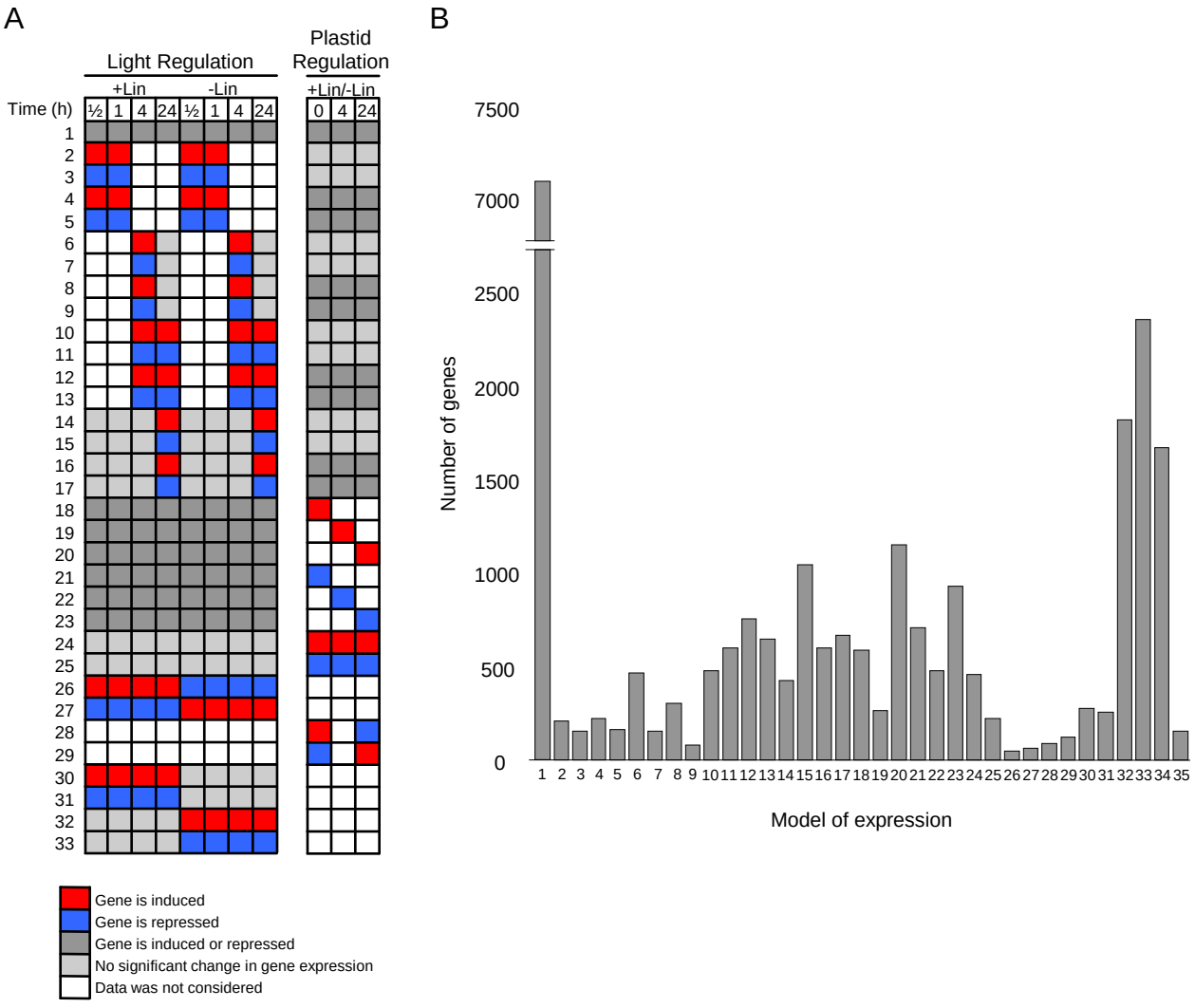

A
Early responsive genes
Genes
Log2 fold change
Cluster
R
S
T
U
V
W
X
1h
0.5h
0.5h
1h
+Lin
-Lin
B
Late responsive genes
Genes
Log2 fold change
Cluster
Y
Z
AA
BB
CC
DD
EE
FF
GG
24h
4h
4h
24h
+Lin
-Lin
C
Light-regulated gene clusters
Cluster A
(64 genes)
Cluster B
(750 genes)
Cluster C
(166 genes)
Cluster D
(1486 genes)
Cluster E
(932 genes)
Cluster F
(876 genes)
Cluster G
(814 genes)
Cluster H
(1846 genes)
Cluster I
(171 genes)
24 4 1 0.5 0.5 1 4 24
+Lin -Lin
D
Plastid-regulated gene clusters
Cluster J
(1167 genes)
Cluster K
(649 genes)
Cluster L
(897 genes)
Cluster M
(1585 genes)
Cluster N
(1648 genes)
Cluster O
(595 genes)
Cluster P
(193 genes)
Cluster Q
(370 genes)
0 4 24
E
Early light-regulated gene clusters
Cluster R
(130 genes)
Cluster S
(858 genes)
Cluster T
(574 genes)
Cluster U
(250 genes)
Cluster V
(545 genes)
Cluster W
(793 genes)
Cluster X
(210 genes)
1 0.5 0.5 1
+Lin -Lin
F
Late light-regulated gene clusters
Cluster Y
(660 genes)
Cluster Z
(1120 genes)
Cluster AA
(218 genes)
Cluster BB
(132 genes)
Cluster CC
(687 genes)
Cluster DD
(1033 genes)
Cluster EE
(590 genes)
Cluster FF
(921 genes)
Cluster GG
(1743 genes)
24 4 4 24
+Lin -Lin

Supplemental Figure S2. Agglomerative clustering of early time points (i.e., 0.5 h and 1 h) and late time points (i.e., 4 h and 24 h).

A, Agglomerative hierarchical clustering of the 7104 active gene sets based on their regulation by light at 0.5 h and 1 h in lincomycin-treated and untreated seedlings. Up-regulated expression is indicated with red and down-regulated expression is indicated with blue. Color intensity is proportional to the degree of regulation.

B, Agglomerative hierarchical clustering of the 7104 active gene sets based on their regulation by the light at 4 h and 24 h in lincomycin-treated and untreated seedlings. Data are colored as in A.

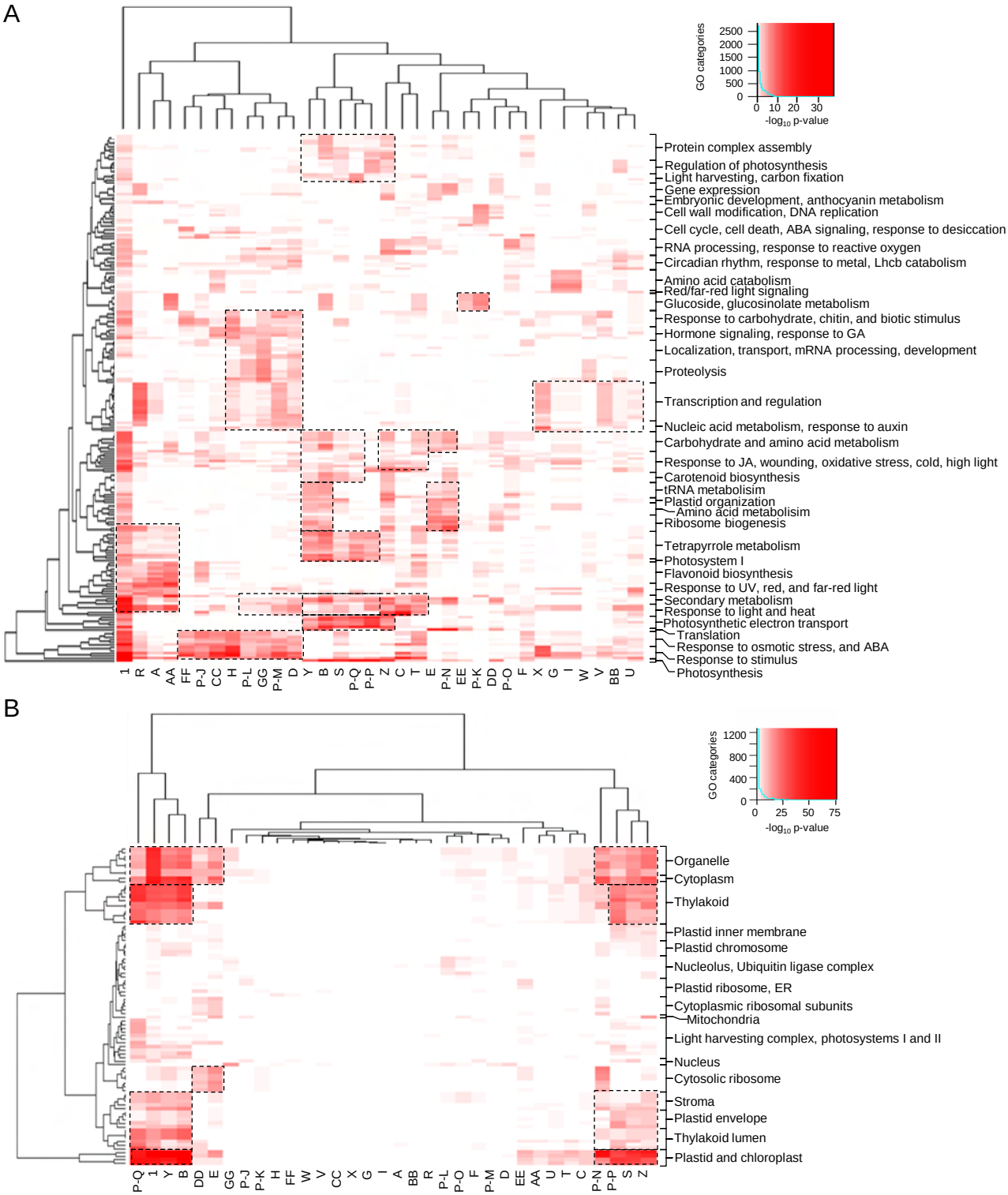
C-F, The average gene expression level (log_2) and number of genes represented by each of the clusters from Fig. 2E (C), Fig. 2F (D), Supplemental Fig. S2A (E), and Supplemental Fig. S2B (F).


A
Light Regulation
Plastid Regulation
+Lin
-Lin
+Lin/-Lin
Time (h)
½ 1 4 24 ½ 1 4 24
0 4 24
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33
Gene is induced
Gene is repressed
Gene is induced or repressed
No significant change in gene expression
Data was not considered
B
Number of genes
7500
7000
2500
2000
1500
1000
500
0
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35
Model of expression

Supplemental Figure S3. Distribution of user-defined expression patterns among light- and plastid-regulated genes.

A, Expression patterns of light- and plastid-regulated genes. We defined 33 models of expression that arise from the interactions between light and plastid signaling. Gene expression was described in four possible ways: induced (red); repressed (blue); induced or repressed (dark gray); no significant change (light gray); data were not considered (white). Genes were considered induced (red) or repressed (blue) if the change in expression was greater than twofold ($p \leq 0.01$). The expression patterns were: pattern 1, genes are induced or repressed; patterns 2-5, early-light-responsive genes (i.e., genes are regulated by light only at 0.5 h and 1 h); patterns 6-9, transiently responsive genes (i.e., genes that are regulated by light only at 4 h); patterns 10-13, light induction or repression at 4 h is maintained at 24 h in lincomycin-treated and/or untreated seedlings; patterns 14-17, late-responsive genes (i.e., genes that are regulated by light only at 24 h); patterns 18-25, plastid-responsive genes (i.e., genes that are regulated in lincomycin-treated seedlings at 0 h, 4 h, or at 24 h); patterns 26-27, genes that are oppositely regulated by light at the same time point in lincomycin-treated and untreated seedlings; patterns 28-29, genes that are oppositely regulated in lincomycin-treated and untreated seedlings 24 h after the BR-fluence-rate shift; patterns 30-31, genes that are either induced or repressed by light in lincomycin-treated but not in untreated seedlings; patterns 32-33 genes that are induced or repressed by light in untreated seedlings but not in lincomycin-treated seedlings.

B, Number of genes in each of the expression models described in A. The 33 expression patterns from A and two additional patterns, 34 and 35, are shown. Pattern 34 (positive correlation) describes genes that exhibit a similar response to the BR-fluence-rate shift regardless of whether seedlings are treated with lincomycin. For these genes, the correlation coefficient between the expression patterns in lincomycin-treated and untreated seedlings is greater than 0.95. Pattern 35 (negative correlation) describes genes that have an opposite response to the BR-fluence-rate shift in lincomycin-treated and untreated seedlings. For these genes, the correlation coefficient between the expression pattern in lincomycin-treated and untreated seedlings is less than -0.95.

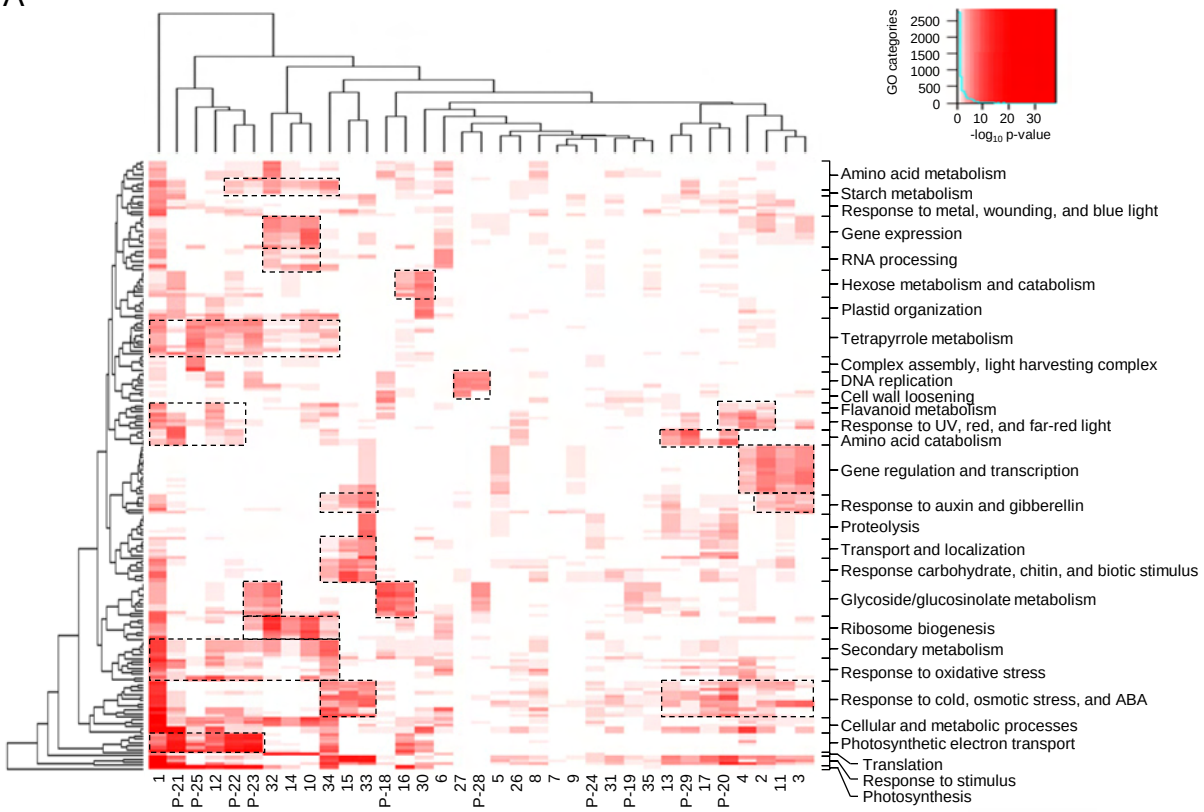

A
GO categories
2500
2000
1500
1000
500
0
0 10 20 30
-log10 p-value
Protein complex assembly
Regulation of photosynthesis
Light harvesting, carbon fixation
Gene expression
Embryonic development, anthocyanin metabolism
Cell wall modification, DNA replication
Cell cycle, cell death, ABA signaling, response to desiccation
RNA processing, response to reactive oxygen
Circadian rhythm, response to metal, Lhcb catabolism
Amino acid catabolism
Red/far-red light signaling
Glucoside, glucosinolate metabolism
Response to carbohydrate, chitin, and biotic stimulus
Hormone signaling, response to GA
Localization, transport, mRNA processing, development
Proteolysis
Transcription and regulation
Nucleic acid metabolism, response to auxin
Carbohydrate and amino acid metabolism
Response to JA, wounding, oxidative stress, cold, high light
Carotenoid biosynthesis
tRNA metabolism
Plastid organization
Amino acid metabolism
Ribosome biogenesis
Tetrapyrrole metabolism
Photosystem I
Flavonoid biosynthesis
Response to UV, red, and far-red light
Secondary metabolism
Response to light and heat
Photosynthetic electron transport
Translation
Response to osmotic stress, and ABA
Response to stimulus
Photosynthesis
1 R A AA FF P-J CC H P-L GG P-M D Y B S P-Q P-P Z C T E P-N EE P-K DD P-O F X G I W V BB U
B
GO categories
1200
800
400
0
0 25 50 75
-log10 p-value
Organelle
Cytoplasm
Thylakoid
Plastid inner membrane
Plastid chromosome
Nucleolus, Ubiquitin ligase complex
Plastid ribosome, ER
Cytoplasmic ribosomal subunits
Mitochondria
Light harvesting complex, photosystems I and II
Nucleus
Cytosolic ribosome
Stroma
Plastid envelope
Thylakoid lumen
Plastid and chloroplast
P-Q 1 Y B DD E GG P-J P-K H FF W V CC X G I A BB R P-L P-O F P-M D EE AA U T C P-N P-P S Z

Supplemental Figure S4. Agglomerative hierarchical clustering of significantly enriched GO terms with expression clusters.

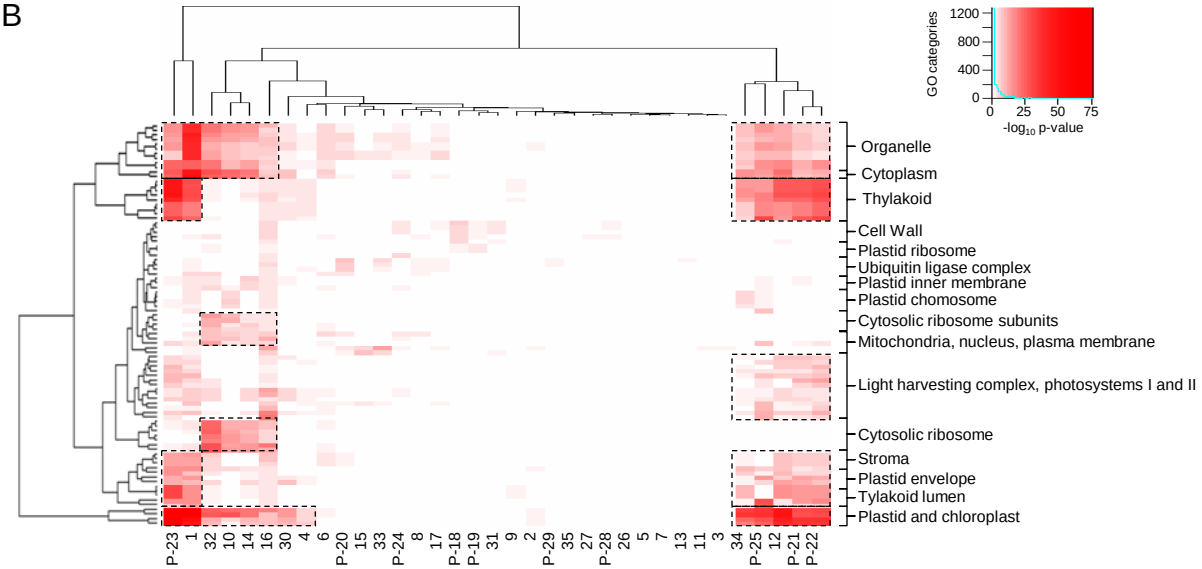
A, Agglomerative hierarchical clustering of GO terms defined as a biological process with expression clusters. We analyzed 205 GO terms and judged them to be enriched in at least one of the expression clusters if $p \leq 0.01$ after a Westfall-Young correction. GO terms were included if they were enriched in at least one expression pattern and $p \leq 0.01$. The negative $\log_{10}$ of the uncorrected p-value for each pattern was clustered. Clusters of GO terms are shown as a dendrogram at the left of the cluster matrix. Summary GO terms are shown at the right of the cluster matrix. These summary terms contain a representative group of genes from multiple GO categories. For example, tetrapyrrole metabolism is a summary term that contains a representative group of genes from the following GO categories: tetrapyrrole metabolic process, 0033013; porphyrin metabolic process, 0006778; chlorophyll metabolic process, 0015994; cofactor metabolic process, 0051186; tetrapyrrole biosynthetic process, 0033014; porphyrin biosynthetic process, 0006779; cofactor biosynthetic process, 0051188; chlorophyll biosynthetic process, 0015995. Expression clusters from Fig. 2 and Supplemental Fig. S2 are shown as a dendrogram at the top of the cluster matrix. Names of expression clusters from Fig. 2 and Supplemental Fig. S2 that correspond to each branch of the dendrogram are indicated at the bottom of the cluster matrix. The letter P next to the cluster letter indicates regulation by plastid dysfunction. No letter P next to the cluster letter indicates regulation by the BR-fluence-rate shift. The branch of the dendrogram labeled 1 contains all of the significantly regulated genes in the dataset. The intensity of the red color is proportional to the degree of enrichment. Co-regulated GO terms are indicated with dashed boxes.

B, Agglomerative hierarchical clustering of GO terms defined as cellular components with expression clusters. Eighty-eight GO terms defined as cellular components were enriched as described in A. The labeling of this heat map is as described for A.

A


GO categories
2500
2000
1500
1000
500
0
0 10 20 30
-log10 p-value
Amino acid metabolism
Starch metabolism
Response to metal, wounding, and blue light
Gene expression
RNA processing
Hexose metabolism and catabolism
Plastid organization
Tetrapyrrole metabolism
Complex assembly, light harvesting complex
DNA replication
Cell wall loosening
Flavanoid metabolism
Response to UV, red, and far-red light
Amino acid catabolism
Gene regulation and transcription
Response to auxin and gibberellin
Proteolysis
Transport and localization
Response carbohydrate, chitin, and biotic stimulus
Glycoside/glucosinolate metabolism
Ribosome biogenesis
Secondary metabolism
Response to oxidative stress
Response to cold, osmotic stress, and ABA
Cellular and metabolic processes
Photosynthetic electron transport
Translation
Response to stimulus
Photosynthesis
1 P-21 P-25 12 P-22 P-23 32 14 10 34 15 33 P-18 16 30 6 27 P-28 5 26 8 7 9 P-24 31 P-19 35 13 P-29 17 P-20 4 2 11 3

B

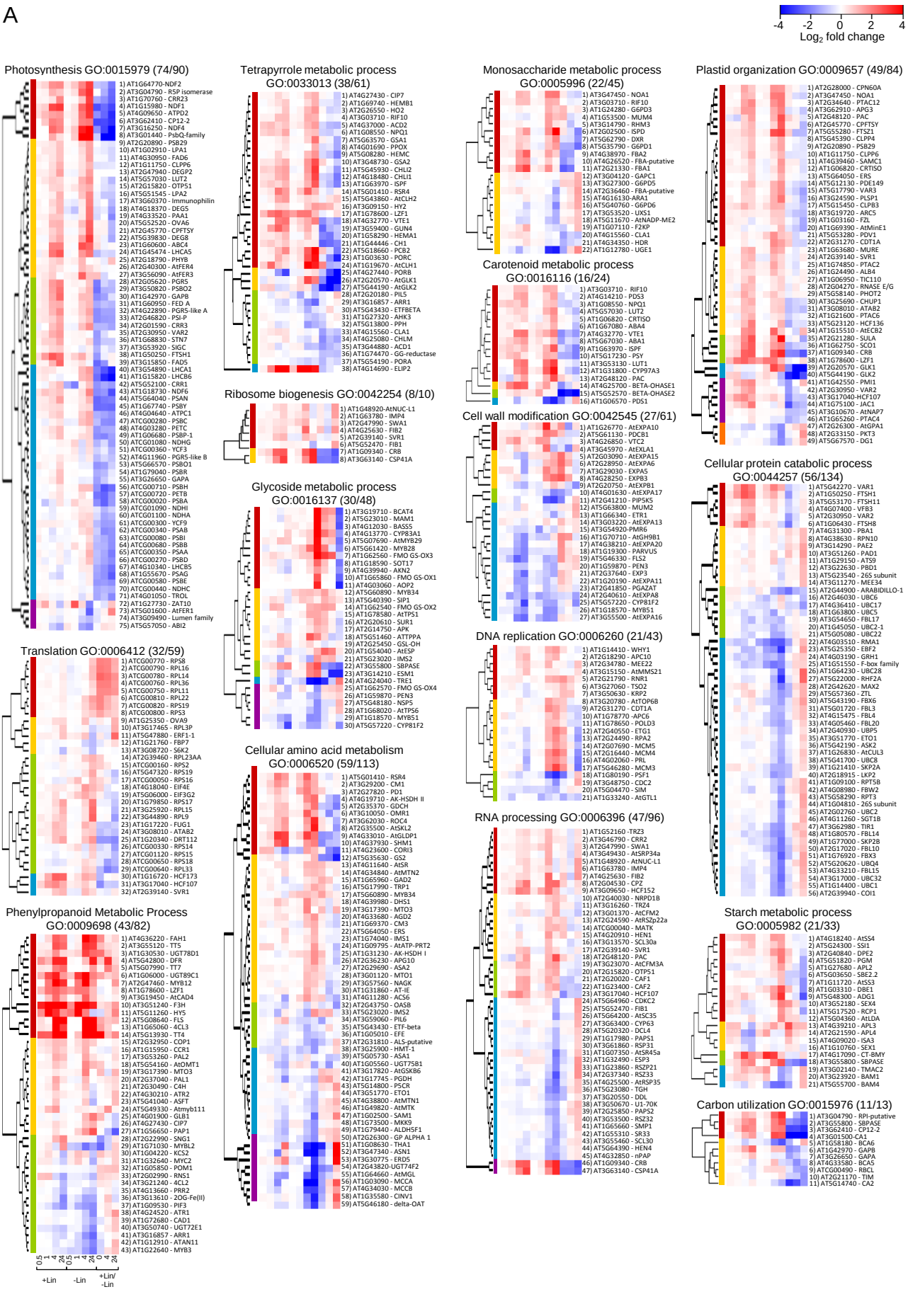

GO categories
1200
800
400
0
0 25 50 75
-log10 p-value
Organelle
Cytoplasm
Thylakoid
Cell Wall
Plastid ribosome
Ubiquitin ligase complex
Plastid inner membrane
Plastid chomosome
Cytosolic ribosome subunits
Mitochondria, nucleus, plasma membrane
Light harvesting complex, photosystems I and II
Cytosolic ribosome
Stroma
Plastid envelope
Tylakoid lumen
Plastid and chloroplast
P-23 1 32 10 14 16 30 4 6 P-20 15 33 P-24 8 17 P-18 P-19 31 9 2 P-29 35 27 P-28 26 5 7 13 11 3 34 P-25 12 P-21 P-22

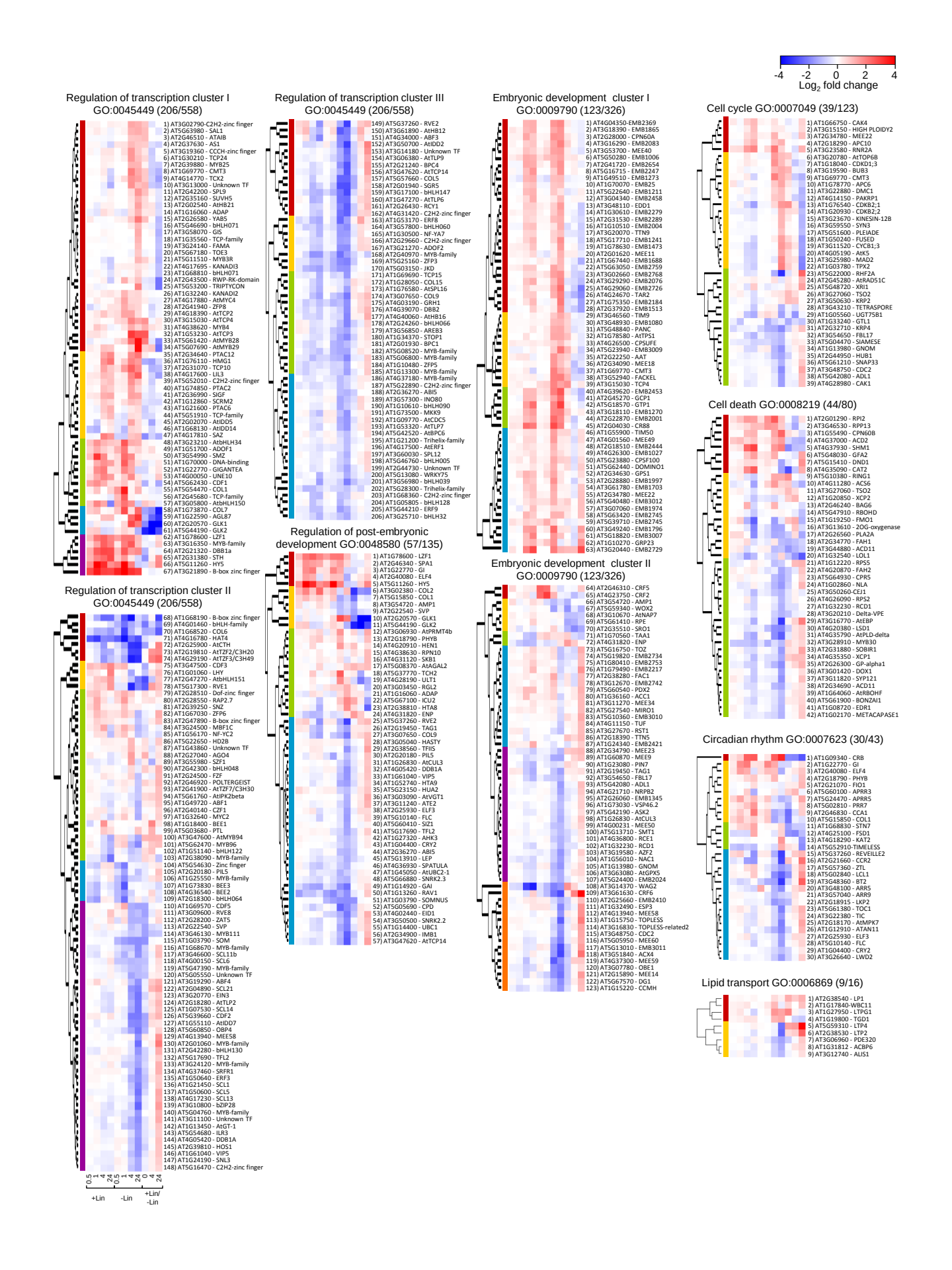
Supplemental Figure S5. Clustering of significantly enriched GO terms with user-defined expression patterns.

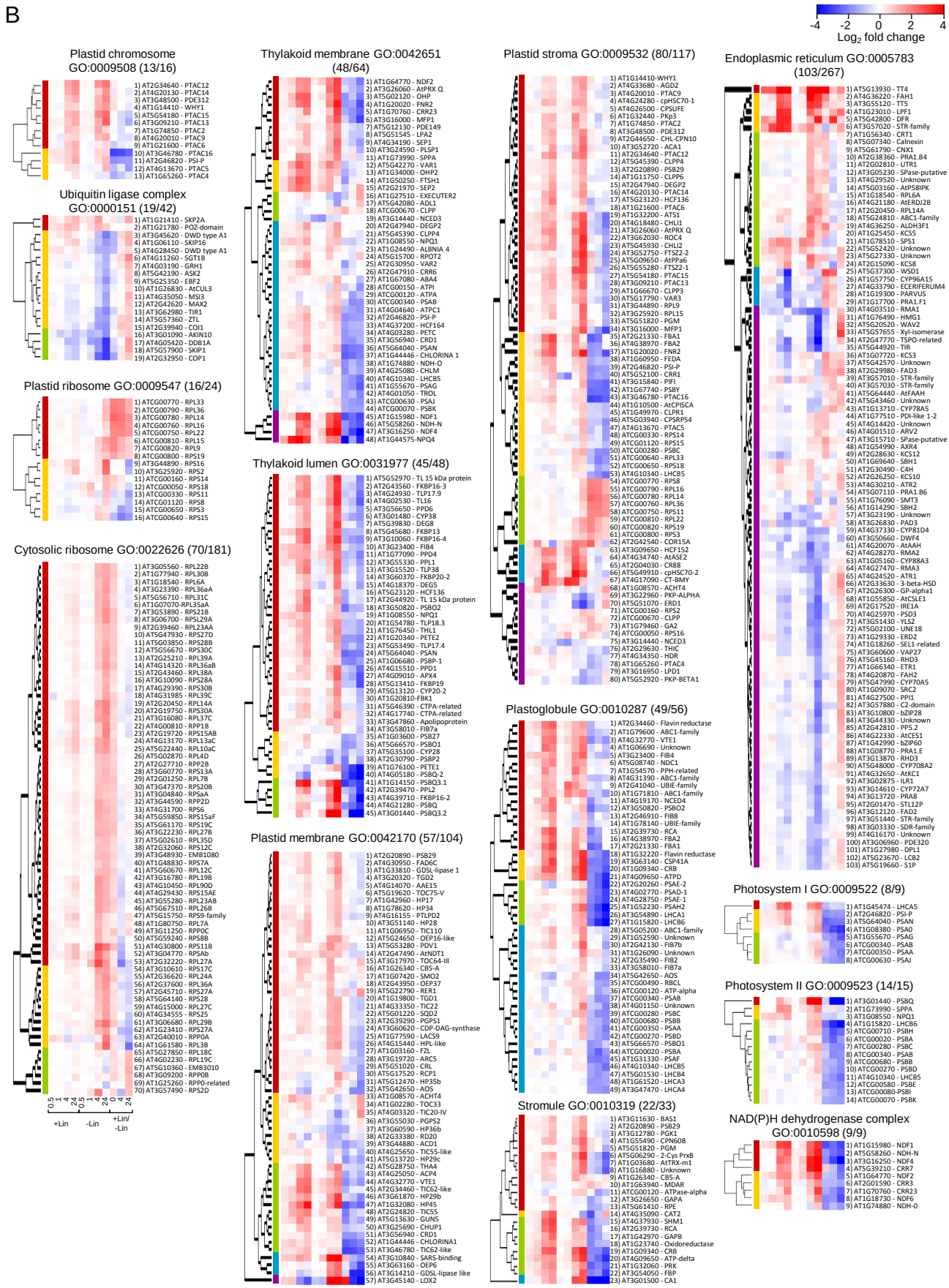
A, Agglomerative hierarchical clustering of GO terms defined as biological processes with expression patterns. One hundred ninety-eight active GO terms assigned as a biological process were considered enriched if $p \leq 0.01$ after a Westfall-Young correction of at least one of the expression clusters. GO terms were included if they were enriched in at least one expression pattern and $p \leq 0.01$. The negative $\log_{10}$ of the uncorrected p-values for each pattern was clustered. These one hundred ninety-eight GO clusters are shown as a dendrogram at the left of the cluster matrix. Summary terms that represent a cluster of GO terms are shown at the right of the cluster matrix and are as described in Supplemental Fig. S4A. User-defined expression patterns from Supplemental Fig. S3 are shown as a dendrogram at the top of the cluster matrix. User-defined expression pattern numbers from Supplemental Fig. S3 that correspond to each branch of the dendrogram are indicated at the bottom of the cluster matrix. The letter P next to the cluster number indicates regulation by the lincomycin treatment. No letter P next to the cluster letter indicates regulation by the BR-fluence-rate shift. The intensity of the red color is proportional to the degree of enrichment. Clusters of patterns are indicated with dashed boxes.

B, Agglomerative hierarchical clustering of GO terms defined as cellular components with expression patterns. Eighty-seven GO terms assigned as cellular components were enriched as described in A. Labeling of this heat map is as described in A.

A


-4 -2 0 2 4
Log2 fold change
Photosynthesis GO:0015979 (74/90)
1) AT1G64770-NDF2
2) AT3G04790 - RSP isomerase
3) AT1G70760 - CRR23
4) AT1G15980 - NDF1
5) AT4G09650 - ATPD2
6) AT3G62410 - CP12-2
7) AT3G16250 - NDF4
8) AT3G01440 - PsbQ-family
9) AT2G20890 - PSB29
10) AT1G02910 - LPA1
11) AT4G30950 - FAD6
12) AT1G11750 - CLPP6
13) AT2G47940 - DEGP2
14) AT5G57030 - LUT2
15) AT2G15820 - OTP51
16) AT5G51545 - LPA2
17) AT3G60370 - Immunophilin
18) AT4G18370 - DEG5
19) AT4G33520 - PAA1
20) AT5G52520 - OVA6
21) AT2G45770 - CPFTSY
22) AT5G39830 - DEG8
23) AT1G60600 - ABC4
24) AT1G45474 - LHCA5
25) AT2G18790 - PHYB
26) AT2G40300 - AtFER4
27) AT3G56090 - AtFER3
28) AT2G05620 - PGR5
29) AT3G50820 - PSBO2
30) AT1G42970 - GAPB
31) AT1G60950 - FED A
32) AT4G22890 - PGR5-like A
33) AT2G46820 - PSI-P
34) AT2G01590 - CRR3
35) AT2G30950 - VAR2
36) AT1G68830 - STN7
37) AT3G53920 - SIGC
38) AT1G50250 - FTSH1
39) AT3G15850 - FAD5
40) AT3G54890 - LHCA1
41) AT1G15820 - LHCB6
42) AT5G52100 - CRR1
43) AT1G18730 - NDF6
44) AT5G64040 - PSAN
45) AT1G67740 - PSBY
46) AT4G04640 - ATPC1
47) ATCG00280 - PSBC
48) AT4G03280 - PETC
49) AT1G06680 - PSBP-1
50) ATCG01080 - NDHG
51) ATCG00360 - YCF3
52) AT4G11960 - PGR5-like B
53) AT5G66570 - PSBO1
54) AT1G79040 - PSBR
55) AT3G26650 - GAPA
56) ATCG00710 - PSBH
57) ATCG00720 - PETB
58) ATCG00020 - PSBA
59) ATCG01090 - NDHI
60) ATCG01100 - NDHA
61) ATCG00300 - YCF9
62) ATCG00340 - PSAB
63) ATCG00080 - PSBI
64) ATCG00680 - PSBB
65) ATCG00350 - PSAA
66) ATCG00270 - PSBD
67) AT4G10340 - LHCB5
68) AT1G55670 - PSAG
69) ATCG00580 - PSBE
70) ATCG00440 - NDHC
71) AT4G01050 - TROL
72) AT1G27730 - ZAT10
73) AT5G01600 - AtFER1
74) AT3G09490 - Lumen family
75) AT5G57050 - ABI2
Tetrapyrrole metabolic process GO:0033013 (38/61)
1) AT4G27430 - CIP7
2) AT1G69740 - HEMB1
3) AT2G26550 - HO2
4) AT3G03710 - RIF10
5) AT4G37000 - ACD2
6) AT1G08550 - NPQ1
7) AT5G63570 - GSA1
8) AT4G01690 - PPOX
9) AT5G08280 - HEMC
10) AT1G48730 - GSA2
11) AT5G45930 - CHLI2
12) AT4G18480 - CHLI1
13) AT1G63970 - ISPF
14) AT5G01410 - RSR4
15) AT5G43860 - AtCLH2
16) AT3G09150 - HY2
17) AT1G78600 - LZF1
18) AT2G32770 - VTE1
19) AT3G59400 - GUN4
20) AT1G58290 - HEMA1
21) AT1G44446 - CH1
22) AT5G18660 - PCB2
23) AT1G03630 - PORC
24) AT1G19670 - AtCLH1
25) AT4G27440 - PORB
26) AT2G20180 - PIL5
27) AT5G44190 - AtGLK2
28) AT2G20180 - PIL5
29) AT3G16857 - ARR1
30) AT5G43430 - ETFBETA
31) AT1G27320 - AHK3
32) AT5G13800 - PPH
33) AT4G19560 - CLA1
34) AT4G25080 - CHLM
35) AT3G44880 - ACD1
36) AT1G74470 - GG-reductase
37) AT5G54190 - PORA
38) AT4G14690 - ELIP2
Ribosome biogenesis GO:0042254 (8/10)
1) AT1G48920-AtNUC-L1
2) AT1G63780 - IMP4
3) AT2G47990 - SWA1
4) AT4G25630 - FIB2
5) AT2G39140 - SVR1
6) AT5G52470 - FIB1
7) AT1G09340 - CR8
8) AT3G63140 - CSP41A
Glycoside metabolic process GO:0016137 (30/48)
1) AT3G19710 - BCAT4
2) AT5G23010 - MAM1
3) AT4G12030 - BASS5
4) AT4G13770 - CYP83A1
5) AT5G07690 - AtMYB29
6) AT5G61420 - MYB28
7) AT1G62560 - FMO GS-OX3
8) AT1G18590 - SOT17
9) AT4G39940 - AKN2
10) AT1G65860 - FMO GS-OX1
11) AT4G03060 - AOP2
12) AT5G60890 - MYB34
13) AT5G40390 - SIP1
14) AT1G62540 - FMO GS-OX2
15) AT1G78580 - AtTPS1
16) AT2G20610 - SUR1
17) AT2G14750 - APK
18) AT5G51460 - AtTTPA
19) AT2G25450 - GSL-OH
20) AT1G54040 - AtESP
21) AT5G23020 - IMS2
22) AT3G55800 - SBPASE
23) AT3G14210 - ESM1
24) AT4G24040 - TRE1
25) AT1G62570 - FMO GS-OX4
26) AT1G59870 - PEN3
27) AT5G48180 - NSP5
28) AT1G68020 - AtTPS6
29) AT1G18570 - MYB51
30) AT5G57220 - CYP81F2
Cellular amino acid metabolism GO:0006520 (59/113)
1) AT5G01410 - RSR4
2) AT3G29200 - CM1
3) AT2G27820 - PD1
4) AT4G19710 - AK-HSDH II
5) AT2G33270 - GDCH
6) AT3G10050 - OMR1
7) AT3G62030 - ROC4
8) AT2G35500 - AtSKL2
9) AT4G33010 - AtGLDP1
10) AT4G37930 - SHM1
11) AT4G23600 - CORI3
12) AT5G35630 - GS2
13) AT4G11640 - MSR
14) AT4G34840 - AtMTN2
15) AT1G65960 - GAD2
16) AT5G17990 - TRP1
17) AT5G60890 - MYB34
18) AT4G39980 - DHS1
19) AT3G17390 - MTO3
20) AT4G33680 - AGD2
21) AT1G69370 - CM3
22) AT5G64050 - ERS
23) AT1G74040 - IMS1
24) AT1G09795 - AtATP-PRT2
25) AT1G31230 - AK-HSDH I
26) AT2G36230 - APG10
27) AT2G29690 - ASA2
28) AT3G01120 - MTO1
29) AT3G57560 - NAGK
30) AT1G31860 - AT-IE
31) AT4G11280 - ACS6
32) AT1G58602 - OAS8
33) AT5G23020 - IMS2
34) AT3G59060 - PIL6
35) AT5G43430 - ETF-beta
36) AT1G05010 - EFE
37) AT2G31810 - ALS-putative
38) AT3G25900 - HMT-1
39) AT5G05730 - ASA1
40) AT1G09360 - UGT75B1
41) AT3G17820 - AtGSKB6
42) AT1G17745 - PGDH
43) AT5G14800 - PSCR
44) AT3G51770 - ETO1
45) AT4G38800 - AtMTN1
46) AT1G49820 - AtMTK
47) AT1G02500 - SAM1
48) AT1G03500 - MKK9
49) AT1G79440 - ALDH5F1
50) AT2G26300 - GP ALPHA 1
51) AT1G08630 - THA1
52) AT3G47340 - ASN1
53) AT3G30775 - ERD5
54) AT2G43820-UGT74F2
55) AT1G64660 - AtMGL
56) AT1G03090 - MCCA
57) AT4G34030 - MCCB
58) AT1G35580 - CINV1
59) AT5G46180 - delta-OAT
Monosaccharide metabolic process GO:0005996 (22/45)
1) AT3G47450 - NOA1
2) AT3G03710 - RIF10
3) AT1G24280 - G6PD3
4) AT1G53500 - MUM4
5) AT3G14790 - RHM3
6) AT2G02500 - PPD
7) AT5G62790 - DXR
8) AT5G35790 - G6PD1
9) AT4G38970 - FBA2
10) AT4G26520 - FBA-putative
11) AT2G21330 - FBA1
12) AT3G04120 - GAPC1
13) AT3G27300 - G6PD5
14) AT2G36460 - FBA-putative
15) AT4G16130-ARA1
16) AT5G40760 - G6PD6
17) AT3G53620 - UXS1
18) AT5G11670 - AtNADP-ME2
19) AT1G07110 - F2KP
20) AT4G15560 - CLA1
21) AT4G14350 - HDR
22) AT1G12780 - UGE1
Carotenoid metabolic process GO:0016116 (16/24)
1) AT3G03710 - RIF10
2) AT4G14210 - PDS3
3) AT1G08550 - NPQ1
4) AT5G57030 - LUT2
5) AT1G06820 - CRTISO
6) AT1G67080 - ABA4
7) AT4G32770 - VTE1
8) AT5G67030 - ABA1
9) AT1G63970 - ISPF
10) AT5G17230 - PSY
11) AT3G53130 - LUT1
12) AT1G31800 - CYP97A3
13) AT2G48120 - PAC
14) AT4G25700 - BETA-OHASE1
15) AT5G52570 - BETA-OHASE2
16) AT1G06570 - PDS1
Cell wall modification GO:0042545 (27/61)
1) AT1G26770 - AtEXPA10
2) AT5G61130 - PDCB1
3) AT4G26850 - VTC2
4) AT3G45970 - AtEXLA1
5) AT2G03090 - AtEXPA15
6) AT2G28950 - AtEXPA6
7) AT3G29030 - EXPA5
8) AT4G28250 - EXPB3
9) AT2G20750 - AtEXPB1
10) AT4G01630 - AtEXPA17
11) AT2G41210 - PIP5K5
12) AT5G63800 - MUM2
13) AT1G66340 - ETR1
14) AT3G03220 - AtEXPA13
15) AT3G59620-PMR6
16) AT1G70710 - AtGH9B1
17) AT4G38210 - AtEXPA20
18) AT1G19300 - PARVUS
19) AT5G46330 - FLS2
20) AT1G59870 - PEN3
21) AT2G37640 - EXP3
22) AT1G20190 - AtEXPA11
23) AT2G41850 - PGAZAT
24) AT2G40610 - AtEXPA8
25) AT5G57220 - CYP81F2
26) AT1G18570 - MYB51
27) AT3G55500 - AtEXPA16
DNA replication GO:0006260 (21/43)
1) AT1G14410 - WHY1
2) AT2G18290 - APC10
3) AT2G34780 - MEE22
4) AT3G15150 - AtMMS21
5) AT2G21790 - RNR1
6) AT4G27060 - SOZ2
7) AT3G50630 - KRP2
8) AT3G20780 - AtTOP6B
9) AT2G31210 - CDT1A
10) AT1G78770 - APC6
11) AT1G78650 - POLD3
12) AT2G40550 - ETG1
13) AT3G24490 - RPA2
14) AT2G07690 - MCM5
15) AT2G16440 - MCM4
16) AT4G02060 - PRL
17) AT5G46280 - MCM3
18) AT1G80190 - PSF1
19) AT3G48750 - CDC2
20) AT5G04470 - SIM
21) AT1G33240 - AtGTL1
RNA processing GO:0006396 (47/96)
1) AT1G52160 - TRZ3
2) AT3G46790 - CRR2
3) AT3G47990 - SWA1
4) AT3G49430 - AtSRP34a
5) AT1G48920 - AtNUC-L1
6) AT1G63780 - IMP4
7) AT4G25630 - FIB2
8) AT2G04530 - CPZ
9) AT3G09650 - HCF152
10) AT2G40030 - NRPD1B
11) AT3G16260 - TRZ4
12) AT3G01370 - AtCFM2
13) AT2G24590 - AtRSZp22a
14) ATCG00040 - MATK
15) AT4G20910 - HEN1
16) AT3G13570 - SCL30a
17) AT2G39140 - SVR1
18) AT2G48120 - PAC
19) AT2G23070 - AtCFM3A
20) AT2G15820 - OTP51
21) AT2G20020 - CAF1
22) AT1G23400 - CAF2
23) AT3G17040 - HCF107
24) AT5G64960 - CDKC2
25) AT5G52470 - FIB1
26) AT5G64200 - AtSC35
27) AT3G63400 - CYP63
28) AT5G20320 - DCL4
29) AT1G17980 - PAPS1
30) AT3G61860 - RSP31
31) AT1G07350 - AtSR45a
32) AT1G32490 - ESP3
33) AT1G23860 - RSZP21
34) AT2G37340 - RSZ33
35) AT4G25500 - AtRSP35
36) AT5G23080 - TGH
37) AT3G20550 - DDL
38) AT4G50670 - U1-70K
39) AT2G25850 - PAPS2
40) AT3G53500 - RSZ32
41) AT1G65660 - SMP1
42) AT1G55310 - SR33
43) AT3G55460 - SCL30
44) AT5G64390 - HEN4
45) AT4G32850 - nPAP
46) AT1G09340 - CR8
47) AT3G63140 - CSP41A
Plastid organization GO:0009657 (49/84)
1) AT2G28000 - CPN60A
2) AT3G47450 - NOA1
3) AT2G34640 - PTAC12
4) AT3G62910 - APG3
5) AT2G48120 - PAC
6) AT2G45770 - CPFTSY
7) AT5G55280 - FTSZ1
8) AT5G45390 - CLPP4
9) AT2G20890 - PSB29
10) AT1G11750 - CLPP6
11) AT4G39460 - SAMC1
12) AT1G06820 - CRTISO
13) AT5G64050 - ERS
14) AT5G12130 - PDE149
15) AT5G17790 - VAR3
16) AT3G24590 - PLSP1
17) AT5G15450 - CLPB3
18) AT3G19720 - ARC5
19) AT1G03160 - FZL
20) AT1G69390 - AtMinE1
21) AT5G53280 - PDV1
22) AT2G31270 - CDT1A
23) AT1G63680 - MURE
24) AT2G39140 - SVR1
25) AT1G74850 - PTAC2
26) AT1G24490 - ALB4
27) AT1G06950 - TIC110
28) AT2G04270 - RNASE E/G
29) AT5G58140 - PHOT2
30) AT3G25690 - CHUP1
31) AT3G08010 - ATAB2
32) AT1G21600 - PTAC6
33) AT5G23120 - HCF136
34) AT1G55510 - AtECB2
35) AT2G21280 - SULA
36) AT1G62750 - SCO1
37) AT1G09340 - CR8
38) AT1G78600 - LZF1
39) AT2G20570 - GLK1
40) AT5G44190 - GLK2
41) AT1G42550 - PMI1
42) AT2G30950 - VAR2
43) AT3G17040-HCF107
44) AT1G75100 - JAC1
45) AT3G10670 - AtNAP7
46) AT1G65260 - PTAC4
47) AT2G26300 - AtGPA1
48) AT2G33150 - PKT3
49) AT5G67570 - DG1
Cellular protein catabolic process GO:0044257 (56/134)
1) AT5G42270 - VAR1
2) AT1G50250 - FTSH1
3) AT5G53170 - FTSH11
4) AT4G07540 - VFB3
5) AT2G30950 - VAR2
6) AT1G06430 - FTSH8
7) AT4G31300 - PBA1
8) AT4G38630 - RPN10
9) AT3G14290 - PAE2
10) AT3G51260 - PAD1
11) AT1G29150 - ATS9
12) AT3G22630 - PBD1
13) AT5G23540 - 26S subunit
14) AT3G11270 - MEE34
15) AT2G44900 - ARABIDILLO-1
16) AT2G46030 - UBC6
17) AT4G36410 - UBC17
18) AT1G63800 - UBC5
19) AT3G54650 - FBL17
20) AT1G45050 - UBC2-1
21) AT5G05080 - UBC22
22) AT4G03510 - RMA1
23) AT5G25350 - EBF2
24) AT4G03190 - GRH1
25) AT1G51550 - F-box family
26) AT1G64230 - UBC28
27) AT5G22000 - RHF2A
28) AT2G42620 - MAX2
29) AT5G57360 - ZTL
30) AT5G43190 - FBX6
31) AT5G01720 - FBL3
32) AT4G15475 - FBL4
33) AT4G05460 - FBL20
34) AT2G40930 - UBP5
35) AT3G51770 - ETO1
36) AT5G42190 - ASK2
37) AT1G26830 - AtCUL3
38) AT5G41700 - UBC8
39) AT1G21410 - SKP2A
40) AT2G18915 - LKP2
41) AT1G09100 - RPT5B
42) AT4G08980 - FBW2
43) AT5G58290 - RPT3
44) AT1G04810 - 26S subunit
45) AT2G02760 - UBC2
46) AT4G11260 - SGT1B
47) AT3G62980 - TIR1
48) AT1G80570 - FBL14
49) AT1G77000 - SKP2B
50) AT2G17020 - FBL10
51) AT1G76920 - FBX3
52) AT5G20620 - UBQ4
53) AT4G33210 - FBL15
54) AT3G17000 - UBC32
55) AT1G14400 - UBC1
56) AT2G39940 - COI1
Starch metabolic process GO:0005982 (21/33)
1) AT4G18240 - AtSS4
2) AT5G24300 - SSI1
3) AT2G40840 - DPE2
4) AT5G51820 - PGM
5) AT1G27680 - APL2
6) AT5G03650 - SBE2.2
7) AT1G11720 - AtSS3
8) AT1G03310 - DBE1
9) AT5G48300 - ADG1
10) AT3G52180 - SEX4
11) AT5G17520 - RCP1
12) AT5G04360 - AtLDA
13) AT4G39210 - APL3
14) AT2G21590 - APL4
15) AT4G09020 - ISA3
16) AT1G10760 - SEX1
17) AT4G17090 - CT-BMY
18) AT3G55800 - SBPASE
19) AT3G02140 - TMAC2
20) AT3G23920 - BAM1
21) AT5G55700 - BAM4
Carbon utilization GO:0015976 (11/13)
1) AT3G04790 - RPI-putative
2) AT3G55800 - SBPASE
3) AT3G62410 - CP12-2
4) AT3G01500-CA1
5) AT1G58180 - BCA6
6) AT1G42970 - GAPB
7) AT3G26650 - GAPA
8) AT4G33580 - BCA5
9) ATCG00490 - RBCL
10) AT2G21170 - TIM
11) AT5G14740 - CA2
Translation GO:0006412 (32/59)
1) ATCG00770 - RPS8
2) ATCG00790 - RPL16
3) ATCG00780 - RPL14
4) ATCG00760 - RPL36
5) ATCG00750 - RPL11
6) ATCG00810 - RPL22
7) ATCG00820 - RPS19
8) ATCG00800 - RPS3
9) AT1G25350 - OVA9
10) AT3G17465 - RPL3P
11) AT5G47880 - ERF1-1
12) AT1G21760 - FBP7
13) AT3G08720 - S6K2
14) AT2G39460 - RPL23AA
15) ATCG00160 - RPS2
16) AT5G47320 - RPS19
17) ATCG00050 - RPS16
18) AT4G18040 - EIF4E
19) AT5G06000 - EIF3G2
20) AT1G79850 - RPS17
21) AT3G25920 - RPL15
22) AT3G44890 - RPL9
23) AT1G17220 - FUG1
24) AT3G08010 - ATAB2
25) AT1G20340 - DRT112
26) ATCG00330 - RPS14
27) ATCG01120 - RPS15
28) ATCG00650 - RPS18
29) ATCG00640 - RPL33
30) AT1G16720 - HCF173
31) AT3G17040 - HCF107
32) AT2G39140 - SVR1
Phenylpropanoid Metabolic Process GO:0009698 (43/82)
1) AT4G36220 - FAH1
2) AT3G55120 - TT5
3) AT1G30530 - UGT78D1
4) AT5G42800 - DFR
5) AT5G07990 - TT7
6) AT1G06000 - UGT89C1
7) AT2G47460 - MYB12
8) AT1G78600 - LZF1
9) AT3G19450 - AtCAD4
10) AT5G01240 - F3H
11) AT5G11260 - HY5
12) AT5G08640 - FLS
13) AT1G65060 - 4CL3
14) AT5G13930 - TT4
15) AT2G32950 - COP1
16) AT1G15950 - CCR1
17) AT3G53260 - PAL2
18) AT1G54160 - AtOMT1
19) AT3G17390 - MTO3
20) AT2G37040 - PAL1
21) AT2G30490 - C4H
22) AT4G30210 - ATR2
23) AT5G41040 - ASFT
24) AT5G49330 - Atmyb111
25) AT4G01900 - GLB1
26) AT1G67430 - CIP7
27) AT1G56650 - PAP1
28) AT2G22990 - SNG1
29) AT1G71030 - MYBL2
30) AT1G04220 - KCS2
31) AT1G32640 - MYC2
32) AT1G05850 - POM1
33) AT2G02990 - RNS1
34) AT3G21240 - 4CL2
35) AT4G13660 - PRR2
36) AT3G13610 - 2OG-Fe(II)
37) AT1G09530 - PIF3
38) AT4G24520 - ATR1
39) AT1G72680 - CAD1
40) AT3G50740 - UGT72E1
41) AT3G16857 - ARR1
42) AT1G12910 - ATAN11
43) AT1G22640 - MYB3
0.5 1 4 24 0.5 1 4 24 0 4
+Lin -Lin +Lin/ -Lin


-4 -2 0 2 4
Log2 fold change
Regulation of transcription cluster I
GO:0045449 (206/558)
1) AT3G02790-C2H2-zinc finger
2) AT5G63980 - SAL1
3) AT2G46510 - ATAIB
4) AT2G37630 - AS1
5) AT3G19360 - CCCH-zinc finger
6) AT1G30210 - TCP24
7) AT2G39880 - MYB25
8) AT1G69770 - CMT3
9) AT4G14770 - TCX2
10) AT3G13000 - Unknown TF
11) AT2G42200 - SPL9
12) AT2G35160 - SUVH5
13) AT2G02540 - AtHB21
14) AT1G16060 - ADAP
15) AT2G26580 - YAB5
16) AT5G46690 - bHLH071
17) AT3G58070 - GIS
18) AT1G55560 - TCP-family
19) AT3G24140 - FAMA
20) AT5G67180 - TOE3
21) AT5G11510 - MYB3R
22) AT4G27695 - KANADI3
23) AT1G68810 - bHLH071
24) AT2G43500 - RWP-RK-domain
25) AT5G53200 - TRIPTYCON
26) AT1G32240 - KANADI2
27) AT4G17880 - AtMYC4
28) AT2G41940 - ZFP8
29) AT4G18390 - AtTCP2
30) AT3G15030 - AtTCP4
31) AT4G38620 - MYB4
32) AT1G53230 - AtTCP3
33) AT5G61420 - AtMYB28
34) AT5G07690 - AtMYB29
35) AT2G34640 - PTAC12
36) AT1G76110 - HMG1
37) AT2G31070 - TCP10
38) AT4G17600 - LIL3
39) AT5G52010 - C2H2-zinc finger
40) AT1G74850 - PTAC2
41) AT2G36990 - SIGF
42) AT1G12860 - SCRM2
43) AT1G21600 - PTAC6
44) AT5G51910 - TCP-family
45) AT2G02070 - AtIDD5
46) AT1G68130 - AtIDD14
47) AT4G17810 - SAZ
48) AT3G23210 - AttbHLH34
49) AT1G51700 - ADOF1
50) AT3G54990 - SMZ
51) AT1G70000 - DNA-binding
52) AT1G22770 - GIGANTEA
53) AT4G00050 - UNE10
54) AT5G62430 - CDF1
55) AT5G54470 - COL1
56) AT2G45680 - TCP-family
57) AT3G05800 - AtbHLH150
58) AT1G73870 - COL7
59) AT1G22590 - AGL87
60) AT2G20570 - GLK1
61) AT5G44190 - GLK2
62) AT1G78600 - LZF1
63) AT3G16350 - MYB-family
64) AT2G21320 - DBB1a
65) AT2G31380 - STH
66) AT5G61260 - HY5
67) AT3G21890 - B-box zinc finger
Regulation of transcription cluster II
GO:0045449 (206/558)
68) AT1G68190 - B-box zinc finger
69) AT4G01460 - bHLH-family
70) AT1G68520 - COL6
71) AT4G16780 - HAT4
72) AT2G25900 - AtCTH
73) AT2G19810 - AtTZF2/C3H20
74) AT4G29190 - AtTZF3/C3H49
75) AT3G47500 - CDF3
76) AT1G01060 - LHY
77) AT2G47270 - AtbHLH151
78) AT5G17300 - RVE1
79) AT5G28510 - Dof-zinc finger
80) AT2G28550 - RAP2.7
81) AT2G39250 - SNZ
82) AT1G67030 - ZFP6
83) AT4G37890 - B-box zinc finger
84) AT3G24500 - MBF1C
85) AT1G56170 - NF-YC2
86) AT5G22650 - HD2B
87) AT1G43860 - Unknown TF
88) AT2G27040 - AGO4
89) AT3G55980 - SZF1
90) AT2G42300 - bHLH048
91) AT2G24500 - FZF
92) AT2G46920 - POLTERGEIST
93) AT2G41900 - AtTZF7/C3H30
94) AT5G61760 - AtIPK2beta
95) AT1G49720 - ABF1
96) AT2G40140 - CZF1
97) AT1G32640 - MYC2
98) AT1G18400 - BEE1
99) AT5G03680 - PTL
100) AT3G47600 - AtMYB94
101) AT5G62470 - MYB96
102) AT1G55140 - bHLH122
103) AT2G38090 - MYB-family
104) AT5G54630 - Zinc finger
105) AT2G20180 - PIL5
106) AT2G25550 - MYB-family
107) AT1G73830 - BEE3
108) AT4G36540 - BEE2
109) AT2G18300 - bHLH064
110) AT1G69570 - CDF5
111) AT3G09600 - RVE8
112) AT2G28200 - ZAT5
113) AT2G22540 - SVP
114) AT3G46130 - MYB111
115) AT1G03790 - SOM
116) AT1G68670 - MYB-family
117) AT3G46600 - SCL11b
118) AT4G00150 - SCL6
119) AT5G47390 - MYB-family
120) AT5G05550 - Unknown TF
121) AT3G19290 - ABF4
122) AT2G04890 - SCL21
123) AT3G20770 - EIN3
124) AT2G18280 - AtTLP2
125) AT1G07530 - SCL14
126) AT5G39660 - CDF2
127) AT1G55110 - AtIDD7
128) AT5G60850 - OBP4
129) AT4G13940 - MEE58
130) AT2G01060 - MYB-family
131) AT2G42280 - bHLH130
132) AT5G17690 - TFL2
133) AT3G24120 - MYB-family
134) AT4G37460 - SRFR1
135) AT1G50640 - ERF3
136) AT1G21450 - SCL1
137) AT1G50600 - SCL5
138) AT4G17230 - SCL13
139) AT3G10800 - bZIP28
140) AT5G04760 - MYB-family
141) AT3G11100 - Unknown TF
142) AT1G13450 - AtGT-1
143) AT5G54680 - ILR3
144) AT4G05420 - DDB1A
145) AT2G39810 - HOS1
146) AT1G61040 - VIP5
147) AT1G24190 - SNL3
148) AT5G16470 - C2H2-zinc finger
0.5 1 1.4 2.4 0.5 1 1.4 2.0 2.4
+Lin -Lin +Lin/-Lin
Regulation of transcription cluster III
GO:0045449 (206/558)
149) AT5G37260 - RVE2
150) AT3G61890 - AtHB12
151) AT4G34000 - ABF3
152) AT3G50700 - AtIDD2
153) AT3G14180 - Unknown TF
154) AT3G06380 - AtTLP9
155) AT2G31270 - ERF8
156) AT3G47620 - AtTCP14
157) AT5G57660 - COL5
158) AT2G01940 - SGR5
159) AT3G17100 - bHLH147
160) AT1G47270 - AtTLP6
161) AT2G26430 - RCY1
162) AT4G31420 - C2H2-zinc finger
163) AT2G53170 - ERF8
164) AT3G57800 - bHLH060
165) AT1G30500 - NF-YA7
166) AT2G29660 - C2H2-zinc finger
167) AT3G21270 - ADOF2
168) AT2G40970 - MYB-family
169) AT5G25160 - ZFP3
170) AT5G50450 - JKD
171) AT1G69690 - TCP15
172) AT1G28050 - COL15
173) AT1G76580 - AtSPL16
174) AT3G07650 - COL9
175) AT4G03190 - GRH1
176) AT4G39070 - DBB2
177) AT4G40060 - AtHB16
178) AT2G42260 - bHLH066
179) AT3G56850 - AREB3
180) AT1G34370 - STOP1
181) AT2G01930 - BPC1
182) AT5G08520 - MYB-family
183) AT5G06800 - MYB-family
184) AT1G10480 - ZFP5
185) AT1G13300 - MYB-family
186) AT4G37180 - MYB-family
187) AT5G22890 - C2H2-zinc finger
188) AT2G36270 - ABI5
189) AT3G57300 - INO80
190) AT1G10610 - bHLH090
191) AT1G73500 - MKK9
192) AT1G09770 - AtCDC5
193) AT1G53320 - AtTLP7
194) AT5G42520 - AtBPC6
195) AT1G21200 - Trihelix-family
196) AT4G17500 - AtERF1
197) AT3G60030 - SPL12
198) AT5G46760 - bHLH005
199) AT2G44730 - Unknown TF
200) AT5G13080 - WRKY75
201) AT3G56980 - bHLH039
202) AT5G28300 - Trihelix-family
203) AT1G68360 - C2H2-zinc finger
204) AT1G05805 - bHLH128
205) AT5G44210 - ERF9
206) AT3G25710 - bHLH32
Regulation of post-embryonic
development GO:0048580 (57/135)
1) AT1G78600 - LZF1
2) AT2G46340 - SPA1
3) AT1G22770 - GI
4) AT2G40080 - ELF4
5) ATSG11260 - HY5
6) AT3G02380 - HIL2
7) ATSG15850 - COL1
8) AT3G54720 - AMP1
9) AT2G22540 - SVP
10) AT2G20570 - GLK1
11) AT5G44190 - GLK2
12) AT3G06930 - AtPRMT4b
13) AT2G37290 - PHYB
14) AT4G20910 - HEN1
15) AT4G38630 - RPN10
16) AT4G31120 - SKB1
17) AT4G03870 - AtAGAL2
18) AT5G37770 - TCH2
19) AT4G28190 - ULT1
20) AT3G03450 - RGL2
21) AT5G48150 - ADAP
22) AT5G67100 - ICU2
23) AT2G38810 - HTA8
24) AT4G31820 - ENP
25) AT5G37260 - RVE2
26) AT2G19450 - TAG1
27) AT3G07650 - COL9
28) AT3G05040 - HASTY
29) AT4G38560 - TTIS
30) AT2G20180 - PIL5
31) AT1G26830 - AtCUL3
32) AT4G05420 - DDB1A
33) AT4G16040 - VIP5
34) AT1G52740 - HTA9
35) AT5G23150 - HUA2
36) AT3G03090 - AtVGT1
37) AT1G11910 - ATE2
38) AT2G25930 - ELF3
39) AT5G10140 - FLC
40) AT5G60410 - SIZ1
41) AT5G17690 - TFL2
42) AT1G27320 - AHK3
43) AT1G04400 - CRY2
44) AT3G63270 - ABI5
45) AT5G13910 - LEP
46) AT4G36930 - SPATULA
47) AT1G45050 - AtUBC2-1
48) AT1G66280 - SNRK2.3
49) AT1G14920 - GAI
50) AT1G13260 - RAV1
51) AT1G03790 - SOMNUS
52) AT5G05690 - CPD
53) AT4G02440 - EID1
54) AT3G50500 - SNRK2.2
55) AT1G14400 - UBC1
56) AT2G34900 - IMB1
57) AT3G47620 - AtTCP14
Embryonic development cluster I
GO:0009790 (123/326)
1) AT4G04350-EMB2369
2) AT3G18390 - EMB1865
3) AT2G28000 - CPN60A
4) AT3G16290 - EMB2083
5) AT3G53700 - MEE40
6) AT5G50280 - EMB1006
7) AT2G41720 - EMB2654
8) AT5G16715 - EMB2247
9) AT1G49510 - EMB1273
10) AT1G70070 - EMB825
11) AT5G22640 - EMB1211
12) AT3G04340 - EMB2458
13) AT3G48110 - EDD1
14) AT1G30610 - EMB2279
15) AT2G31530 - EMB2289
16) AT1G10510 - EMB2004
17) AT3G20070 - TTN9
18) AT5G17710 - EMB1241
19) AT1G78630 - EMB1473
20) AT2G01620 - MEE11
21) AT1G67440 - EMB1688
22) AT5G63050 - EMB2759
23) AT3G02660 - EMB2768
24) AT3G29290 - EMB2076
25) AT4G29060 - EMB2726
26) AT4G24670 - TAR2
27) AT1G75350 - EMB2184
28) AT2G37920 - EMB1513
29) AT3G46560 - TIM9
30) AT5G48930 - EMB1080
31) AT5G48840 - PANC
32) AT1G78580 - AtTPS1
33) AT4G26500 - CPSUFE
34) AT5G23940 - EMB3009
35) AT2G22250 - AAT
36) AT2G34090 - MEE18
37) AT1G69770 - CMT3
38) AT3G52940 - FACKEL
39) AT3G15030 - TCP4
40) AT4G39620 - EMB2453
41) AT2G45270 - GCP1
42) AT5G18570 - GTP1
43) AT3G18110 - EMB1270
44) AT2G22870 - EMB2001
45) AT2G04030 - CRB8
46) AT1G55900 - TIM50
47) AT4G01560 - MEE49
48) AT2G18510 - EMB2444
49) AT4G26300 - EMB1027
50) AT5G23880 - CPSF100
51) AT5G62440 - DOMINO1
52) AT2G34630 - GPS1
53) AT2G28880 - EMB1997
54) AT3G61780 - EMB1703
55) AT2G34780 - MEE22
56) AT5G40480 - EMB3012
57) AT3G07060 - EMB1974
58) AT5G63420 - EMB2745
59) AT5G39710 - EMB2745
60) AT3G49240 - EMB1796
61) AT5G18820 - EMB3007
62) AT1G10270 - GRP23
63) AT3G20440 - EMB2729
Embryonic development cluster II
GO:0009790 (123/326)
64) AT2G46310 - CRF5
65) AT4G23750 - CRF2
66) AT3G47470 - AMP1
67) AT5G59340 - WOX2
68) AT3G10670 - AtNAP7
69) AT5G61410 - RPE
70) AT4G35510 - SRO1
71) AT1G70560 - TAA1
72) AT4G31820 - ENP
73) AT5G16750 - TOZ
74) AT5G19820 - EMB2734
75) AT1G80410 - EMB2753
76) AT1G79490 - EMB2217
77) AT2G38280 - FAC1
78) AT3G12670 - EMB2742
79) AT5G60540 - PDX2
80) AT1G36160 - ACC1
81) AT3G11270 - MEE34
82) AT5G27540 - MIRO1
83) AT5G10360 - EMB3010
84) AT4G11150 - TUF
85) AT3G27670 - RST1
86) AT2G18390 - TTN5
87) AT1G24340 - EMB2421
88) AT2G34790 - MEE23
89) AT1G60870 - MEE9
90) AT1G23080 - PIN7
91) AT2G19450 - TAG1
92) AT3G54650 - FBL17
93) AT5G42080 - ADL1
94) AT4G21710 - NRPB2
95) AT2G26060 - EMB1345
96) AT3G30300 - VPS46.2
97) AT5G42190 - ASK2
98) AT1G26830 - AtCUL3
99) AT4G00231 - MEE50
100) AT5G13710 - SMT1
101) AT4G36800 - RCE1
102) AT1G32230 - RCD1
103) AT3G19580 - AZF2
104) AT1G56010 - NAC1
105) AT1G13980 - GNOM
106) AT3G63080 - AtGPX5
107) AT5G24440 - EMB2024
108) AT3G14370 - WAG2
109) AT3G61630 - CRF6
110) AT2G25660 - EMB2410
111) AT1G32490 - ESP3
112) AT4G13940 - MEE58
113) AT1G15750 - TOPLESS
114) AT3G16830 - TOPLESS-related2
115) AT5G48750 - CDC2
116) AT5G05950 - MEE60
117) AT5G13010 - EMB3011
118) AT3G51840 - ACX4
119) AT4G37300 - MEE59
120) AT3G07780 - OBE1
121) AT2G15890 - MEE14
122) AT5G67570 - DG1
123) AT1G15220 - CCMH
Cell cycle GO:0007049 (39/123)
1) AT1G66750 - CAK4
2) AT3G15150 - HIGH PLOIDY2
3) AT2G34780 - MEE22
4) AT2G18290 - APC10
5) AT3G23580 - RNR2A
6) AT3G20780 - ATOP6B
7) AT1G18040 - DDKD1;3
8) AT3G19590 - BUB3
9) AT1G69770 - CMT3
10) AT1G78770 - APC6
11) AT3G22880 - DMC1
12) AT4G14150 - PAKRP1
13) AT1G76540 - CDKB2;1
14) AT1G20930 - CDKB2;2
15) AT3G23670 - KINESIN-12B
16) AT3G59550 - SYN3
17) AT5G51600 - PLEIADE
18) AT1G50240 - FUSED
19) AT3G11520 - CYCB1;3
20) AT4G05190 - AtK5
21) AT3G25980 - MAD2
22) AT1G03780 - TPX2
23) AT5G22000 - RHF2A
24) AT2G45280 - AtRAD51C
25) AT5G48720 - XRI1
26) AT3G27060 - TSO2
27) AT3G50630 - KRP2
28) AT3G43210 - TETRASPORE
29) AT1G05560 - UGT75B1
30) AT1G33240 - GTL1
31) AT2G32710 - KRP4
32) AT3G54650 - FBL17
33) AT5G04470 - SIAMESE
34) AT1G13980 - GNOM
35) AT2G44950 - HUB1
36) AT5G61210 - SNAP33
37) AT3G48750 - CDC2
38) AT5G42080 - ADL1
39) AT4G28980 - CAK1
Cell death GO:0008219 (44/80)
1) AT2G01290 - RPI2
2) AT3G46530 - RPP13
3) AT1G55490 - CPN60B
4) AT4G37000 - ACD2
5) AT4G37930 - SHM1
6) AT5G48030 - GFA2
7) AT5G15410 - DND1
8) AT4G35090 - CAT2
9) AT5G10380 - RING1
10) AT4G11280 - ACS6
11) AT3G27060 - TSO2
12) AT1G20850 - XCP2
13) AT2G46240 - BAG6
14) AT5G47910 - RBOHD
15) AT1G19250 - FMO1
16) AT3G13610 - 2OG-oxygenase
17) AT2G26560 - PLA2A
18) AT2G34770 - FAH1
19) AT3G44880 - ACD11
20) AT1G32540 - LOL1
21) AT1G12220 - RPS5
22) AT4G20870 - FAH2
23) AT5G64930 - CPR5
24) AT1G02860 - NLA
25) AT3G50260 - CEI1
26) AT4G26090 - RPS2
27) AT1G32230 - RCD1
28) AT3G20210 - Delta-VPE
29) AT3G16770 - AtEBP
30) AT2G30380 - LSD1
31) AT4G35790 - AtPLD-delta
32) AT3G28910 - MYB30
33) AT3G51840 - SOBIR1
34) AT5G35350 - XCP1
35) AT2G26300 - GP-alpha1
36) AT3G01420 - DOX1
37) AT3G11820 - SYP121
38) AT2G34690 - ACD11
39) AT1G64060 - ATRBOHF
40) AT5G61900 - BONZAI1
41) AT1G08720 - EDR1
42) AT1G02170 - METACAPASE1
Circadian rhythm GO:0007623 (30/43)
1) AT1G09340 - CRB
2) AT1G22770 - GI
3) AT2G40080 - ELF4
4) AT4G18790 - PHYB
5) AT2G21070 - FIO1
6) AT5G60100 - APRR3
7) AT5G24470 - APRR5
8) AT5G02810 - PRR7
9) AT2G46830 - CCA1
10) AT5G15850 - COL1
11) AT1G68830 - STN7
12) AT4G25100 - FSD1
13) AT4G18290 - KAT2
14) AT5G52910-TIMELESS
15) AT5G37260 - REVEILLE2
16) AT2G21660 - GRP7
17) AT5G57360 - ZTL
18) AT5G02840 - LCL1
19) AT3G48360 - BT2
20) AT3G48100 - ARR5
21) AT3G57040 - ARR9
22) AT2G18915 - LKP2
23) AT5G61380 - TOC1
24) AT3G22380 - TIC
25) AT2G18170 - AtMPK7
26) AT1G12910 - ATAN11
27) AT2G25930 - ELF3
28) AT5G10140 - FLC
29) AT1G04400 - CRY2
30) AT3G26640 - LWD2
Lipid transport GO:0006869 (9/16)
1) AT2G38540 - LP1
2) AT1G17840-WBC11
3) AT1G27950 - LTPG1
4) AT1G19800 - TGD1
5) AT5G59310 - LTP4
6) AT2G38530 - LTP2
7) AT3G06960 - PDE320
8) AT1G31812 - ACBP6
9) AT3G12740 - ALIS1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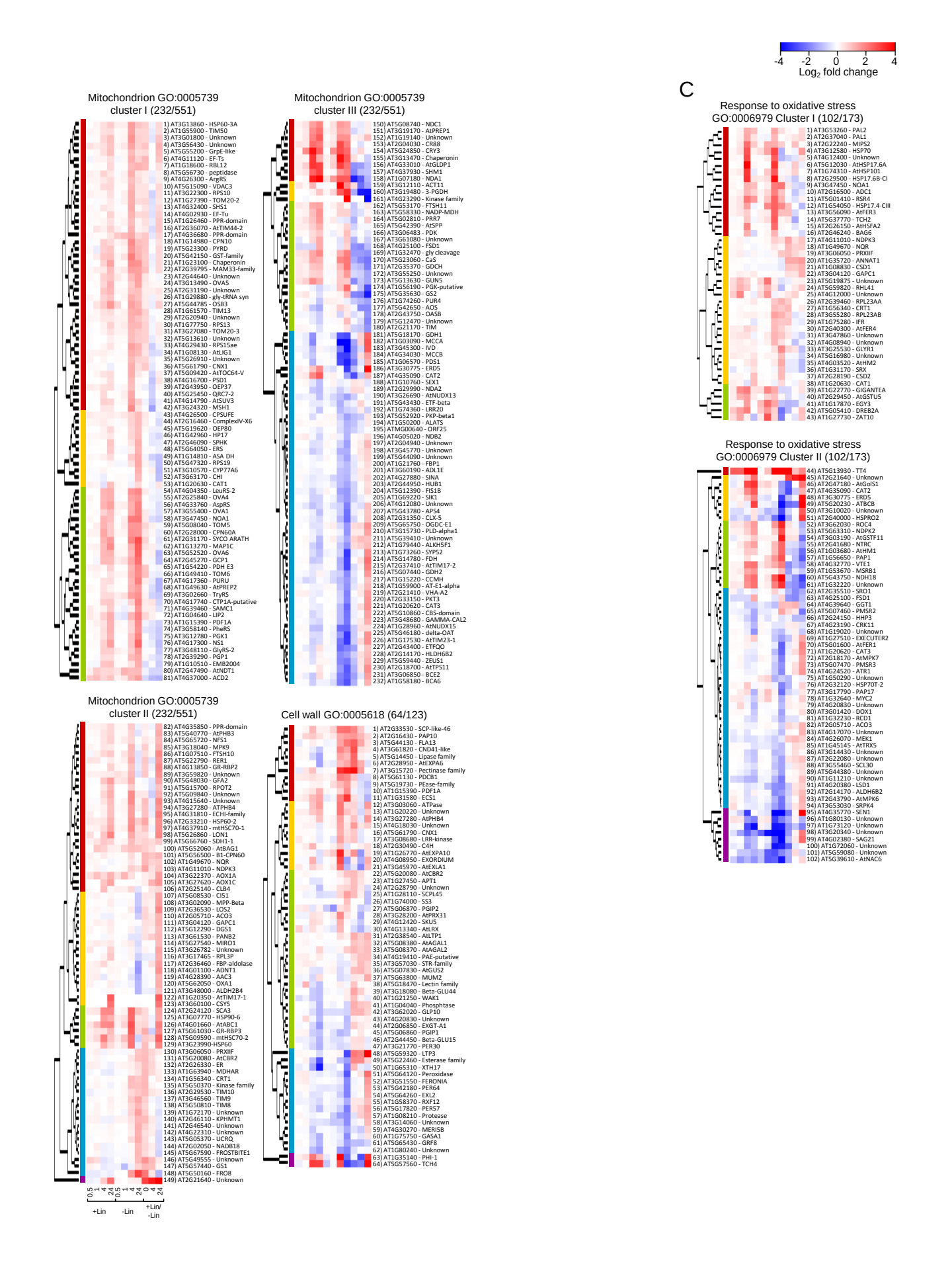
-4 -2 0 2 4
Log2 fold change
Plastid chromosome GO:0009508 (13/16)
1) AT2G34640 - PTAC12
2) AT4G20130 - PTAC14
3) AT3G48500 - PDE312
4) AT1G14410 - WHY1
5) AT5G54180 - PTAC15
6) AT3G09210 - PTAC13
7) AT1G74850 - PTAC2
8) AT4G20010 - PTAC9
9) AT1G21600 - PTAC6
10) AT3G46780 - PTAC16
11) AT2G46820 - PSI-P
12) AT4G13670 - PTAC5
13) AT1G65260 - PTAC4
Ubiquitin ligase complex GO:0000151 (19/42)
1) AT1G21410 - SKP2A
2) AT1G21780 - POZ-domain
3) AT3G45620 - DWD type A1
4) AT1G60110 - SKIP16
5) AT4G28450 - DWD type A1
6) AT4G11260 - SGT1B
7) AT4G03190 - GRH1
8) AT5G42190 - ASK2
9) AT3G25350 - EBF2
10) AT1G26830 - AtCUL3
11) AT4G35050 - MSI3
12) AT2G42620 - MAX2
13) AT3G62980 - TIR1
14) AT5G57360 - ZTL
15) AT2G39940 - COI1
16) AT3G01090 - AKIN10
17) AT4G05420 - DDB1A
18) AT5G57900 - SKIP1
19) AT2G32950 - COP1
Plastid ribosome GO:0009547 (16/24)
1) ATCG00770 - RPL33
2) ATCG00790 - RPL36
3) ATCG00780 - RPL14
4) ATCG00760 - RPL16
5) ATCG00750 - RPL22
6) ATCG00810 - RPL15
7) ATCG00820 - RPL9
8) ATCG00800 - RPS19
9) AT3G44890 - RPS16
10) AT3G25920 - RPS2
11) ATCG00160 - RPS14
12) ATCG00050 - RPS18
13) ATCG00330 - RPS11
14) ATCG01120 - RPS8
15) ATCG00650 - RPS3
16) ATCG00640 - RPS15
Cytosolic ribosome GO:0022626 (70/181)
1) AT3G05560 - RPL22B
2) AT1G77940 - RPL30B
3) AT1G18540 - RPL6A
4) AT3G23390 - RPL36aA
5) AT5G56710 - RPL31C
6) AT1G07070-RPL35aA
7) AT3G53890 - RPS21B
8) AT3G67000 - RPSL29A
9) AT2G39460 - RPL23AA
10) AT5G47930 - RPS27D
11) AT5G03850 - RPS28B
12) AT4G36670 - RPS30C
13) AT2G25210 - RPL39A
14) AT4G14320 - RPL36aB
15) AT2G43460 - RPL38A
16) AT3G10090 - RPS28A
17) AT4G29390 - RPS30B
18) AT4G31985 - RPL39C
19) AT2G20450 - RPL14A
20) AT2G19750 - RPS30A
21) AT3G16080 - RPL37C
22) AT4G00810 - RPP1B
23) AT2G19720 - RPS15AB
24) AT4G13170 - RPL13aC
25) AT5G22440 - RPL10aC
26) AT5G02870 - RPL4D
27) AT4G27710 - RPP2B
28) AT3G60770 - RPS13A
29) AT2G01250 - RPL7B
30) AT3G47370 - RPS20B
31) AT3G04840 - RPSaA
32) AT3G44590 - RPP2D
33) AT4G31700 - RPS6
34) AT5G59850 - RPS15aF
35) AT5G61170 - RPS19C
36) AT3G22230 - RPL27B
37) AT5G02610 - RPL35D
38) AT2G32060 - RPS12C
39) AT3G48930 - EMB1080
40) AT1G48830 - RPS7A
41) AT5G60670 - RPL12C
42) AT3G16780 - RPL19B
43) AT4G10450 - RPL90D
44) AT4G29430 - RPS15AE
45) AT3G55280 - RPL23AB
46) AT5G67510 - RPL26B
47) AT5G15750 - RPS9-family
48) AT1G80750 - RPL7A
49) AT3G11250 - RPP0C
50) AT5G59240 - RPS8B
51) AT4G30800 - RPS11B
52) AT3G04770 - RPSAb
53) AT2G32220 - RPL27A
54) AT3G09610 - RPS17C
55) AT2G36620 - RPL24A
56) AT2G37600 - RPL36A
57) AT2G45710 - RPS27A
58) AT5G64140 - RPS28
59) AT4G15000 - RPL27C
60) AT4G34555 - RPS25
61) AT3G06680 - RPL29B
62) AT1G23410 - RPS27A
63) AT2G40010 - RPP0A
64) AT1G61580 - RPL3B
65) AT5G27850 - RPL18C
66) AT4G02230 - RPL19C
67) AT5G10360 - EMB3010
68) AT3G09200 - RPP0B
69) AT1G25260 - RPP0-related
70) AT3G57490 - RPS2D
0.5 1 2 4 0.5 1 2 4 0 4 24
+Lin -Lin +Lin/ -Lin
Thylakoid membrane GO:0042651 (48/64)
1) AT1G64770 - NDF2
2) AT3G26060 - AtPRX Q
3) ATSG02120 - OHP
4) AT1G20020 - FNR2
5) AT1G70760 - CRR23
6) AT3G16000 - MFP1
7) ATSG12130 - PDE149
8) ATSG51545 - LPA2
9) AT4G34190 - SEP1
10) AT3G55090 - PLSP1
11) AT1G73990 - SPPA
12) AT5G42270 - VAR1
13) AT1G34000 - OHP2
14) AT1G50250 - FTSH1
15) AT2G21970 - SEP2
16) AT1G27510 - EXECUTER2
17) AT5G42080 - ADL1
18) ATCG00670 - CLPP
19) AT3G14440 - NCED3
20) AT2G47940 - DEGP2
21) ATSG45390 - CLPP4
22) AT1G08550 - NPQ1
23) AT1G24490 - ALBINIA 4
24) ATSG15700 - RPOT2
25) AT2G30950 - VAR2
26) AT2G47910 - CRR6
27) AT1G67080 - ABA4
28) ATCG00150 - ATPI
29) ATCG00120 - ATPA
30) ATCG00340 - PSAB
31) AT4G04640 - ATPC1
32) AT2G46820 - PSI-P
33) AT4G37200 - HCF164
34) AT4G03280 - PETC
35) AT3G56940 - CRD1
36) AT5G64040 - PSAN
37) AT1G44446 - CHLORINA 1
38) AT1G74880 - NDH-O
39) AT4G25080 - CHLM
40) AT4G10340 - LHCB5
41) AT1G55670 - PSAG
42) AT4G01050 - TROL
43) ATCG00630 - PSAJ
44) ATCG00070 - PSBK
45) AT1G15980 - NDF1
46) AT5G58260 - NDH-N
47) AT3G16250 - NDF4
48) AT1G44575 - NPQ4
Thylakoid lumen GO:0031977 (45/48)
1) AT5G52970 - TL 15 kDa protein
2) AT2G43560 - FKBP16-3
3) AT4G24930 - TLP17.9
4) AT4G02530 - TL16
5) ATSG56650 - PPD6
6) AT3G01480 - CYP38
7) ATSG39830 - DEG8
8) AT5G45680 - FKBP13
9) AT3G10060 - FKBP16-4
10) AT3G23400 - FIB4
11) AT1G77090 - PPD4
12) AT3G55330 - PPL1
13) AT3G15520 - TLP38
14) AT3G60370 - FKBP20-2
15) AT4G18370 - DEG5
16) AT5G23120 - HCF136
17) AT2G44920 - TL 15 kDa protein
18) AT3G50820 - PSBO2
19) AT1G08550 - NPQ1
20) AT1G54780 - TLP18.3
21) AT1G76450 - THL1
22) AT1G20340 - PETE2
23) AT5G53490 - TLP17.4
24) AT5G64040 - PSAN
25) AT1G06680 - PSBP-1
26) AT4G15510 - PPD1
27) AT4G09010 - APX4
28) AT5G13410 - FKBP19
29) AT5G13120 - CYP20-2
30) AT1G20810-FBK1
31) AT5G46390 - CTPA-related
32) AT4G17740 - CTPA-related
33) AT3G47860 - Apolipoprotein
34) AT3G58010 - FIB7a
35) AT1G03600 - PSB27
36) AT5G66570 - PSBO1
37) AT5G35100 - CYP28
38) AT2G30790 - PSBP2
39) AT1G76100 - PETE1
40) AT5G05180 - PSBQ-2
41) AT1G14150 - PSBQ3.1
42) AT2G39470 - PPL2
43) AT4G39710 - FKBP16-2
44) AT4G21280 - PSBQ
45) AT3G01440 - PSBQ3.2
Plastid membrane GO:0042170 (57/104)
1) AT2G20890 - PSB29
2) AT4G30950 - FAD6C
3) AT1G33810 - GDSL-lipase 1
4) AT3G20320 - TGD2
5) AT4G14070 - AAE15
6) AT5G19620 - TOC75-V
7) AT1G42960 - HP17
8) AT1G78620 - HP34
9) AT4G16155 - PTLPD2
10) AT3G51140 - HP28
11) AT1G06950 - TIC110
12) ATSG45550 - OEP16-like
13) AT5G53280 - PDV1
14) AT2G47490 - AtNDT1
15) AT3G17970 - TOC64-III
16) AT1G26340 - CBS-A
17) AT1G07420 - SMO2
18) AT2G43950 - OEP37
19) AT5G22790 - RER1
20) AT1G19800 - TGD1
21) AT4G33350 - TIC22
22) AT5G01220 - SQD2
23) AT3G59970 - PGP51
24) AT3G60620 - CDP-DAG-synthase
25) AT1G77590 - LACS9
26) AT4G15440 - HPL-like
27) AT1G03160 - FZL
28) AT3G19720 - ARC5
29) AT5G51020 - CRL
30) AT5G17520 - RCP1
31) AT5G12470 - HP35b
32) AT5G42650 - AOS
33) AT1G08570 - ACHT4
34) AT1G02280 - TOC33
35) AT4G03320 - TIC20-IV
36) AT3G55030 - PGPS2
37) AT3G60590 - HP36b
38) AT2G33380 - RD20
39) AT3G44880 - ACD1
40) AT4G25650 - TIC55-like
41) AT5G13720 - HP29c
42) AT5G28750 - THA4
43) AT4G25050 - ACP4
44) AT4G32770 - VTE1
45) AT2G34460 - TIC62-like
46) AT3G61870 - HP29b
47) AT1G32080 - HP45
48) AT2G24820 - TIC55
49) AT5G13630 - GUN5
50) AT3G25690 - CHUP1
51) AT3G56940 - CRD1
52) AT1G44446 - CHLORINA1
53) AT3G46780 - TIC62-like
54) AT3G10840 - SAR5-binding
55) AT3G63160 - OEP6
56) AT3G14210 - GDSL-lipase like
57) AT3G45140 - LOX2
Plastid stroma GO:0009532 (80/117)
1) AT1G14410-WHY1
2) AT4G33680 - AGD2
3) AT4G20010 - PTAC9
4) AT4G24280 - cpHSC70-1
5) AT4G26500 - CPSUFE
6) AT1G32440 - PKp3
7) AT1G74850 - PTAC2
8) AT3G48500 - PDE312
9) AT2G44650 - CHL-CPN10
10) AT3G52720 - ACA1
11) AT2G34640 - PTAC12
12) AT5G45390 - CLPP4
13) AT2G20890 - PSB29
14) AT1G11750 - CLPP6
15) AT2G47940 - DEGP2
16) AT4G20130 - PTAC14
17) AT5G23120 - HCF136
18) AT1G21600 - PTAC6
19) AT1G32200 - ATS1
20) AT4G18480 - CHL11
21) AT3G26060 - AtPRX Q
22) AT3G62030 - ROC4
23) AT5G45930 - CHL12
24) AT3G52750 - FTSZ2-2
25) ATSG09650 - AtPPa6
26) AT5G55280 - FTSZ2-1
27) AT5G54180 - PTAC15
28) AT3G09210 - PTAC13
29) AT1G66670 - CLPP3
30) AT5G17790 - VAR3
31) AT3G44890 - RPL9
32) AT3G25920 - RPL15
33) AT5G51820 - PGM
34) AT3G16000 - MFP1
35) AT2G21330 - FBA1
36) AT4G38970 - FBA2
37) AT1G20020 - FNR2
38) AT1G60950 - FEDA
39) AT2G46820 - PSI-P
40) AT5G52100 - CRR1
41) AT3G15840 - PIFI
42) AT1G67740 - PSBY
43) AT3G46780 - PTAC16
44) AT1G10500 - AtCPYSCA
45) AT1G49970 - CLPR1
46) AT5G03940 - CPSRP54
47) AT4G13670 - PTAC5
48) ATCG00330 - RPS14
49) ATCG01120 - RPS15
50) ATCG00280 - PSBC
51) ATCG00640 - RPL33
52) ATCG00650 - RPS18
53) AT4G10340 - LHCB5
54) ATCG00770 - RPS8
55) ATCG00790 - RPL16
56) ATCG00780 - RPL14
57) ATCG00760 - RPL36
58) ATCG00750 - RPS11
59) ATCG00810 - RPL22
60) ATCG00820 - RPS19
61) ATCG00800 - RPS3
62) AT2G42540 - COR15A
63) AT3G09650 - HCF152
64) AT4G34740 - AtASE2
65) AT2G04030 - CR88
66) ATSG49910 - cpHSC70-2
67) AT4G17090 - CT-BMY
68) AT1G08570 - ACHT4
69) AT3G22960 - PKP-ALPHA
70) AT5G51070 - ERD1
71) ATCG00160 - RPS2
72) ATCG00670 - CLPP
73) AT1G79460 - GA2
74) ATCG00050 - RPS16
75) AT3G14440 - NCED3
76) AT2G29630 - THIC
77) AT4G34350 - HDR
78) AT1G65260 - PTAC4
79) AT3G16950 - LPD1
80) AT5G52920 - PKP-BETA1
Plastoglobule GO:0010287 (49/56)
1) AT2G34460 - Flavin reductase
2) AT1G79600 - ABC1-family
3) AT4G32770 - VTE1
4) AT1G06690 - Unknown
5) AT3G23400 - FIB4
6) ATSG08740 - NDC1
7) AT1G54570 - PPH-related
8) AT4G31390 - ABC1-family
9) AT2G41040 - UBIE-family
10) AT1G71810 - ABC1-family
11) AT4G19170 - NCED4
12) AT3G50820 - PSBO2
13) AT2G46910 - FIB8
14) AT1G78140 - UBIE-family
15) AT2G39730 - RCA
16) AT4G38970 - FBA2
17) AT2G21330 - FBA1
18) AT1G32220 - Flavin reductase
19) AT3G63140 - CSP41A
20) AT1G09340 - CRB
21) AT4G09650 - ATPD
22) AT2G20260 - PSAE-2
23) AT4G02770 - PSAD-1
24) AT4G28750 - PSAE-1
25) AT1G52230 - PSAH2
26) AT3G54890 - LHCA1
27) AT1G15820 - LHCB6
28) AT5G05200 - ABC1-family
29) AT1G52590 - Unknown
30) AT2G42130 - FIB7b
31) AT1G26090 - Unknown
32) AT2G35490 - FIB2
33) AT3G58010 - FIB7a
34) AT5G42650 - AOS
35) ATCG00490 - RBCL
36) ATCG00120 - ATP-alpha
37) ATCG00340 - PSAB
38) AT4G01150 - Unknown
39) ATCG00280 - PSBC
40) ATCG00680 - PSB6
41) ATCG00350 - PSAA
42) ATCG00270 - PSBD
43) AT5G66570 - PSBO1
44) ATCG00020 - PSBA
45) AT1G31330 - PSAF
46) AT4G10340 - LHCB5
47) AT5G01530 - LHCB4
48) AT4G15510 - LHCA3
49) AT3G47470 - LHCA4
Stromule GO:0010319 (22/33)
1) AT3G11630 - BAS1
2) AT2G20890 - PSB29
3) AT3G12780 - PGK1
4) AT1G55490 - CPN60B
5) AT5G51820 - PGM
6) AT5G06290 - 2-Cys PrxB
7) AT1G60580 - ATFRX-m1
8) AT1G16880 - Unknown
9) AT1G26340 - CBS-A
10) AT1G19940 - NMAR
11) ATCG00120 - ATPase-alpha
12) AT3G26650 - GAPA
13) ATSG61410 - RPE
14) AT4G35090 - CAT2
15) AT4G37930 - SHM1
16) AT2G39730 - RCA
17) AT1G42970 - GAPB
18) AT1G23740 - Oxidoreductase
19) AT1G09340 - CRB
20) AT4G09650 - ATP-delta
21) AT1G32060 - PRK
22) AT3G54050 - FBP
23) AT3G01500 - CA1
Endoplasmic reticulum GO:0005783 (103/267)
1) AT5G13930 - TT4
2) AT4G36220 - FAH1
3) AT3G55120 - TT5
4) AT1G23010 - LPF1
5) AT5G42800 - DFR
6) AT3G57020 - STR-family
7) AT1G56340 - CRT1
8) AT5G07340 - Calnexin
9) AT5G61790 - CNX1
10) AT2G38360 - PRA1.B4
11) AT2G02810 - UTR1
12) AT3G05230 - SPase-putative
13) AT4G29520 - Unknown
14) AT5G03160 - At5S8IPK
15) AT1G18540 - RPL6A
16) AT4G21180 - AtERDJ2B
17) AT2G20450 - RPL14A
18) AT5G24810 - ABC1-family
19) AT4G36250 - ALDH3F1
20) AT1G25450 - KCS5
21) AT1G78510 - SPS1
22) AT5G52420 - Unknown
23) AT5G27330 - Unknown
24) AT2G15090 - KCS8
25) AT5G37300 - WSD1
26) AT1G57750 - CYP96A15
27) AT4G33790 - ECERIFERUM4
28) AT1G19300 - PARVUS
29) AT1G17700 - PRA1.F1
30) AT4G03510 - RMA1
31) AT1G76490 - HMG1
32) AT5G20520 - WAX2
33) AT5G57655 - Xyl-isomerase
34) AT2G47770 - TSPO-related
35) AT5G44920 - TIR
36) AT1G07720 - KCS3
37) AT5G42570 - Unknown
38) AT2G29980 - FAD3
39) AT3G57010 - STR-family
40) AT3G57030 - STR-family
41) AT5G64440 - AtFAAH
42) AT5G43460 - Unknown
43) AT1G13710 - CYP78A5
44) AT1G77510 - PDI-like 1-2
45) AT4G14420 - Unknown
46) AT4G01510 - ARV2
47) AT3G15710 - SPase-putative
48) AT1G54990 - AXR4
49) AT2G28630 - KCS12
50) AT1G69640 - SBH1
51) AT2G30490 - C4H
52) AT2G26250 - KCS10
53) AT4G30210 - ATR2
54) AT5G07110 - PRA1.B6
55) AT1G76090 - SMT3
56) AT1G14290 - SBH2
57) AT3G23190 - Unknown
58) AT3G26830 - PAD3
59) AT4G37330 - CYP81D4
60) AT3G50660 - DWF4
61) AT4G20070 - AtAAH
62) AT4G28270 - RMA2
63) AT1G05160 - CYP88A3
64) AT4G27470 - RMA3
65) AT4G24520 - ATR1
66) AT2G33630 - 3-beta-HSD
67) AT2G26300 - GP-alpha1
68) AT1G55850 - AtCSLE1
69) AT2G17520 - IRE1A
70) AT4G25970 - PSD3
71) AT3G51430 - YLS2
72) AT5G02100 - UNE18
73) AT1G29330 - ERD2
74) AT1G18260 - SEL1-related
75) AT3G60600 - VAP27
76) AT5G65160 - RHD3
77) AT1G66340 - ETR1
78) AT4G20870 - FAH2
79) AT5G47990 - CYP70A5
80) AT1G09070 - SRC2
81) AT4G27500 - PPI1
82) AT3G57880 - C2-domain
83) AT3G10800 - b2IP28
84) AT3G44330 - Unknown
85) AT2G42810 - PPS.2
86) AT4G22330 - AtCES1
87) AT1G42990 - b2IP60
88) AT1G08770 - PRA1.E
89) AT3G13870 - RHD3
90) AT5G48000 - CYP708A2
91) AT4G32650 - AtKC1
92) AT3G02875 - ILR1
93) AT3G14610 - CYP72A7
94) AT3G13720 - PRA8
95) AT2G01470 - STL12P
96) AT3G12120 - FAD2
97) AT3G51440 - STR-family
98) AT3G03330 - SDR-family
99) AT4G16170 - Unknown
100) AT3G06960 - PDE320
101) AT1G27980 - DPL1
102) AT5G23670 - LCB2
103) AT5G19660 - S1P
Photosystem I GO:0009522 (8/9)
1) AT1G45474 - LHCA5
2) AT2G46820 - PSI-P
3) AT5G64040 - PSAN
4) AT1G08380 - PSAO
5) AT5G56720 - PSAG
6) ATCG00340 - PSAB
7) ATCG00350 - PSAA
8) ATCG00630 - PSAJ
Photosystem II GO:0009523 (14/15)
1) AT3G01440 - PSBQ
2) AT1G73990 - SPPA
3) AT1G08550 - NPQ1
4) AT1G15820 - LHCB6
5) ATCG00710 - PSBH
6) ATCG00020 - PSBA
7) ATCG00280 - PSBC
8) ATCG00340 - PSAB
9) ATCG00680 - PSB6
10) ATCG00270 - PSBD
11) AT4G10340 - LHCB5
12) ATCG00580 - PSBE
13) ATCG00480 - PSBI
14) ATCG00070 - PSBK
NAD(P)H dehydrogenase complex GO:0010598 (9/9)
1) AT1G15980 - NDF1
2) AT5G58260 - NDH-N
3) AT3G16250 - NDF4
4) AT5G39210 - CRR7
5) AT1G64770 - NDF2
6) AT2G01590 - CRR3
7) AT1G70760 - CRR23
8) AT1G18730 - NDF6
9) AT1G74880 - NDH-O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Response to oxidative stress
GO:0006979 Cluster I (102/173)
1) AT3G53260 - PAL2
2) AT2G37040 - PAL1
3) AT2G22240 - MIPS2
4) AT3G12580 - HSP70
5) AT4G12400 - Unknown
6) AT5G12030 - AtHSP17.6A
7) AT1G74310 - AtHSP101
8) AT2G29500 - HSP17.6B-CI
9) AT3G47450 - NOA1
10) AT2G16500 - ADC1
11) AT5G01410 - RSR4
12) AT1G54050 - HSP17.4-CIII
13) AT3G56090 - AtFER3
14) AT5G37770 - TCH2
15) AT2G26150 - AtHSFA2
16) AT2G46240 - BAG6
17) AT4G11010 - NDPK3
18) AT1G49670 - NQR
19) AT3G06050 - PRXIIF
20) AT1G35720 - ANNAT1
21) AT1G08830 - CSD1
22) AT3G04120 - GAPC1
23) AT5G19875 - Unknown
24) AT5G59820 - RHL41
25) AT4G12000 - Unknown
26) AT2G39460 - RPL23AA
27) AT1G56340 - CRT1
28) AT3G55280 - RPL23AB
29) AT1G75280 - IFR
30) AT2G40300 - AtFER4
31) AT3G47860 - Unknown
32) AT4G08940 - Unknown
33) AT3G25530 - GLYR1
34) AT5G16980 - Unknown
35) AT4G03520 - AtHM2
36) AT1G31170 - SRX
37) AT2G28190 - CSD2
38) AT1G20630 - CAT1
39) AT1G22770 - GIGANTEA
40) AT2G29450 - AtGSTU5
41) AT1G17870 - EGY3
42) AT5G05410 - DREB2A
43) AT1G27730 - ZAT10
Response to oxidative stress
GO:0006979 Cluster II (102/173)
44) AT5G13930 - TT4
45) AT2G21640 - Unknown
46) AT2G47180 - AtGolS1
47) AT4G35090 - CAT2
48) AT3G30775 - ERD5
49) AT5G20230 - ATBCB
50) AT3G10020 - Unknown
51) AT2G40000 - HSPRO2
52) AT3G62030 - ROC4
53) AT5G63310 - NDPK2
54) AT3G03190 - AtGSTF11
55) AT2G41680 - NTRC
56) AT1G03680 - AtHM1
57) AT1G56650 - PAP1
58) AT4G32770 - VTE1
59) AT1G53670 - MSRB1
60) AT5G43750 - NDH18
61) AT1G32220 - Unknown
62) AT2G35510 - SRO1
63) AT4G25100 - FSD1
64) AT4G39640 - GGT1
65) AT5G07460 - PMSR2
66) AT2G24150 - HHP3
67) AT4G23190 - CRK11
68) AT1G19020 - Unknown
69) AT1G27510 - EXECUTER2
70) AT5G01600 - AtFER1
71) AT1G20620 - CAT3
72) AT2G18170 - AtMPK7
73) AT5G07470 - PMSR3
74) AT4G24520 - ATR1
75) AT1G50290 - Unknown
76) AT2G32120 - HSP70T-2
77) AT3G17790 - PAP17
78) AT1G32640 - MYC2
79) AT4G20830 - Unknown
80) AT3G01420 - DOX1
81) AT1G32230 - RCD1
82) AT2G05710 - ACO3
83) AT4G17070 - Unknown
84) AT4G26070 - MEK1
85) AT1G45145 - AtTRX5
86) AT3G14430 - Unknown
87) AT2G20080 - Unknown
88) AT3G55460 - SCL30
89) AT5G44380 - Unknown
90) AT1G11210 - Unknown
91) AT4G20380 - LSD1
92) AT2G14170 - ALDH6B2
93) AT2G43790 - AtMPK6
94) AT3G53030 - SRPK4
95) AT4G35770 - SEN1
96) AT1G80130 - Unknown
97) AT1G73120 - Unknown
98) AT3G20340 - Unknown
99) AT4G02380 - SAG21
100) AT1G72060 - Unknown
101) AT5G59080 - Unknown
102) AT5G39610 - AtNAC6
Mitochondrion GO:0005739
cluster I (232/551)
1) AT3G13860 - HSP60-3A
2) AT1G55900 - TIM50
3) AT3G01800 - Unknown
4) AT3G56430 - Unknown
5) AT5G55200 - GrpE-like
6) AT4G11120 - EF-Ts
7) AT1G18600 - RBL12
8) AT5G56730 - peptidase
9) AT4G26300 - ArgRS
10) AT5G15090 - VDAC3
11) AT3G22300 - RPS10
12) AT1G27390 - TOM20-2
13) AT4G32400 - SHS1
14) AT4G02930 - EF-Tu
15) AT1G26460 - PPR-domain
16) AT2G36070 - AtTIM44-2
17) AT4G36680 - PPR-domain
18) AT1G14980 - CPN10
19) AT5G23300 - PYRD
20) AT5G42150 - GST-family
21) AT1G23100 - Chaperonin
22) AT2G39795 - MAM33-family
23) AT2G44640 - Unknown
24) AT3G13490 - OVA5
25) AT2G31190 - Unknown
26) AT1G29880 - gly-tRNA syn
27) AT5G44785 - OSB3
28) AT1G61570 - TIM13
29) AT2G20940 - Unknown
30) AT1G77750 - RPS13
31) AT3G27080 - TOM20-3
32) AT5G13610 - Unknown
33) AT4G29430 - RPS15ae
34) AT1G08130 - AtLIG1
35) AT5G26910 - Unknown
36) AT5G61790 - CNX1
37) AT5G09420 - AtTOC64-V
38) AT4G16700 - PSD1
39) AT2G43950 - OEP37
40) AT5G25450 - QRC7-2
41) AT4G14790 - AtSUV3
42) AT3G24320 - MSH1
43) AT4G26500 - CPSUFE
44) AT2G16460 - ComplexIV-X6
45) AT5G19620 - OEP80
46) AT1G42960 - HP17
47) AT2G46090 - SPHK
48) AT5G64050 - ERS
49) AT1G14810 - ASA_DH
50) AT5G47320 - RPS19
51) AT3G10570 - CYP77A6
52) AT3G63170 - CHI
53) AT1G20630 - CAT1
54) AT4G04350 - LeuRS-2
55) AT2G25840 - OVA4
56) AT4G33760 - AspRS
57) AT3G55400 - OVA1
58) AT3G47450 - NOA1
59) AT5G08040 - TOM5
60) AT2G28000 - CPN60A
61) AT2G31170 - SYCO ARATH
62) AT1G13270 - MAP1C
63) AT5G52520 - OVA6
64) AT2G45270 - GCP1
65) AT1G54220 - PDH E3
66) AT1G49410 - TOM6
67) AT4G17360 - PURU
68) AT1G49630 - AtPREP2
69) AT3G02660 - TryRS
70) AT4G17740 - CTP1A-putative
71) AT4G39460 - SAMC1
72) AT1G04640 - LIP2
73) AT1G15390 - PDF1A
74) AT3G58140 - PheRS
75) AT3G12780 - PGK1
76) AT4G17300 - NS1
77) AT3G48110 - GlyRS-2
78) AT2G39290 - PGP1
79) AT1G10510 - EMB2004
80) AT2G47490 - AtNDT1
81) AT4G37000 - ACD2
Mitochondrion GO:0005739
cluster III (232/551)
150) AT5G08740 - NDC1
151) AT3G19170 - AtPREP1
152) AT1G19140 - Unknown
153) AT2G04030 - CR88
154) AT5G24850 - CRY3
155) AT3G13470 - Chaperonin
156) AT4G33010 - AtGLDP1
157) AT4G37930 - SHM1
158) AT1G07180 - NDA1
159) AT3G12110 - ACT11
160) AT3G19480 - 3-PGDH
161) AT4G23290 - Kinase family
162) AT5G53170 - FTSH11
163) AT5G58330 - NADP-MDH
164) AT5G02810 - PRR7
165) AT5G42390 - AtSPP
166) AT3G06483 - PDK
167) AT3G61080 - Unknown
168) AT4G25100 - FSD1
169) AT1G32470 - gly cleavage
170) AT5G23060 - CaS
171) AT2G35370 - GDCH
172) AT3G55250 - Unknown
173) AT5G13630 - GUN5
174) AT1G56190 - PGK-putative
175) AT5G35630 - GS2
176) AT1G74260 - PUR4
177) AT5G42650 - AOS
178) AT2G43750 - OASB
179) AT5G12470 - Unknown
180) AT2G21170 - TIM
181) AT5G18170 - GDH1
182) AT1G03090 - MCCA
183) AT3G45300 - IVD
184) AT4G34030 - MCCB
185) AT1G06570 - PDS1
186) AT3G30775 - ERD5
187) AT4G35090 - CAT2
188) AT1G10760 - SEX1
189) AT2G29990 - NDA2
190) AT3G26690 - AtNUDX13
191) AT5G43430 - ETF-beta
192) AT1G74360 - LRR20
193) AT5G52920 - PKP-beta1
194) AT1G50200 - ALATS
195) ATMG00640 - ORF25
196) AT4G05020 - NDB2
197) AT2G04940 - Unknown
198) AT3G45770 - Unknown
199) AT5G44090 - Unknown
200) AT1G21760 - FBP1
201) AT3G60190 - ADL1E
202) AT4G27880 - SINA
203) AT2G44950 - HUB1
204) AT5G12390 - FIS1B
205) AT1G69220 - SIK1
206) AT4G12080 - Unknown
207) AT5G43780 - APS4
208) AT2G31350 - CLK-5
209) AT5G65750 - OGDC-E1
210) AT3G15730 - PLD-alpha1
211) AT5G39410 - Unknown
212) AT1G79440 - ALKHSF1
213) AT1G73260 - SYP52
214) AT5G14780 - FDH
215) AT2G37410 - AtTIM17-2
216) AT5G07440 - GDH2
217) AT1G15220 - CCMH
218) AT1G59900 - AT-E1-alpha
219) AT2G21410 - VHA-A2
220) AT2G33150 - PKT3
221) AT1G20620 - CAT3
222) AT5G10860 - CBS-domain
223) AT3G48680 - GAMMA-CAL2
224) AT1G28960 - AtNUDX15
225) AT5G46180 - delta-OAT
226) AT1G17530 - AtTIM23-1
227) AT2G43400 - ETFQO
228) AT2G14170 - HLDH6B2
229) AT5G59440 - ZEUS1
230) AT2G18700 - AtTPS11
231) AT3G06850 - BCE2
232) AT1G58180 - BCA6
Mitochondrion GO:0005739
cluster II (232/551)
82) AT4G35850 - PPR-domain
83) AT5G40770 - AtPHB3
84) AT5G65720 - NFS1
85) AT3G18040 - MPK9
86) AT1G07510 - FTSH10
87) AT5G22790 - RER1
88) AT4G13850 - GR-RBP2
89) AT3G59820 - Unknown
90) AT5G48030 - GFA2
91) AT5G15700 - RPOT2
92) AT5G09840 - Unknown
93) AT4G15640 - Unknown
94) AT3G27280 - ATPHB4
95) AT4G31810 - ECHI-family
96) AT2G33210 - HSP60-2
97) AT4G37910 - mtHSC70-1
98) AT5G26860 - LON1
99) AT5G66760 - SDH1-1
100) AT5G52060 - AtBAG1
101) AT5G56500 - B1-CPN60
102) AT1G49670 - NQR
103) AT4G11010 - NDPK3
104) AT3G22370 - AOX1A
105) AT3G27620 - AOX1C
106) AT3G25140 - CL84
107) AT5G08530 - CIS1
108) AT3G02090 - MPP-Beta
109) AT2G36530 - LOS2
110) AT2G05710 - ACO3
111) AT3G04120 - GAPC1
112) AT5G12290 - DGS1
113) AT3G61530 - PANB2
114) AT3G27540 - MRP1
115) AT3G26782 - Unknown
116) AT3G17465 - RPL3P
117) AT2G36460 - FBP-aldolase
118) AT4G01100 - ADNT1
119) AT4G28390 - AAC3
120) AT5G62050 - OXA1
121) AT3G48000 - ALDH2B4
122) AT1G20350 - AtTIM17-1
123) AT3G60100 - CSY5
124) AT2G24120 - SCA3
125) AT3G07770 - HSP90-6
126) AT4G01660 - AtABC1
127) AT5G61030 - GR-RBP3
128) AT5G09590 - mtHSC70-2
129) AT3G23990-HSP60
130) AT3G06050 - PRXIIF
131) AT5G20080 - AtCBR2
132) AT3G26330 - ER
133) AT1G63940 - MDHAR
134) AT1G56340 - CRT1
135) AT5G50370 - Kinase family
136) AT2G29530 - TIM10
137) AT3G46560 - TIM9
138) AT5G50810 - TIM8
139) AT1G72170 - Unknown
140) AT2G46110 - KPHMT1
141) AT2G46540 - Unknown
142) AT4G22310 - Unknown
143) AT5G05370 - UCRQ
144) AT2G02050 - NAD8I8
145) AT5G67590 - FROSTBITE1
146) AT5G49555 - Unknown
147) AT5G57440 - GS1
148) AT5G50160 - FRO8
149) AT2G21640 - Unknown
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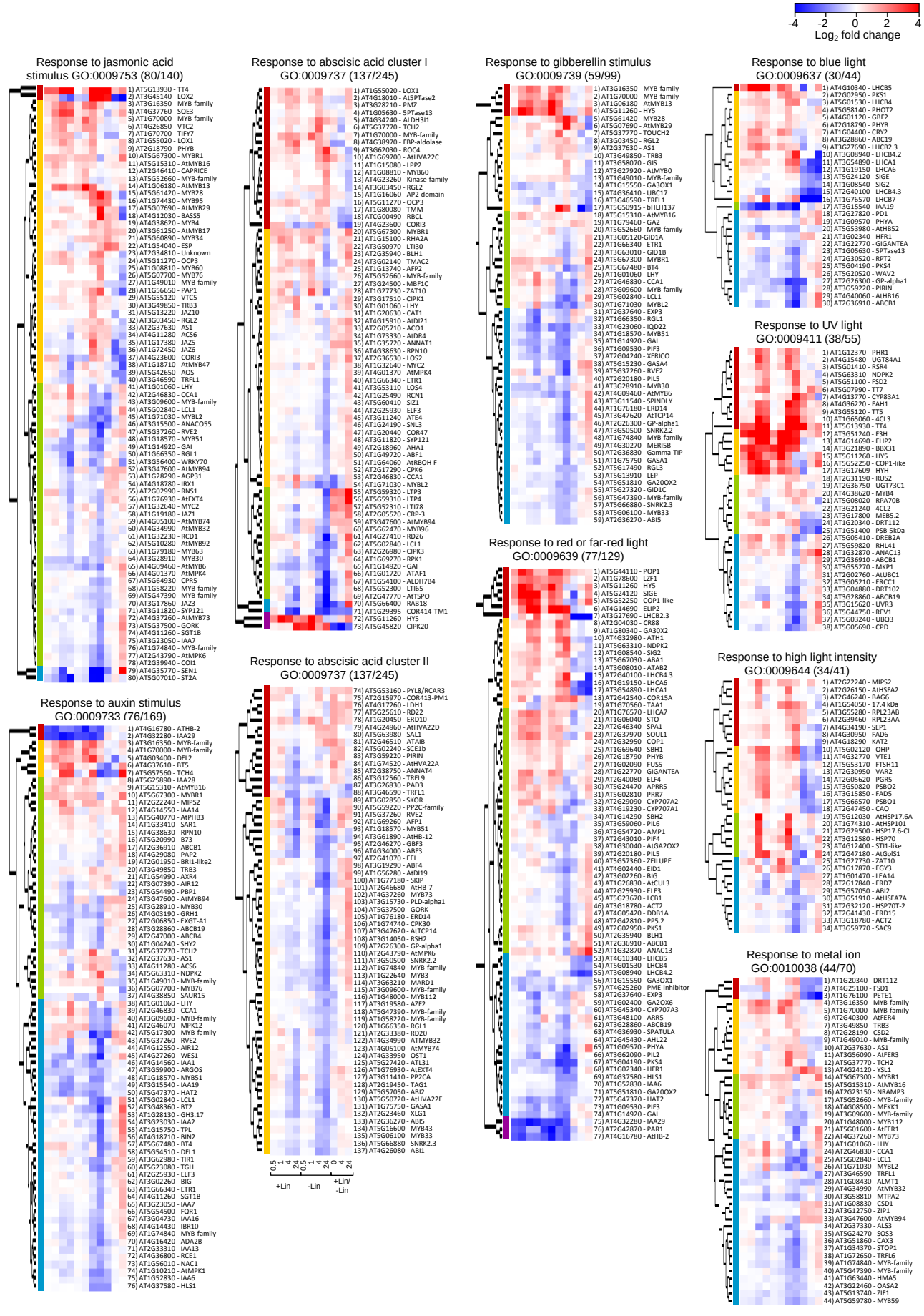
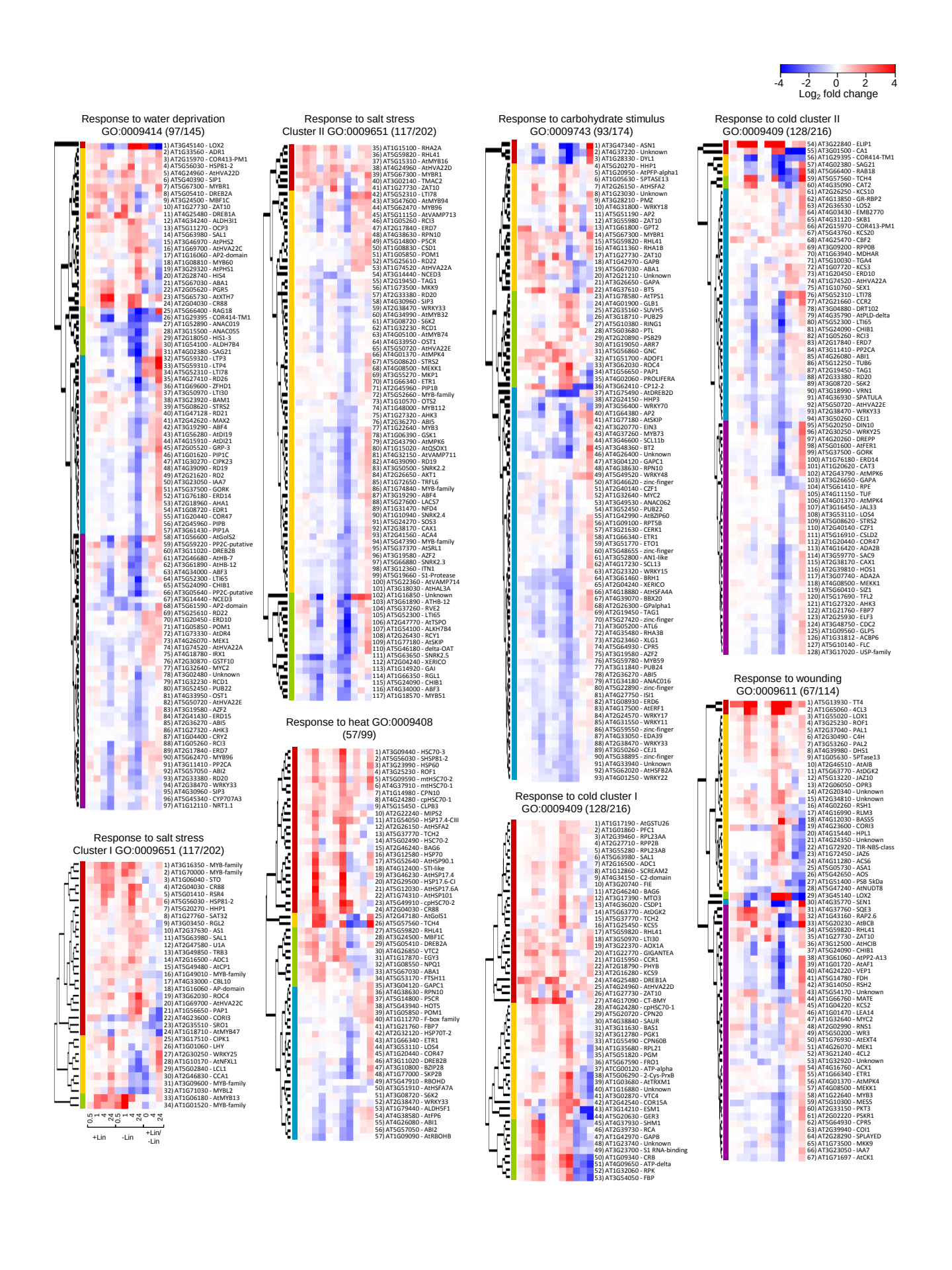
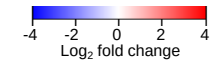
Cell wall GO:0005618 (64/123)
1) AT2G33530 - SCP-like-46
2) AT2G16430 - PAP10
3) AT5G44130 - FLA13
4) AT3G61820 - CND41-like
5) AT5G14450 - Lipase family
6) AT2G28950 - AtEXPA6
7) AT3G15720 - Pectinase family
8) AT5G61130 - PDCB1
9) AT5G19730 - PEase-family
10) AT1G15390 - PDF1A
11) AT1G31580 - ECS1
12) AT3G03060 - ATPase
13) AT1G20220 - Unknown
14) AT3G27280 - AtPHB4
15) AT4G18030 - Unknown
16) AT5G61790 - CNX1
17) AT3G08680 - LRR-kinase
18) AT2G30490 - C4H
19) AT1G26770 - AtEXPA10
20) AT4G08950 - EXORDIUM
21) AT3G45970 - AtEXLA1
22) AT5G20080 - AtCBR2
23) AT1G27450 - APT1
24) AT2G28790 - Unknown
25) AT1G28110 - SCPL45
26) AT1G74000 - SS3
27) AT5G06870 - PGIP2
28) AT3G28200 - AtPRX31
29) AT4G12420 - SKU5
30) AT4G13340 - AtLRX
31) AT2G38540 - AtLTP1
32) AT5G08380 - AtAGAL1
33) AT5G08370 - AtAGAL2
34) AT4G19410 - PAE-putative
35) AT3G57030 - STR-family
36) AT5G07830 - AtGUS2
37) AT5G63800 - MUM2
38) AT5G18470 - Lectin family
39) AT3G18080 - Beta-GLU44
40) AT1G21250 - WAK1
41) AT1G04040 - Phosphtase
42) AT3G62020 - GLP10
43) AT4G20830 - Unknown
44) AT2G06850 - EXGT-A1
45) AT5G06860 - PGIP1
46) AT2G44450 - Beta-GLU15
47) AT3G21770 - PER30
48) AT5G59320 - LTP3
49) AT5G22460 - Esterase family
50) AT1G65310 - XTH17
51) AT5G64120 - Peroxidase
52) AT3G51550 - FERONIA
53) AT5G42180 - PER64
54) AT5G64260 - EXL2
55) AT1G58370 - RXF12
56) AT5G17820 - PER57
57) AT1G08210 - Protease
58) AT3G14060 - Unknown
59) AT4G30270 - MERI5B
60) AT1G75750 - GASA1
61) AT5G65430 - GRF8
62) AT1G80240 - Unknown
63) AT1G35140 - PHI-1
64) AT5G57560 - TCH4

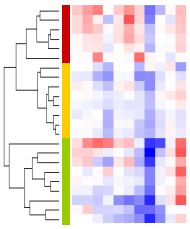

-4 -2 0 2 4
Log2 fold change
Response to jasmonic acid stimulus GO:0009753 (80/140)
1) AT5G13930 - TT4
2) AT3G45140 - LOX2
3) AT3G16350 - MYB-family
4) AT4G37760 - SQE3
5) AT1G70000 - MYB-family
6) AT4G26850 - VTC2
7) AT1G70700 - TIFY7
8) AT1G55020 - LOX1
9) AT2G18790 - PHYB
10) AT5G67300 - MYB81
11) AT5G15310 - AtMYB16
12) AT2G46410 - CAPRICE
13) AT5G52660 - MYB-family
14) AT1G06180 - AtMYB13
15) AT5G61420 - MYB28
16) AT1G74430 - MYB95
17) AT5G07690 - AtMYB29
18) AT5G42030 - BASS5
19) AT4G38620 - MYB4
20) AT3G61250 - AtMYB17
21) AT5G60890 - MYB34
22) AT1G64040 - ESP
23) AT2G34810 - Unknown
24) AT5G11270 - OCP3
25) AT1G08810 - MYB60
26) AT5G60700 - MYB76
27) AT1G49010 - MYB-family
28) AT1G56650 - PAP1
29) AT5G55120 - VTC5
30) AT3G49850 - TRB3
31) AT5G13220 - JAZ10
32) AT3G03450 - RGL2
33) AT2G37630 - AS1
34) AT4G31280 - ACS6
35) AT1G17380 - JAZ5
36) AT1G72450 - JAZ6
37) AT4G23600 - CORI3
38) AT1G28710 - AtMYB47
39) AT5G42650 - AOS
40) AT3G46590 - TRFL1
41) AT1G01060 - LHY
42) AT2G46830 - CCA1
43) AT3G09600 - MYB-family
44) AT5G02840 - LCL1
45) AT1G01030 - MYBL2
46) AT3G15500 - ANACO55
47) AT5G37260 - RVE2
48) AT1G18570 - MYB51
49) AT1G14920 - GAI
50) AT1G66350 - RGL1
51) AT3G56400 - WRKY70
52) AT3G47600 - AtMYB94
53) AT2G28290 - AGP31
54) AT4G18780 - IRX1
55) AT2G02990 - RNS1
56) AT1G76930 - AtEXT4
57) AT1G32640 - MYC2
58) AT1G19180 - JAZ1
59) AT4G05100 - AtMYB74
60) AT4G34990 - AtMYB32
61) AT1G52230 - RCD1
62) AT5G10280 - AtMYB92
63) AT1G79180 - MYB63
64) AT3G28910 - MYB30
65) AT4G09460 - AtMYB6
66) AT4G01370 - AtMPK4
67) AT5G64930 - CPR5
68) AT1G58220 - MYB-family
69) AT5G47390 - MYB-family
70) AT3G17860 - JAZ3
71) AT3G11820 - SYP121
72) AT4G37260 - AtMYB73
73) AT5G37500 - GORK
74) AT4G11260 - SGT1B
75) AT3G23050 - IAA7
76) AT1G74840 - MYB-family
77) AT2G43790 - AtMPK6
78) AT2G39940 - COI1
79) AT4G35770 - SEN1
80) AT5G07010 - ST2A
Response to auxin stimulus GO:0009733 (76/169)
1) AT4G16780 - ATHB-2
2) AT4G32280 - IAA29
3) AT3G16350 - MYB-family
4) AT1G70000 - MYB-family
5) AT4G03400 - DFL2
6) AT4G37610 - BT5
7) AT5G57560 - TCH4
8) AT5G25890 - IAA28
9) AT5G15310 - AtMYB16
10) AT5G67300 - MYB81
11) AT2G22240 - MIPS2
12) AT4G14550 - IAA14
13) AT4G40370 - AtPHB3
14) AT1G33410 - SAR1
15) AT4G38630 - RPN10
16) AT5G20990 - B73
17) AT4G09810 - ABCB1
18) AT4G29080 - PAP2
19) AT2G01950 - BRI1-like2
20) AT3G49850 - TRB3
21) AT1G54990 - AXR4
22) AT3G07390 - AIR12
23) AT5G54490 - PBP1
24) AT3G47600 - AtMYB94
25) AT3G28910 - MYB30
26) AT4G03190 - GRH1
27) AT2G06850 - EXGT-A1
28) AT3G28860 - ABCB19
29) AT2G47000 - ABCB4
30) AT1G04240 - SHY2
31) AT5G37770 - TCH2
32) AT2G37630 - AS1
33) AT4G31280 - ACS6
34) AT5G63310 - NDPK2
35) AT1G49010 - MYB-family
36) AT5G07700 - MYB76
37) AT4G38850 - SAUR15
38) AT1G01060 - LHY
39) AT2G46830 - CCA1
40) AT3G09600 - MYB-family
41) AT2G46070 - MPK12
42) AT5G17300 - MYB-family
43) AT5G37260 - RVE2
44) AT4G12550 - AIR12
45) AT4G27260 - WES1
46) AT4G14560 - IAA1
47) AT3G59900 - ARGOS
48) AT1G18570 - MYB51
49) AT3G15540 - IAA19
50) AT5G47370 - HAT2
51) AT5G02840 - LCL1
52) AT3G58360 - BT2
53) AT1G28130 - GH3.17
54) AT3G23030 - IAA2
55) AT1G15750 - TPL
56) AT4G18710 - BIN2
57) AT5G67480 - BT4
58) AT5G54510 - DFL1
59) AT3G62980 - TIR1
60) AT5G03080 - TGH
61) AT2G25930 - ELF3
62) AT3G02260 - BIG
63) AT1G66340 - ETR1
64) AT4G11260 - SGT1B
65) AT3G23050 - IAA7
66) AT5G54500 - FQR1
67) AT3G04730 - IAA16
68) AT4G14430 - IBR10
69) AT1G74840 - MYB-family
70) AT4G16420 - ADA2B
71) AT2G33310 - IAA13
72) AT4G36800 - RCE1
73) AT1G56010 - NAC1
74) AT1G10210 - AtMPK1
75) AT1G52830 - IAA6
76) AT4G37580 - HLS1
Response to abscisic acid cluster I GO:0009737 (137/245)
1) AT1G55020 - LOX1
2) AT4G18010 - At5PTase2
3) AT3G28210 - PMZ
4) AT1G05630 - 5PTase13
5) AT4G34240 - ALDH3I1
6) AT5G37770 - TCH2
7) AT1G70000 - MYB-family
8) AT4G38970 - FBP-aldolase
9) AT3G62030 - ROC4
10) AT1G69700 - AtHVA22C
11) AT1G15080 - LPP2
12) AT1G08810 - MYB60
13) AT4G23260 - Kinase-family
14) AT3G03450 - RGL2
15) AT4G01060 - AP2-domain
16) AT5G11270 - OCP3
17) AT1G80080 - TMM
18) AT4G00490 - RBCL
19) AT4G23600 - CORI3
20) AT5G67300 - MYB81
21) AT1G15100 - RHA2A
22) AT3G59970 - LTI30
23) AT2G35940 - BLH1
24) AT3G02140 - TMAC2
25) AT1G13740 - AFP2
26) AT5G52660 - MYB-family
27) AT3G24500 - MBF1C
28) AT1G27730 - ZAT10
29) AT3G17510 - CIPK1
30) AT1G01060 - LHY
31) AT1G20630 - CAT1
32) AT4G15910 - AtDI21
33) AT2G05710 - ACO1
34) AT1G73330 - AtDR4
35) AT1G35720 - ANNAT1
36) AT4G38630 - RPN10
37) AT2G36530 - LOS2
38) AT1G32640 - MYC2
39) AT4G01370 - AtMPK4
40) AT1G66340 - ETR1
41) AT3G53110 - LOS4
42) AT1G25490 - RCN1
43) AT5G60410 - SIZ1
44) AT2G25930 - ELF3
45) AT3G11240 - ATE4
46) AT1G71030 - MYBL2
47) AT1G20440 - COR47
48) AT3G11820 - SYP121
49) AT2G18960 - AHA1
50) AT1G69720 - ABF1
51) AT1G64060 - AtRBOH F
52) AT2G17290 - CPK6
53) AT2G46830 - CCA1
54) AT1G71030 - MYBL2
55) AT5G59320 - LTP3
56) AT5G59310 - LTP4
57) AT5G52310 - LTI78
58) AT2G05520 - CRP-3
59) AT3G47600 - AtMYB94
60) AT5G62470 - MYB96
61) AT4G27410 - RD26
62) AT5G02840 - LCL1
63) AT2G26980 - CIPK3
64) AT1G69270 - RPK1
65) AT1G14920 - GAI
66) AT1G01720 - ATAF1
67) AT1G54100 - ALDH7B4
68) AT5G52300 - LTI65
69) AT2G47770 - AtTPO
70) AT5G66400 - RAB18
71) AT1G29395 - COR414-TM1
72) AT5G11260 - HYS
73) AT5G45820 - CIPK20
Response to abscisic acid cluster II GO:0009737 (137/245)
74) AT5G53160 - PYL8/RCAR3
75) AT2G15970 - COR413-PM1
76) AT4G17260 - LDH1
77) AT5G25610 - RD22
78) AT1G20450 - ERD10
79) AT4G29360 - AtHVA22D
80) AT5G63980 - SAL1
81) AT2G46510 - ATAIB
82) AT5G02240 - SCE1b
83) AT3G04120 - PIRIN
84) AT1G74520 - AtHVA22A
85) AT2G38750 - ANNAT4
86) AT3G12360 - TRFL9
87) AT3G28860 - PAD3
88) AT3G46590 - TRFL1
89) AT3G02850 - SKOR
90) AT5G59220 - PP2C-family
91) AT5G37260 - RVE2
92) AT1G69260 - AFP1
93) AT1G18570 - MYB51
94) AT3G50890 - AtHB-12
95) AT2G46270 - GBF3
96) AT4G34000 - ABF3
97) AT2G41070 - EEL
98) AT3G62420 - ABF4
99) AT1G56280 - AtDi19
100) AT1G77180 - SKIP
101) AT2G46680 - AtHB-7
102) AT4G37260 - MYB73
103) AT3G15730 - PLD-alpha1
104) AT5G37500 - GORK
105) AT1G76180 - ERD14
106) AT1G74740 - CPK30
107) AT3G47620 - AtTCP14
108) AT3G14050 - RSH2
109) AT2G46300 - GP-alpha1
110) AT2G43790 - AtMPK6
111) AT3G50500 - SNRK2.2
112) AT1G74840 - MYB-family
113) AT1G22640 - MYB3
114) AT3G63210 - MARD1
115) AT3G09600 - MYB-family
116) AT1G48000 - MYB112
117) AT3G19580 - AZF2
118) AT5G47390 - MYB-family
119) AT1G58220 - MYB-family
120) AT1G66350 - RGL1
121) AT2G33380 - RD20
122) AT4G34990 - ATMYB32
123) AT4G05100 - AtMYB74
124) AT4G33950 - OST1
125) AT5G27420 - ATL31
126) AT1G76930 - AtEXT4
127) AT3G14410 - PP2CA
128) AT2G19450 - TAG1
129) AT5G57050 - ABI2
130) AT5G50720 - AtHVA22E
131) AT1G75750 - GASA1
132) AT2G23460 - XLG1
133) AT2G36270 - ABI5
134) AT5G16600 - MYB43
135) AT5G06100 - MYB33
136) AT5G66880 - SNRK2.3
137) AT4G26080 - ABI1
0.5 4 24 0.5 4 24 0 24
+Lin -Lin +Lin/ -Lin
Response to gibberellin stimulus GO:0009739 (59/99)
1) AT3G16350 - MYB-family
2) AT1G70000 - MYB-family
3) AT3G06180 - AtMYB13
4) AT5G11260 - HY5
5) AT5G61420 - MYB28
6) AT5G07690 - AtMYB29
7) AT5G37770 - TOUCH2
8) AT3G03450 - RGL2
9) AT2G37630 - AS1
10) AT1G55310 - AtMYB16
11) AT3G58070 - GIS
12) AT3G27920 - AtMYB0
13) AT1G49010 - MYB-family
14) AT5G01550 - GA3OX1
15) AT4G36410 - UBC17
16) AT3G46590 - TRFL1
17) AT5G50915 - bHLH137
18) AT5G15310 - AtMYB16
19) AT1G79460 - GA2
20) AT5G52660 - MYB-family
21) AT3G05120-GID1A
22) AT1G66340 - ETR1
23) AT3G63010 - GID1B
24) AT5G67300 - MYB81
25) AT5G67480 - BT4
26) AT5G01060 - LHY
27) AT2G46830 - CCA1
28) AT3G09600 - MYB-family
29) AT5G02840 - LCL1
30) AT1G71030 - MYBL2
31) AT2G37640 - EXP3
32) AT1G66350 - RGL1
33) AT4G23060 - KDJ22
34) AT1G18570 - MYB51
35) AT1G14920 - GAI
36) AT1G09530 - PIF3
37) AT2G04240 - XERICO
38) AT5G15230 - GASA4
39) AT5G37260 - RVE2
40) AT2G20180 - PIL5
41) AT3G28910 - MYB30
42) AT4G09460 - AtMYB6
43) AT3G11540 - SPINDLY
44) AT1G76180 - ERD14
45) AT3G47620 - AtTCP14
46) AT2G26300 - GP-alpha1
47) AT3G50500 - SNRK2.2
48) AT1G74840 - MYB-family
49) AT4G38270 - MERI5B
50) AT2G36830 - Gamma-TIP
51) AT1G75750 - GASA1
52) AT5G17490 - RGL3
53) AT5G13910 - LEP
54) AT5G51810 - GA2OX2
55) AT5G27320 - GID1C
56) AT5G47390 - MYB-family
57) AT5G66880 - SNRK2.3
58) AT5G06100 - MYB33
59) AT2G36270 - ABI5
Response to red or far-red light GO:0009639 (77/129)
1) AT5G44110 - POP1
2) AT1G78600 - LZF1
3) AT5G11260 - HY5
4) AT5G24120 - SIGE
5) AT5G52250 - COP1-like
6) AT4G14690 - ELIP2
7) AT3G27690 - LHCB2.3
8) AT2G04030 - CR88
9) AT1G80340 - GA3OX2
10) AT4G32980 - ATH1
11) AT5G63310 - NDPK2
12) AT1G08540 - SIG2
13) AT5G67030 - ABA1
14) AT3G08010 - ATAB2
15) AT2G40100 - LHCB4.3
16) AT1G19150 - LHCA6
17) AT3G54890 - LHCA1
18) AT2G42540 - COR15A
19) AT1G70560 - TAA1
20) AT1G76570 - LHCA7
21) AT1G06040 - STO
22) AT2G46340 - SPA1
23) AT2G37970 - SOUL1
24) AT2G32950 - COP1
25) AT1G69640 - SBH1
26) AT2G18790 - PHYB
27) AT1G02090 - FUS5
28) AT1G22770 - GIGANTEA
29) AT2G40080 - ELF4
30) AT5G24470 - APRR5
31) AT5G02810 - PRR7
32) AT2G29090 - CYP707A2
33) AT4G19230 - CYP707A1
34) AT1G14290 - SBH2
35) AT3G59060 - PIL6
36) AT3G54720 - AMP1
37) AT2G43010 - PIF4
38) AT1G30040 - AtGA2OX2
39) AT2G20180 - PIL5
40) AT5G57360 - ZEILUPE
41) AT4G02440 - EID1
42) AT5G02260 - BIG
43) AT1G26830 - AtCUL3
44) AT2G25930 - ELF3
45) AT5G23670 - LCB1
46) AT3G18780 - ACT2
47) AT4G05420 - DDB1A
48) AT2G42810 - PP5.2
49) AT2G02950 - PKS1
50) AT2G35940 - BLH1
51) AT2G36910 - ABCB1
52) AT1G32870 - ANAC13
53) AT4G10340 - LHCB5
54) AT5G01530 - LHCB4
55) AT3G08940 - LHCB4.2
56) AT1G15550 - GA3OX1
57) AT4G25260 - PHE-inhibitor
58) AT2G37640 - EXP3
59) AT1G02400 - GA2OX6
60) AT5G45340 - CYP707A3
61) AT3G48100 - ARR5
62) AT3G28860 - ABCB19
63) AT4G36930 - SPATULA
64) AT2G45430 - AHL22
65) AT1G09570 - PHYA
66) AT3G62090 - PIL2
67) AT5G04190 - PKS4
68) AT1G02340 - HFR1
69) AT4G37580 - HLS1
70) AT1G52830 - IAA6
71) AT5G51810 - GA2OX2
72) AT5G47370 - HAT2
73) AT1G09530 - PIF3
74) AT1G14920 - GAI
75) AT4G32280 - IAA29
76) AT2G42870 - PAR1
77) AT4G16780 - ATHB-2
Response to blue light GO:0009637 (30/44)
1) AT4G10340 - LHCB5
2) AT2G05990 - PKS1
3) AT5G01530 - LHCB4
4) AT5G58140 - PHOT2
5) AT4G01120 - GBF2
6) AT2G18790 - PHYB
7) AT1G04400 - CRY2
8) AT3G28860 - ABC19
9) AT3G27690 - LHCB2.3
10) AT3G08940 - LHCB4.2
11) AT3G54890 - LHCA1
12) AT1G19150 - LHCA6
13) AT5G24120 - SIGE
14) AT1G08540 - SIG2
15) AT2G40100 - LHCB4.3
16) AT1G76570 - LHCB7
17) AT3G15540 - IAA19
18) AT2G27820 - PD1
19) AT1G09570 - PHYA
20) AT5G53980 - AtHB52
21) AT1G02340 - HFR1
22) AT1G22770 - GIGANTEA
23) AT1G05630 - 5PTase13
24) AT2G30520 - RPT2
25) AT5G04190 - PKS4
26) AT5G20520 - WAV2
27) AT2G26300 - GP-alpha1
28) AT3G59220 - PIRIN
29) AT4G40060 - AtHB16
30) AT2G36910 - ABCB1
Response to UV light GO:0009411 (38/55)
1) AT1G12370 - PHR1
2) AT4G15480 - UGT84A1
3) AT5G01410 - RSR4
4) AT5G63310 - NDPK2
5) AT5G51100 - FSD2
6) AT5G07990 - TT7
7) AT4G13770 - CYP83A1
8) AT4G36220 - FAH1
9) AT3G55120 - TT5
10) AT1G65060 - 4CL3
11) AT5G13930 - TT4
12) AT3G51240 - F3H
13) AT4G14690 - ELIP2
14) AT3G21890 - BBX31
15) AT5G11260 - HY5
16) AT5G52250 - COP1-like
17) AT3G17609 - HYH
18) AT2G31190 - RUS2
19) AT2G36750 - UGT73C1
20) AT4G38620 - MYB4
21) AT5G08020 - RPA70B
22) AT3G21240 - 4CL2
23) AT3G17800 - MEB5.2
24) AT1G20340 - DRT112
25) AT1G51400 - PSB-5kDa
26) AT5G05410 - DREB2A
27) AT5G59820 - RHL41
28) AT1G32870 - ANAC13
29) AT2G36910 - ABCB1
30) AT3G55270 - MKP1
31) AT2G02760 - ATUBC1
32) AT3G05210 - ERCC1
33) AT3G04880 - DRT102
34) AT3G28860 - ABCB19
35) AT3G15620 - UVR3
36) AT5G44750 - REV1
37) AT5G03240 - UBQ3
38) AT5G05690 - CPD
Response to high light intensity GO:0009644 (34/41)
1) AT2G22240 - MIPS2
2) AT2G26150 - AtHSFA2
3) AT2G46240 - BAG6
4) AT1G54050 - 17.4 kDa
5) AT3G55280 - RPL23AB
6) AT2G39460 - RPL23AA
7) AT4G34190 - SFR1
8) AT4G30950 - FAD6
9) AT4G18290 - KAT2
10) AT5G02120 - OHP
11) AT4G32770 - VTE1
12) AT5G53170 - FTSH11
13) AT2G30950 - VAR2
14) AT2G05620 - PGR5
15) AT3G50820 - PSBO2
16) AT3G15850 - FAD5
17) AT5G66570 - PSBO1
18) AT2G47450 - CAO
19) AT5G12030 - AtHSP17.6A
20) AT1G74310 - AtHSP101
21) AT2G29500 - HSP17.6-CI
22) AT3G12580 - HSP70
23) AT4G12400 - STT1-like
24) AT2G47180 - AtGolS1
25) AT1G27730 - ZAT10
26) AT1G17870 - EGY3
27) AT1G01470 - LEA14
28) AT2G17840 - ERD7
29) AT5G57050 - ABI2
30) AT3G51910 - AtHSFA7A
31) AT3G22120 - HSP70T-2
32) AT2G41430 - ERD15
33) AT3G18780 - ACT2
34) AT3G59770 - SAC9
Response to metal ion GO:0010038 (44/70)
1) AT1G20340 - DRT112
2) AT4G25100 - FSD1
3) AT1G76100 - PETE1
4) AT3G16350 - MYB-family
5) AT1G70000 - MYB-family
6) AT2G40300 - AtFER4
7) AT3G49850 - TRB3
8) AT2G28190 - CSD2
9) AT1G49010 - MYB-family
10) AT2G37630 - AS1
11) AT3G56090 - AtFER3
12) AT5G37770 - TCH2
13) AT4G24120 - YSL1
14) AT5G67300 - MYB81
15) AT5G15310 - AtMYB16
16) AT2G23150 - NRAMP3
17) AT5G52660 - MYB-family
18) AT4G08500 - MEKK1
19) AT3G09600 - MYB-family
20) AT1G48000 - MYB112
21) AT5G01600 - AtFER1
22) AT4G37260 - MYB73
23) AT1G01060 - LHY
24) AT2G46830 - CCA1
25) AT5G02840 - LCL1
26) AT1G71030 - MYBL2
27) AT3G46590 - TRFL1
28) AT1G08430 - ALMT1
29) AT4G34990 - AtMYB32
30) AT3G58810 - MTPA2
31) AT1G08830 - CSD1
32) AT3G12750 - ZIP1
33) AT3G47600 - AtMYB94
34) AT2G37330 - ALS3
35) AT5G24270 - SOS3
36) AT3G51860 - CAX3
37) AT1G43370 - STOP1
38) AT1G72650 - TRFL6
39) AT1G74840 - MYB-family
40) AT5G47390 - MYB-family
41) AT1G63440 - HMA5
42) AT3G22460 - OASA2
43) AT5G13740 - ZIF1
44) AT5G59780 - MYB59


-4 -2 0 2 4
Log2 fold change
Response to water deprivation
GO:0009414 (97/145)
1) AT3G45140 - LOX2
2) AT1G33560 - ADR1
3) AT2G15970 - COR413-PM1
4) AT5G56030 - HSP81-2
5) AT4G24960 - AtHVA22D
6) AT5G40390 - SIP1
7) AT5G67300 - MYBR1
8) AT1G05410 - DREB2A
9) AT3G24500 - MBF1C
10) AT1G27730 - ZAT10
11) AT4G25480 - DREB1A
12) AT4G34240 - ALDH3I1
13) AT5G11270 - OCP3
14) AT5G63980 - SAL1
15) AT3G46970 - AtPHS2
16) AT1G69700 - AtHVA22C
17) AT1G16060 - AP2-domain
18) AT1G08810 - MYB60
19) AT3G29320 - AtPHS1
20) AT2G28740 - HIS4
21) AT5G67030 - ABA1
22) AT2G05620 - PGR5
23) AT5G65730 - AtXTH7
24) AT2G04030 - CRB8
25) AT5G66400 - RAG18
26) AT1G29395 - COR414-TM1
27) AT1G52890 - ANAC019
28) AT3G15500 - ANAC055
29) AT2G18050 - HIS1-3
30) AT1G54100 - ALDH7B4
31) AT4G02380 - SAG21
32) AT5G59320 - LTP3
33) AT5G59310 - LTP4
34) AT5G52310 - LTI78
35) AT4G27410 - RD26
36) AT1G69600 - ZFHD1
37) AT3G50970 - LTI30
38) AT3G23920 - BAM1
39) AT5G08620 - STRS2
40) AT1G47128 - RD21
41) AT2G42620 - MAX2
42) AT3G19290 - ABF4
43) AT1G56280 - AtDI19
44) AT4G15910 - AtDI21
45) AT2G05520 - GRP-3
46) AT1G01620 - PIP1C
47) AT1G30270 - CIPK23
48) AT4G39090 - RD19
49) AT2G21620 - RD2
50) AT3G23050 - IAA7
51) AT5G37500 - GORK
52) AT1G76180 - ERD14
53) AT2G18960 - AHA1
54) AT1G08720 - EDR1
55) AT1G20440 - COR47
56) AT2G45960 - PIP8
57) AT3G61430 - PIP1A
58) AT1G56600 - AtGolS2
59) AT5G59220 - PP2C-putative
60) AT3G11020 - DREB2B
61) AT2G46680 - AtHB-7
62) AT3G61890 - AtHB-12
63) AT4G34000 - ABF3
64) AT5G52300 - LTI65
65) AT5G24090 - CHIB1
66) AT4G05640 - PP2C-putative
67) AT3G44440 - NCED3
68) AT5G61590 - AP2-domain
69) AT5G25610 - RD22
70) AT1G20450 - ERD10
71) AT1G05850 - POM1
72) AT1G73330 - AtDR4
73) AT4G26070 - MEK1
74) AT1G64520 - AtHVA22A
75) AT4G18780 - IRX1
76) AT2G30870 - GSTF10
77) AT1G32640 - MYC2
78) AT3G05880 - Unknown
79) AT1G32230 - RCD1
80) AT3G52450 - PUB22
81) AT4G33950 - OST1
82) AT5G50720 - AtHVA22E
83) AT3G19580 - AZF2
84) AT2G41430 - ERD15
85) AT2G36270 - ABI5
86) AT4G27320 - AHK3
87) AT1G04400 - CRY2
88) AT1G05260 - RCI3
89) AT2G17840 - ERD7
90) AT5G62470 - MYB96
91) AT3G11410 - PP2CA
92) AT5G57050 - ABI2
93) AT2G33380 - RD20
94) AT2G38470 - WRKY33
95) AT4G30960 - SIP3
96) AT5G45340 - CYP707A3
97) AT1G12110 - NRT1.1
Response to salt stress
Cluster II GO:0009651 (117/202)
35) AT1G15100 - RHA2A
36) AT5G59820 - RHL41
37) AT5G15310 - AtMYB16
38) AT4G24960 - AtHVA22D
39) AT5G67300 - MYBR1
40) AT3G02140 - TMAC2
41) AT1G27730 - ZAT10
42) AT5G52310 - LTI78
43) AT3G47600 - AtMYB94
44) AT5G62470 - MYB96
45) AT5G11150 - AtVAMP713
46) AT1G05260 - RCI3
47) AT2G17840 - ERD7
48) AT4G38630 - RPN10
49) AT5G14800 - PSCR
50) AT1G08830 - CSD1
51) AT1G05850 - POM1
52) AT5G25610 - RD22
53) AT1G74520 - AtHVA22A
54) AT3G14440 - NCED3
55) AT2G19450 - TAG1
56) AT1G73500 - MKK9
57) AT2G33380 - RD20
58) AT4G30960 - SIP3
59) AT2G38470 - WRKY33
60) AT4G34990 - AtMYB32
61) AT3G08720 - SGK2
62) AT1G32230 - RCD1
63) AT4G05100 - AtMYB74
64) AT4G33950 - OST1
65) AT5G50720 - AtHVA22E
66) AT4G01370 - AtMPK4
67) AT5G08620 - STRS2
68) AT4G08570 - MEKK1
69) AT3G55270 - MKP1
70) AT1G66340 - ETR1
71) AT2G45960 - PIP1B
72) AT5G52660 - MYB-family
73) AT1G10570 - OTS2
74) AT1G48000 - MYB112
75) AT1G27320 - AHK3
76) AT2G36270 - ABI5
77) AT1G22640 - MYB3
78) AT1G06390 - GSK1
79) AT2G43790 - AtMPK6
80) AT1G15020 - AtQSOX1
81) AT4G32150 - AtVAMP711
82) AT4G39090 - RD19
83) AT3G50500 - SNRK2.2
84) AT2G26650 - AKT1
85) AT1G72650 - TRFL6
86) AT1G74840 - MYB-family
87) AT3G19290 - ABF4
88) AT5G27600 - LACS7
89) AT1G31450 - NFD4
90) AT1G10940 - SNRK2.4
91) AT5G24270 - SOS3
92) AT2G38170 - CAX1
93) AT2G41560 - CCA4
94) AT5G47390 - MYB-family
95) AT5G37370 - AtSRL1
96) AT3G19580 - AZF2
97) AT5G66880 - SNRK2.3
98) AT3G12360 - ITN1
99) AT5G19660 - S1-Protease
100) AT5G22360 - AtVAMP714
101) AT3G18030 - AtHAL3A
102) AT1G16850 - Unknown
103) AT3G61890 - AtHB-12
104) AT5G37260 - RVE2
105) AT5G52300 - LTI65
106) AT2G47770 - AtTSPO
107) AT1G54100 - ALKH7B4
108) AT2G26430 - RCY1
109) AT1G77180 - AtSKIP
110) AT5G46180 - delta-OAT
111) AT5G63650 - SNRK2.5
112) AT2G04240 - XERICO
113) AT1G14920 - GAI
114) AT1G66150 - RGL1
115) AT5G24090 - CHIB1
116) AT4G34000 - ABF3
117) AT1G18570 - MYB51
Response to carbohydrate stimulus
GO:0009743 (93/174)
1) AT3G47340 - ASN1
2) AT4G37220 - Unknown
3) AT1G28330 - DYL1
4) AT5G20270 - HHP1
5) AT1G20950 - AtPFP-alpha1
6) AT1G05630 - 5PTASE13
7) AT2G26150 - AtHSFA2
8) AT1G23030 - Unknown
9) AT3G28210 - PMZ
10) AT4G31800 - WRKY18
11) AT5G51190 - AP2
12) AT2G55980 - ZAT10
13) AT1G61800 - GPT2
14) AT5G67300 - MYBR1
15) AT5G59820 - RHL41
16) AT4G11360 - RHA1B
17) AT1G27730 - ZAT10
18) AT1G42970 - GAPB
19) AT5G67030 - ABA1
20) AT2G21210 - Unknown
21) AT3G26650 - GAPA
22) AT4G37610 - BT5
23) AT1G78580 - AtTPS1
24) AT4G01900 - GLB1
25) AT2G35160 - SUVH5
26) AT3G18710 - PUB29
27) AT5G10380 - RING1
28) AT5G03680 - PTL
29) AT2G20890 - PSB29
30) AT1G19050 - ARR7
31) AT5G56860 - GNC
32) AT1G51700 - ADOF1
33) AT3G62030 - ROC4
34) AT1G56650 - PAP1
35) AT4G02060 - PROLIFERA
36) AT3G62410 - CP12-2
37) AT1G75490 - AtDREB2D
38) AT2G24150 - HHP3
39) AT3G56400 - WRKY70
40) AT1G64380 - AP2
41) AT1G77180 - AtSKIP
42) AT3G20770 - EIN3
43) AT4G37260 - MYB73
44) AT3G46600 - SCL11b
45) AT3G48360 - BT2
46) AT4G26400 - Unknown
47) AT3G04120 - GAPC1
48) AT4G38630 - RPN10
49) AT5G49520 - WRKY48
50) AT3G46620 - zinc-finger
51) AT5G40140 - CZF1
52) AT1G32640 - MYC2
53) AT3G49530 - ANAC062
54) AT3G52450 - PUB22
55) AT1G42990 - AtBZIP60
56) AT1G09100 - RPT5B
57) AT3G21630 - CERK1
58) AT1G66340 - ETR1
59) AT3G51770 - ETO1
60) AT5G48655 - zinc-finger
61) AT3G52800 - AN1-like
62) AT4G17230 - SCL13
63) AT2G23320 - WRKY15
64) AT3G61460 - BRH1
65) AT2G04240 - XERICO
66) AT4G18880 - AtHSFA4A
67) AT4G39070 - BBX20
68) AT2G26300 - GPalpha1
69) AT2G19450 - TAG1
70) AT5G27420 - zinc-finger
71) AT3G05200 - ATL6
72) AT4G35480 - RHA3B
73) AT2G23460 - XLG1
74) AT5G64930 - CPR5
75) AT3G19580 - AZF2
76) AT5G59780 - MYB59
77) AT3G11840 - PUB24
78) AT2G36270 - ABI5
79) AT1G34180 - ANAC016
80) AT5G22890 - zinc-finger
81) AT4G27750 - ISI1
82) AT1G08930 - ERD6
83) AT4G17500 - AtERF1
84) AT2G24570 - WRKY17
85) AT4G31550 - WRKY11
86) AT5G59550 - zinc-finger
87) AT4G33050 - EDA39
88) AT2G38470 - WRKY33
89) AT3G50260 - CEJ1
90) AT5G38895 - zinc-finger
91) AT4G33940 - Unknown
92) AT5G62020 - AtHSFB2A
93) AT4G01250 - WRKY22
Response to cold cluster II
GO:0009409 (128/216)
54) AT3G22840 - ELIP1
55) AT3G01500 - CA1
56) AT1G29395 - COR414-TM1
57) AT4G02380 - SAG21
58) AT5G66400 - RAB18
59) AT5G57560 - TCH4
60) AT4G35090 - CAT2
61) AT2G26250 - KCS10
62) AT4G13850 - GR-RBP2
63) AT2G36530 - LOS2
64) AT4G03430 - EMB2770
65) AT4G31120 - SKB1
66) AT2G15970 - COR413-PM1
67) AT5G43760 - KCS20
68) AT4G25470 - CBF2
69) AT3G09200 - RPP0B
70) AT1G63940 - MDHAR
71) AT5G10030 - TGA4
72) AT1G07720 - KCS3
73) AT1G20450 - ERD10
74) AT1G74520 - AtHVA22A
75) AT1G10760 - SEX1
76) AT5G52310 - LTI78
77) AT2G21660 - CCR2
78) AT3G04880 - DRT102
79) AT4G35790 - AtPLD-delta
80) AT5G52300 - LTI65
81) AT5G24090 - CHIB1
82) AT1G05260 - RCI3
83) AT2G17840 - ERD7
84) AT3G14310 - PP2CA
85) AT4G26080 - ABI1
86) AT5G12250 - TUB6
87) AT4G25470 - CBF2
88) AT2G33380 - RD20
89) AT3G08720 - SGK2
90) AT3G18990 - VRN1
91) AT4G36930 - SPATULA
92) AT5G50720 - AtHVA22E
93) AT2G38470 - WRKY33
94) AT3G50260 - CEJ1
95) AT5G20250 - DIN10
96) AT2G30250 - WRKY25
97) AT4G20260 - DREPP
98) AT5G01600 - AtFER1
99) AT5G37500 - GORK
100) AT1G76180 - ERD14
101) AT1G20620 - CAT3
102) AT2G43790 - AtMPK6
103) AT3G26650 - GAPA
104) AT5G61410 - RPE
105) AT4G11150 - TUF
106) AT4G01370 - AtMPK4
107) AT3G16450 - JAL33
108) AT3G53110 - LOS4
109) AT5G08620 - STRS2
110) AT2G40140 - CZF1
111) AT5G61850 - CSLD2
112) AT1G20440 - COR47
113) AT4G16420 - ADA2B
114) AT3G59770 - SAG29
115) AT2G38170 - CAX1
116) AT2G39810 - HOS1
117) AT3G07740 - ADA2A
118) AT4G08000 - MEKK1
119) AT5G60410 - SIZ1
120) AT5G17690 - TFL2
121) AT1G27320 - AHK3
122) AT1G21760 - FBP7
123) AT2G25930 - ELF3
124) AT3G48750 - CDC2
125) AT1G09560 - GLP5
126) AT1G31812 - ACBP6
127) AT5G10140 - FLC
128) AT3G17020 - USP-family
Response to heat GO:0009408
(57/99)
1) AT3G09440 - HSC70-3
2) AT5G56030 - SHSP81-2
3) AT3G23990 - HSP60
4) AT3G25230 - ROF1
5) AT5G09590 - mtHSC70-2
6) AT4G37910 - cpHSC70-1
7) AT1G14980 - CPN10
8) AT4G24280 - cpHSC70-1
9) AT5G15450 - CLPB3
10) AT2G22240 - MIPS2
11) AT1G54050 - HSP17.4-CIII
12) AT2G26150 - AtHSFA2
13) AT5G37770 - TCH2
14) AT5G02490 - HSC70-2
15) AT2G46240 - BAG6
16) AT3G12580 - HSP70
17) AT5G52640 - AtHSP90.1
18) AT4G12400 - STI-like
19) AT3G46230 - AtHSP17.4
20) AT2G29500 - HSP17.6-CI
21) AT5G51440 - AtHSP17.6A
22) AT1G74310 - AtHSP101
23) AT5G49910 - cpHSC70-2
24) AT2G04030 - CRB8
25) AT4G27180 - AtGolS1
26) AT5G57560 - TCH4
27) AT5G59820 - RHL41
28) AT3G24500 - MBF1C
29) AT5G05410 - DREB2A
30) AT4G26850 - VTC2
31) AT1G17870 - EGY3
32) AT1G08550 - NPQ1
33) AT5G67030 - ABA1
34) AT5G53170 - FTSH11
35) AT3G04120 - GAPC1
36) AT4G38630 - RPN10
37) AT5G14800 - PSCR
38) AT5G43940 - HOT5
39) AT1G05850 - POM1
40) AT1G11270 - F-box family
41) AT1G67940 - FBP7
42) AT2G32120 - HSP70T-2
43) AT1G66340 - ETR1
44) AT3G53110 - LOS4
45) AT1G22640 - MYB3
46) AT3G11020 - DREB2B
47) AT3G10800 - BZIP28
48) AT1G77000 - SKP2B
49) AT5G47910 - RBOHD
50) AT3G51910 - AtHSFA7A
51) AT3G08720 - SGK2
52) AT2G38470 - WRKY33
53) AT1G79440 - ALDH5F1
54) AT4G38580 - AtPP6
55) AT4G26080 - ABI1
56) AT5G57050 - ABI2
57) AT1G09090 - AtRBOHB
Response to cold cluster I
GO:0009409 (128/216)
1) AT1G17190 - AtGSTU26
2) AT1G01860 - PFC1
3) AT2G39460 - RPL23AA
4) AT2G27710 - RPP2B
5) AT3G55280 - RPL23AB
6) AT5G63980 - SAL1
7) AT2G16500 - ADC1
8) AT1G12860 - SCREAM2
9) AT4G34150 - C2-domain
10) AT3G20740 - FIE
11) AT2G46240 - BAG6
12) AT3G17390 - MTO3
13) AT4G36020 - CSDP1
14) AT5G63770 - AtDGK2
15) AT5G37770 - TCH2
16) AT1G25450 - KCS5
17) AT5G59820 - RHL41
18) AT3G50970 - LTI30
19) AT3G22370 - AOX1A
20) AT1G22770 - GIGANTEA
21) AT1G15950 - CCR1
22) AT2G18790 - PHYB
23) AT2G16280 - KCS9
24) AT4G25480 - DREB1A
25) AT4G24960 - AtHVA22D
26) AT1G27730 - ZAT10
27) AT4G17090 - CT-BMY
28) AT4G24280 - cpHSC70-1
29) AT5G20720 - CPN20
30) AT4G38840 - SAUR
31) AT1G51830 - BAS1
32) AT3G12780 - PGK1
33) AT1G55490 - CPN60B
34) AT1G35680 - RPL21
35) AT5G51820 - PGM
36) AT5G67590 - FRO1
37) ATCG00120 - ATP-alpha
38) AT5G06290 - 2-Cys-Prx8
39) AT1G03680 - AtTRXM1
40) AT1G16880 - Unknown
41) AT3G02870 - VTC4
42) AT2G42540 - COR15A
43) AT3G14210 - ESM1
44) AT5G20630 - GER3
45) AT4G37930 - SHM1
46) AT2G39730 - RCA
47) AT1G42970 - GAPB
48) AT1G23740 - Unknown
49) AT3G23700 - S1 RNA-binding
50) AT1G09340 - CRB
51) AT4G09650 - ATP-delta
52) AT1G32060 - RPK
53) AT3G54050 - FBP
Response to wounding
GO:0009611 (67/114)
1) AT5G13930 - TT4
2) AT1G65060 - 4CL3
3) AT1G55020 - LOX1
4) AT3G25230 - ROF1
5) AT2G37040 - PAL1
6) AT2G30490 - C4H
7) AT3G53260 - PAL2
8) AT4G39980 - DHS1
9) AT1G05630 - 5PTase13
10) AT2G46510 - AtAIB
11) AT5G63770 - AtDGK2
12) AT5G13220 - JAZ10
13) AT2G06050 - OPR3
14) AT2G20340 - Unknown
15) AT2G34810 - Unknown
16) AT4G02260 - RSH1
17) AT4G16990 - RLM3
18) AT4G12030 - BASS5
19) AT4G23600 - CORI3
20) AT4G15440 - HPL1
21) AT4G24350 - Unknown
22) AT1G72920 - TIR-NBS-class
23) AT1G72450 - JAZ6
24) AT4G11280 - ACS6
25) AT5G05730 - ASA1
26) AT5G42650 - AOS
27) AT1G51400 - PSB 5kDa
28) AT5G47240 - ANNUAT8
29) AT3G45140 - LOX2
30) AT4G35770 - SEN1
31) AT4G37760 - SQE1
32) AT1G63160 - RAP2.6
33) AT5G20230 - AtBCB
34) AT5G59820 - RHL41
35) AT1G27730 - ZAT10
36) AT3G61890 - AtHCIB
37) AT5G24090 - CHIB1
38) AT3G61060 - AtPP2-A13
39) AT1G01720 - ATAF1
40) AT4G24220 - VEP1
41) AT5G14780 - FDH
42) AT3G14050 - RSH2
43) AT5G54170 - Unknown
44) AT1G62160 - MATE
45) AT1G04220 - KCS2
46) AT1G01470 - LEA14
47) AT1G32640 - MYC2
48) AT4G02990 - RNS1
49) AT5G50200 - WR3
50) AT1G76930 - AtEXT4
51) AT4G26070 - MEK1
52) AT3G23030 - ACS2
53) AT1G32920 - Unknown
54) AT4G16760 - ACX1
55) AT1G66340 - ETR1
56) AT4G01370 - AtMPK4
57) AT4G08500 - MEKK1
58) AT1G22640 - MYB3
59) AT3G03300 - MES5
60) AT2G33150 - PKT3
61) AT2G02220 - PSKR1
62) AT5G64930 - CPR5
63) AT2G39940 - COI1
64) AT2G28290 - SPLAYED
65) AT1G73500 - MKK9
66) AT3G23050 - IAA7
67) AT1G71697 - AtCK1
Response to salt stress
Cluster I GO:0009651 (117/202)
1) AT3G16350 - MYB-family
2) AT1G70000 - MYB-family
3) AT1G60040 - STO
4) AT2G04030 - CRB8
5) AT5G01410 - RSR4
6) AT5G56030 - HSP81-2
7) AT5G20270 - HHP1
8) AT3G27760 - SAT32
9) AT3G03450 - RGL2
10) AT2G37630 - AS1
11) AT5G63980 - SAL1
12) AT2G47580 - U1A
13) AT1G49850 - TRB3
14) AT2G16500 - ADC1
15) AT5G49480 - AtCP1
16) AT1G49010 - MYB-family
17) AT4G33000 - CBL10
18) AT1G16060 - AP-domain
19) AT3G62030 - ROC4
20) AT1G69700 - AtHVA22C
21) AT1G56650 - PAP1
22) AT4G23600 - CORI3
23) AT2G35510 - SRO1
24) AT1G18710 - AtMYB47
25) AT3G17510 - CIPK1
26) AT1G01060 - LHY
27) AT2G30250 - WRKY25
28) AT1G10170 - AtNFXL1
29) AT5G02840 - LCL1
30) AT2G46830 - CCA1
31) AT3G09600 - MYB-family
32) AT1G71030 - MYBL2
33) AT1G06180 - AtMYB13
34) AT1G01520 - MYB-family
0.5 1 4 24 0.5 1 4 24 0 4
+Lin -Lin +Lin/ -Lin

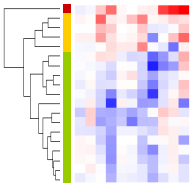
D



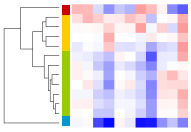
Transcription factors Induced by at least three species of ROS (23/32) p = 9.233E-06



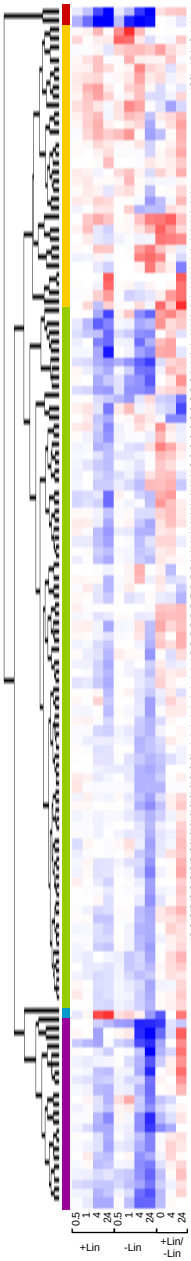
Induced by multiple ROS (19/31) p = 0.001062



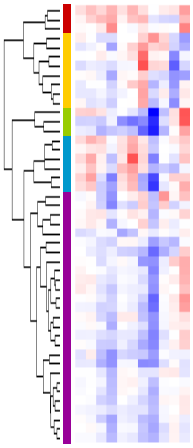
Induced by superoxide in the mitochondria and chloroplast (13/17) p = 0.0003280



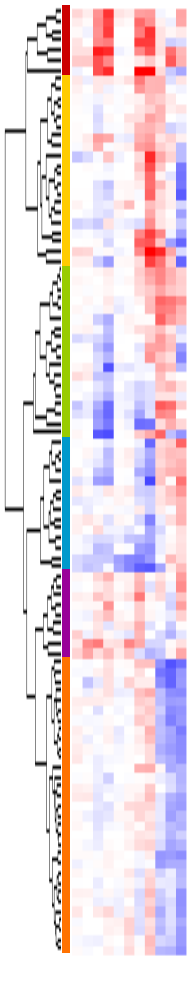
Induced by singlet oxygen (127/267) p = 3.634E-07



Induced by *flu*, ozone, and methyl viologen (47/63) p = 2.9238E-11

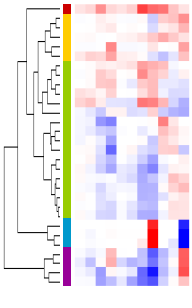


Induced by superoxide in the chloroplast (99/132) p = 3.510E-23

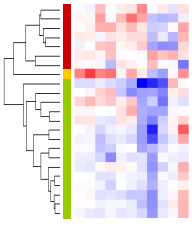


Induced by photorespiratory H_2O_2 (3/6) p = 0.22288

Induced by cytosolic H_2O_2 (30/67) p = 0.01657



Induced by peroxisomal H_2O_2 (23/79) p = 0.06748



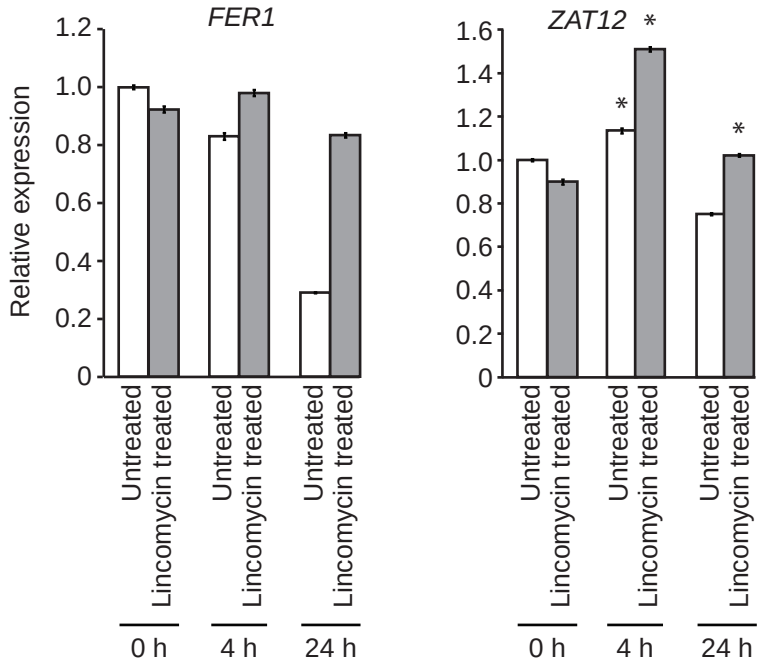
Supplemental Figure S6. Agglomerative hierarchical clustering of significantly regulated genes.

A, Agglomerative hierarchical clustering of significantly regulated genes annotated as contributing to 24 biological processes by their expression profiles. The criteria for significant regulation are described in Fig. 2. Enriched GO terms were identified using the criteria described in Supplemental Fig. S4A. The number of significantly regulated genes from a GO term/total number of genes in each GO term is indicated in parentheses next to each GO term number code. As indicated by the key at the bottom of the leftmost column, squares from the left to the right indicate light-regulated expression at 0.5 h, 1 h, 4 h, and 24 h following the BR-fluence-rate shift in lincomycin-treated seedlings; light-regulated expression at 0.5 h, 1 h, 4 h, and 24 h following the BR-fluence-rate shift in untreated seedlings; and plastid-regulated expression at 0 h, 4 h, and 24 following the fluence-rate shift. Up-regulated expression is indicated with red and down-regulated expression is indicated with blue. Color intensity is proportional to the degree of regulation.

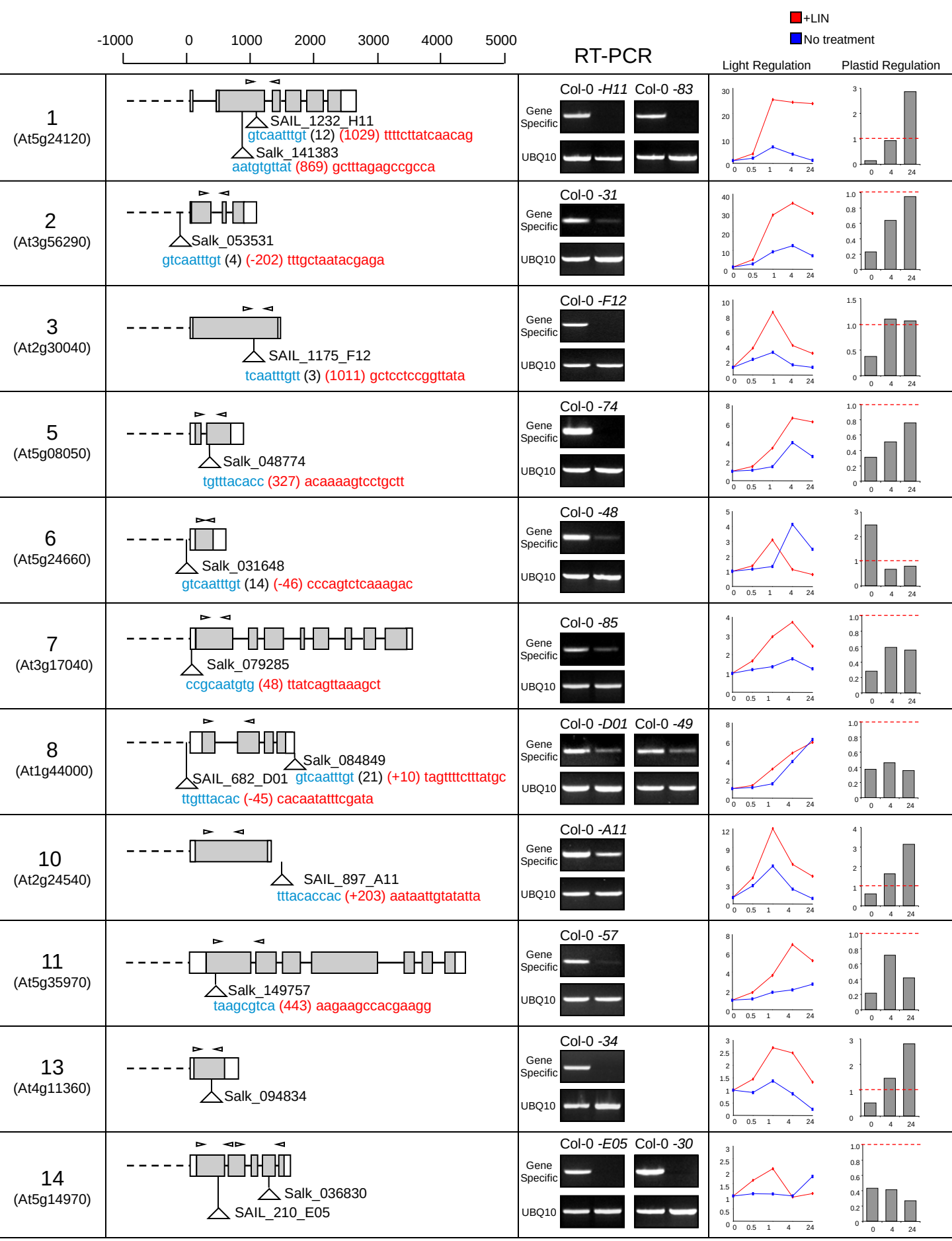
B, Agglomerative hierarchical clustering of significantly regulated genes annotated as contributing to the 14 cell components by their expression profiles. Genes and GO terms were clustered, arranged, and labeled as described in A.

C, Agglomerative hierarchical clustering of significantly regulated genes annotated as contributing to 16 biological responses to stimulus by their expression profiles. Genes and GO terms were clustered, arranged and labeled as described in A.

D, Agglomerative hierarchical clustering of significantly regulated ROS-responsive genes by their expression profiles. Genes whose expression is induced fivefold by ROS were previously described (Gadjev et al., 2006) and were obtained from the AtGenExpress repository. The confidence that each ROS-responsive gene list is enriched in our overall data set is indicated with p-values. Groups of ROS-responsive genes were clustered, arranged, and labeled as described in A.



Supplemental Figure S7. *FER1* and *ZAT12* expression in lincomycin-treated and untreated seedlings.
The expression of *FER1* and *ZAT12* at 0 h, 4 h, and 24 h relative to the BR-fluence-rate shift was quantified with qRT-PCR. The expression of a particular gene in lincomycin-treated seedlings (gray bars) and untreated seedlings (white bars) is normalized to the expression of that same gene in untreated seedlings at 0 h. Error bars indicate standard deviation. *, indicates a statistically significant increase relative to untreated seedlings at 0 h ($P \leq 0.0001$ to 0.003).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0
1000
2000
3000
4000
5000
RT-PCR
+LIN
No treatment
Light Regulation
Plastid Regulation
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gtcaatttgt (12) (1029) ttttcttatcaacag
Salk_141383
aatgtgttat (869) gctttagagccgcca
Col-0 -H11
Col-0 -83
2
(At3g56290)
Salk_053531
gtcaatttgt (4) (-202) tttgctaatacgaga
Col-0 -31
3
(At2g30040)
SAIL_1175_F12
tcaatttgtt (3) (1011) gctcctccggttata
Col-0 -F12
5
(At5g08050)
Salk_048774
tgtttacacc (327) acaaaagtcctgctt
Col-0 -74
6
(At5g24660)
Salk_031648
gtcaatttgt (14) (-46) cccagtctcaaagac
Col-0 -48
7
(At3g17040)
Salk_079285
ccgcaatgtg (48) ttatcagttaaagct
Col-0 -85
8
(At1g44000)
Salk_084849
SAIL_682_D01
gtcaatttgt (21) (+10) tagttttctttatgc
ttgtttacac (-45) cacaatatttcgata
Col-0 -D01
Col-0 -49
10
(At2g24540)
SAIL_897_A11
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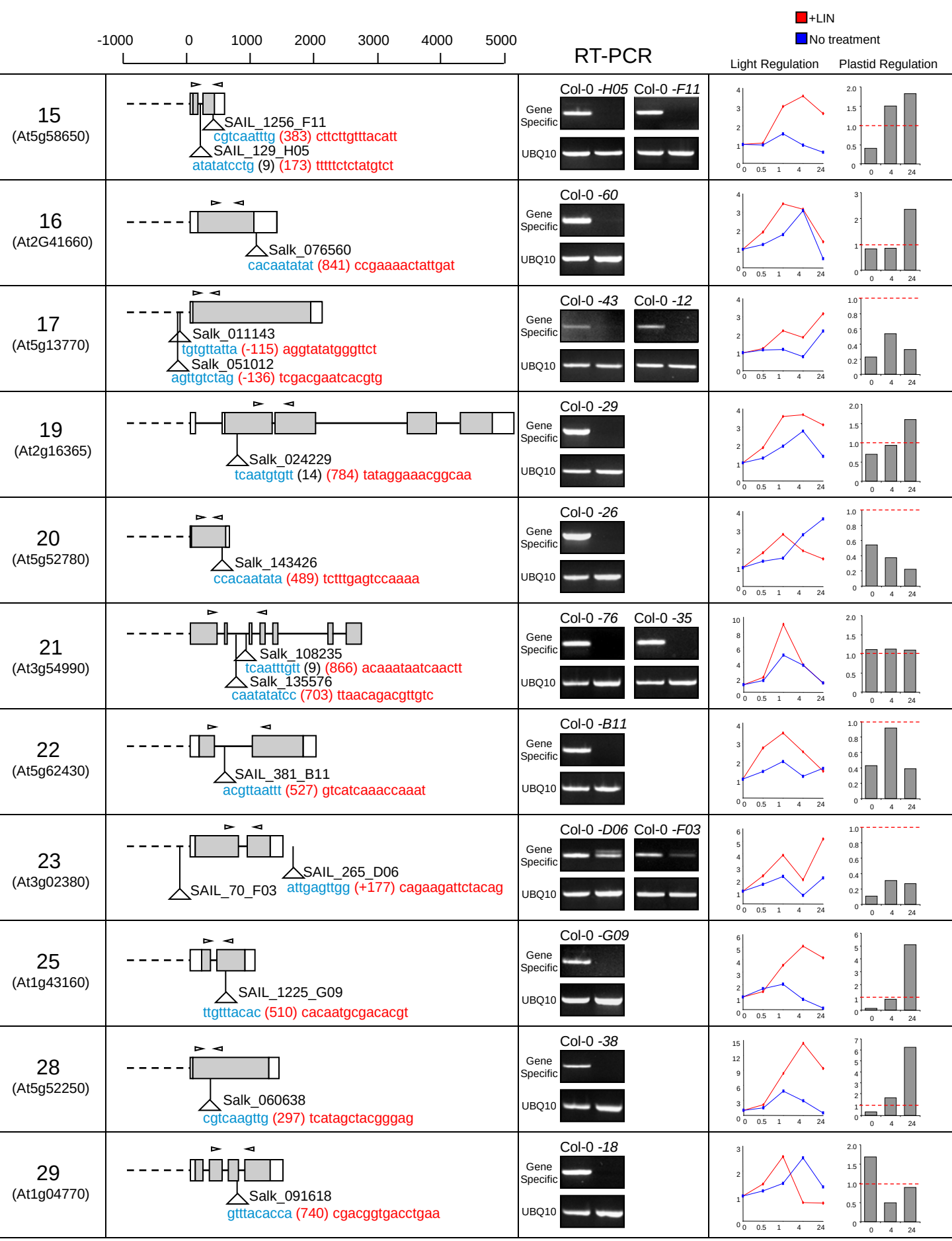
Col-0 -A11
11
(At5g35970)
Salk_149757
taagcgtca (443) aagaagccacgaagg
Col-0 -57
13
(At4g11360)
Salk_094834
Col-0 -34
14
(At5g14970)
Salk_036830
SAIL_210_E05
Col-0 -E05
Col-0 -30
Gene Specific
UBQ10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0
1000
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3000
4000
5000
RT-PCR
+LIN
No treatment
Light Regulation
Plastid Regulation
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SAIL_129_H05
atatatcctg (9) (173) tttttctctatgtct
Col-0 -H05
Col-0 -F11
16
(At2G41660)
Salk_076560
cacaatatat (841) ccgaaaactattgat
Col-0 -60
17
(At5g13770)
Salk_011143
tgtgttatta (-115) aggtatatgggttct
Salk_051012
agttgtctag (-136) tcgacgaatcacgtg
Col-0 -43
Col-0 -12
19
(At2g16365)
Salk_024229
tcaatgtgtt (14) (784) tataggaaacggcaa
Col-0 -29
20
(At5g52780)
Salk_143426
ccacaatata (489) tctttgagtccaaaa
Col-0 -26
21
(At3g54990)
Salk_108235
tcaatttgtt (9) (866) acaaataatcaactt
Salk_135576
caatatatcc (703) ttaacagacgttgtc
Col-0 -76
Col-0 -35
22
(At5g62430)
SAIL_381_B11
acgttaattt (527) gtcatcaaaccaaat
Col-0 -B11
23
(At3g02380)
SAIL_265_D06
attgagttgg (+177) cagaagattctacag
SAIL_70_F03
Col-0 -D06
Col-0 -F03
25
(At1g43160)
SAIL_1225_G09
ttgtttacac (510) cacaatgcgacacgt
Col-0 -G09
28
(At5g52250)
Salk_060638
cgtcaagttg (297) tcatagctacgggag
Col-0 -38
29
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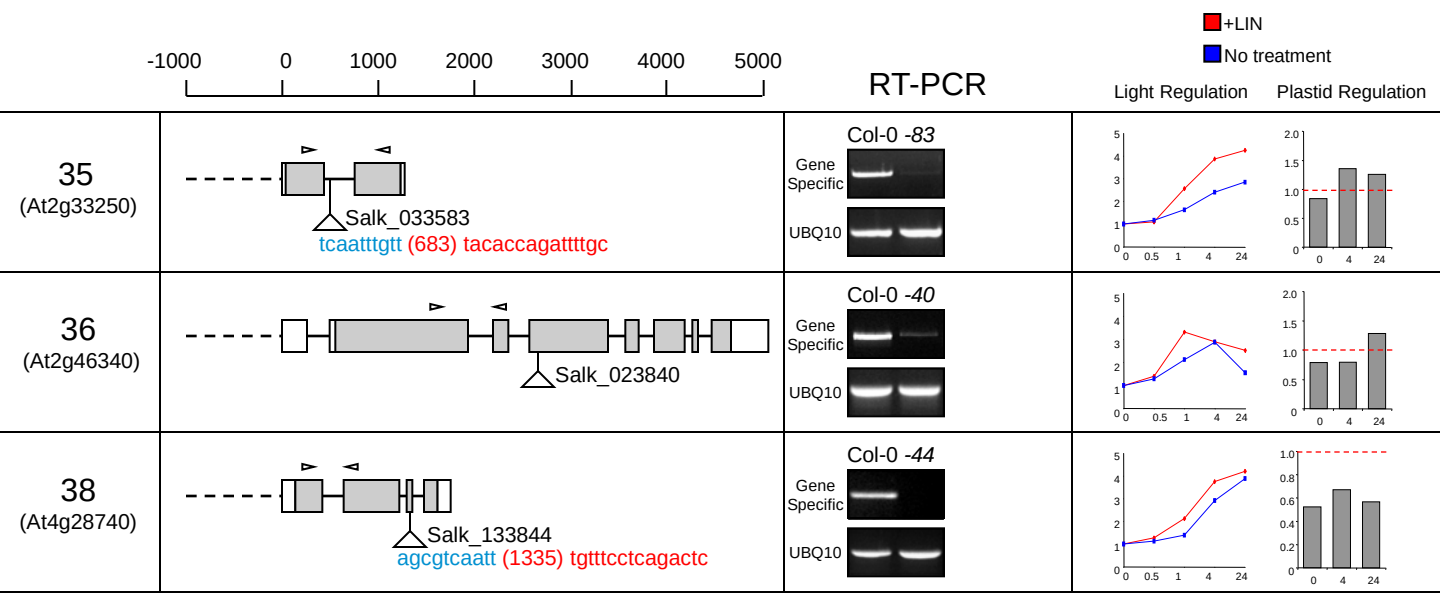
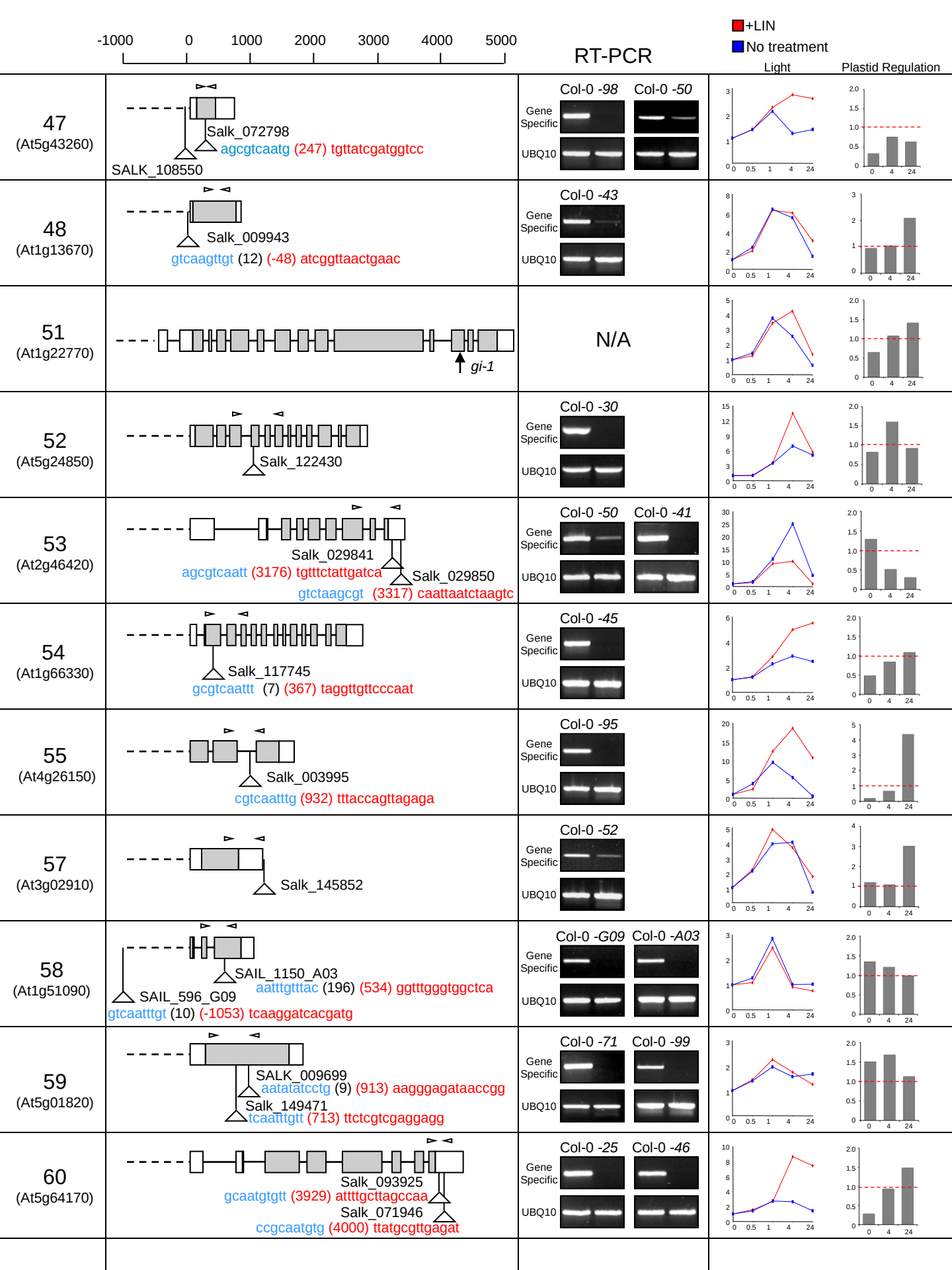
Salk_091618
gtttacacca (740) cgacggtgacctgaa
Col-0 -18
Gene Specific
UBQ10



Supplemental Figure S8. T-DNA insertion alleles of genes whose expression is more highly induced in lincomycin-treated than in untreated seedlings by 1 h following the BR-fluence-rate shift. The leftmost column contains the AGI code and an arbitrary number for each gene. The adjacent column contains the gene models based on information from The Institute for Genomic Research (TIGR). A scale in base pairs (bp) is indicated above this column. White boxes represent 5'- and 3'-untranslated regions (UTRs). Gray boxes represent exons. Dashed lines represent promoter sequences. Solid lines represent introns. The position of each T-DNA insertion is indicated to the left of the respective Salk or SAIL accession code. The sequence of the insertion site is indicated below each Salk or SAIL number and is color coded. The blue bases indicate the T-DNA sequence flanking the insertion site. Black numbers in parentheses indicate the number of bases that match neither the T-DNA nor the genomic sequence. The red bases indicate the genomic sequence flanking the T-DNA insertion. Red numbers in parentheses indicate the distance of the T-DNA insertion from the first base of the 5'-UTR sequence in bp. Negative red numbers indicate the number of bp upstream of the 5'-UTR sequence, and positive red numbers indicate the number of bp downstream of the 5'-UTR sequence. The third column from the left shows the RNA phenotype caused by each T-DNA insertion allele. RNA phenotypes were scored by extracting total RNA from 7-d-old seedlings and using RT-PCR to detect transcripts from genes that contain T-DNA insertions. The location of each gene-specific primer pair is represented as converging arrows above each gene model in the second column from the left. The last two numbers of Salk accession code or the last 3 digits of the SAIL accession code are used to name the T-DNA alleles. For example, the T-DNA alleles of gene number 1 (At5g24120) are SAIL_1232_H11 and Salk_141383. In this figure, these alleles are named -H11 and -83, respectively. RT-PCR detection of *UBQ10* transcripts was used to test whether equal amounts of total RNA from both T-DNA mutants and wild type were used in each experiment. The fourth column from the left contains graphs that indicate the light- and plastid-regulated expression of each gene following the BR-fluence-rate shift. Expression levels are derived from microarray analysis. The leftmost graph indicates the expression level following the BR-fluence-rate shift. Relative transcript levels are indicated on the ordinate. Time in h following the BR-fluence-rate shift is indicated on the abscissa. Transcript levels in lincomycin-treated seedlings (+Lin) are indicated in red. Transcript levels in untreated seedlings (no treatment) are indicated in blue. The rightmost graph is a histogram that quantifies the plastid regulation of each gene. Plastid-regulated gene expression is defined as a ratio of expression in lincomycin-treated to expression in untreated seedlings at 0 h, 4 h, or 24 h following the fluence-rate shift. The dashed-red line indicates no effect of the lincomycin treatment on gene expression.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0
1000
2000
3000
4000
5000
RT-PCR
+LIN
No treatment
Light
Plastid Regulation
47
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Salk_072798
agcgtcaatg (247) tgttatcgatggtcc
SALK_108550
Col-0 -98
Col-0 -50
Gene Specific
UBQ10
48
(At1g13670)
Salk_009943
gtcaagttgt (12) (-48) atcggttaactgaac
Col-0 -43
51
(At1g22770)
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(At5g24850)
Salk_122430
Col-0 -30
53
(At2g46420)
Salk_029841
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Salk_029850
gtctaagcgt (3317) caattaatctaagtc
Col-0 -50
Col-0 -41
54
(At1g66330)
Salk_117745
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Col-0 -45
55
(At4g26150)
Salk_003995
cgtcaatttg (932) tttaccagttagaga
Col-0 -95
57
(At3g02910)
Salk_145852
Col-0 -52
58
(At1g51090)
SAIL_1150_A03
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SAIL_596_G09
gtcaatttgt (10) (-1053) tcaaggatcacgatg
Col-0 -G09
Col-0 -A03
59
(At5g01820)
SALK_009699
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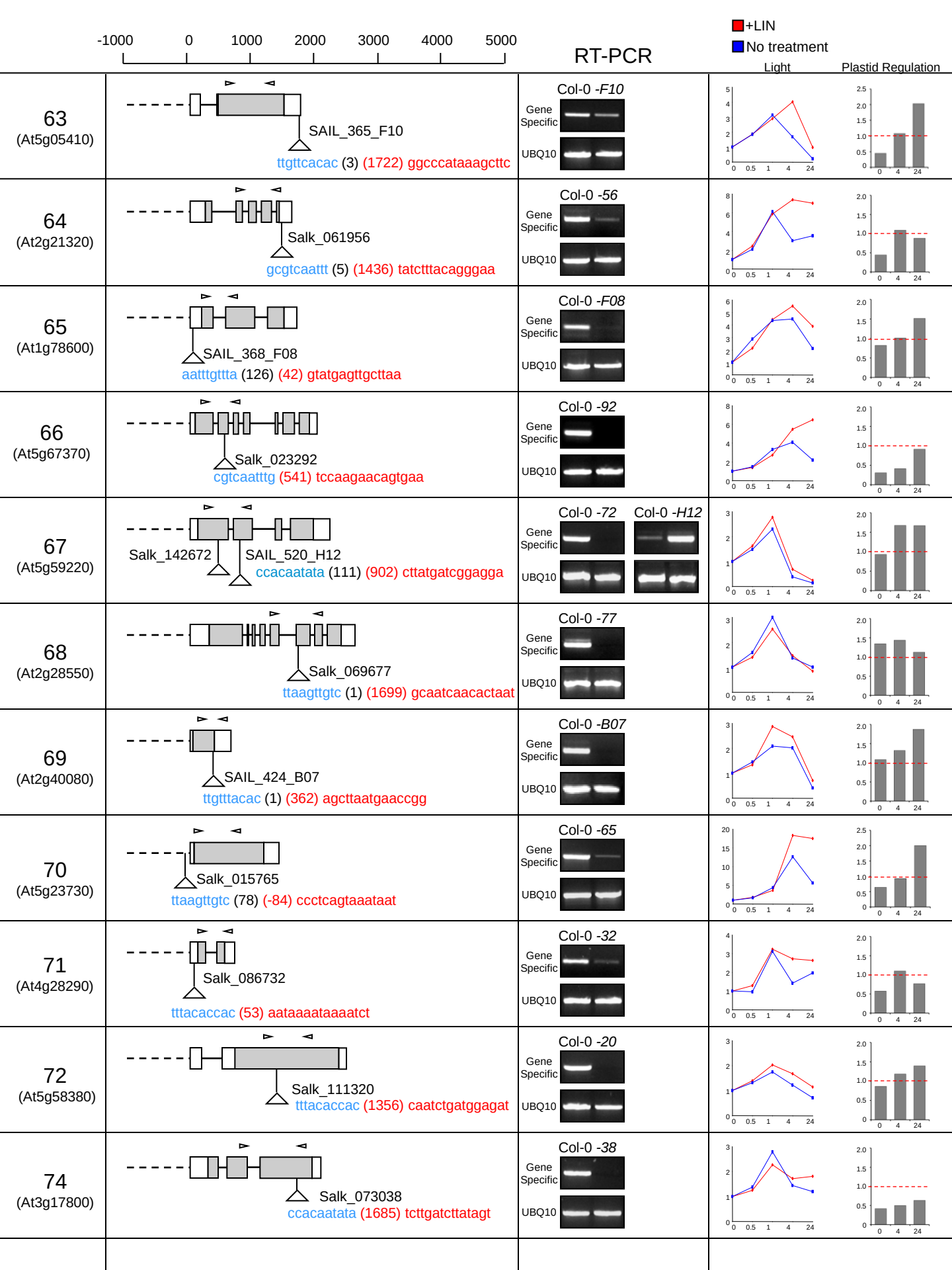
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RT-PCR
+LIN
No treatment
Light
Plastid Regulation
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Col-0 -F10
Gene Specific
UBQ10
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Col-0 -56
65
(At1g78600)
SAIL_368_F08
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(At5g67370)
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Col-0 -92
67
(At5g59220)
Salk_142672
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Col-0 -72
Col-0 -H12
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Salk_069677
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Col-0 -B07
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Salk_086732
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Col-0 -32
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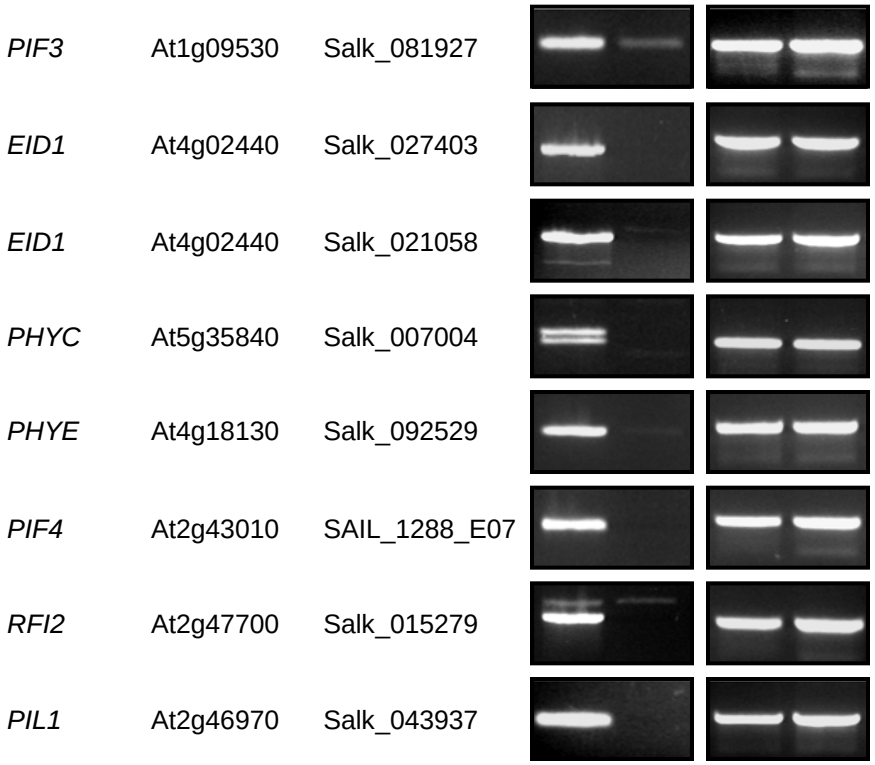
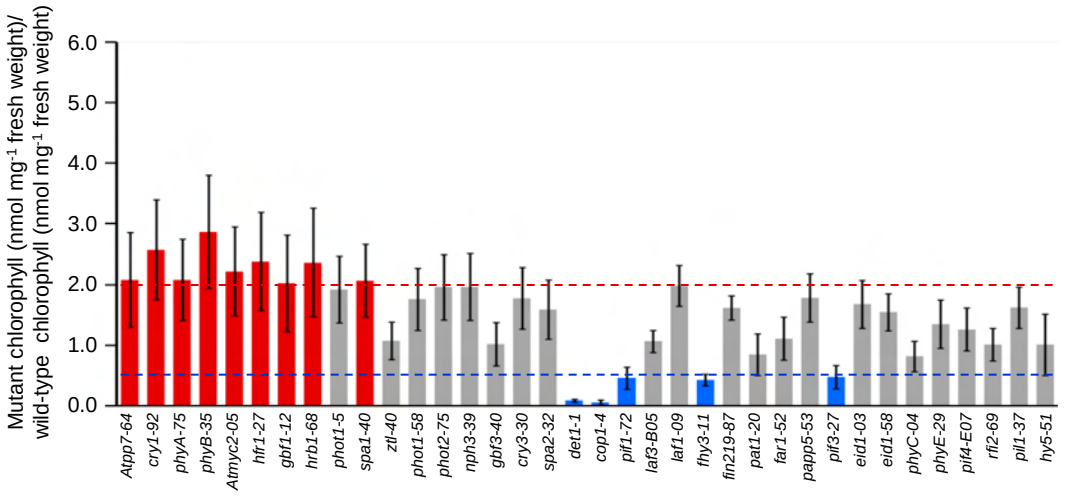
(At5g58380)
Salk_111320
tttacaccac (1356) caatctgatggagat
Col-0 -20
74
(At3g17800)
Salk_073038
ccacaatata (1685) tcttgatcttatagt
Col-0 -38

Supplemental Figure S9. T-DNA insertion alleles of genes whose expression is similarly induced in lincomycin-treated and untreated seedlings by 1 h following the BR-fluence-rate shift. The leftmost column contains the AGI code and an arbitrary number for each gene. The adjacent column contains the gene models based on information from The Institute for Genomic Research (TIGR). The gene models are labeled as described in Supplemental Fig. S8. *gi-1* (a.k.a., mutant 51) is not a T-DNA insertion allele. *gi-1* has a 5-bp deletion that introduces a premature stop codon (indicated with an arrow) and deletes 171 amino acid residues from the carboxy-terminus of the GIGANTEA protein (Park et al., 1999). The third column from the left shows the RNA phenotype caused by each T-DNA insertion allele. RNA phenotypes were scored using RT-PCR as described in Supplemental Fig. S8. The fourth column from the left contains graphs that indicate the light- and plastid-regulated expression of each gene following the BR-fluence-rate shift. The graphs are labeled as described in Supplemental Fig. S8.

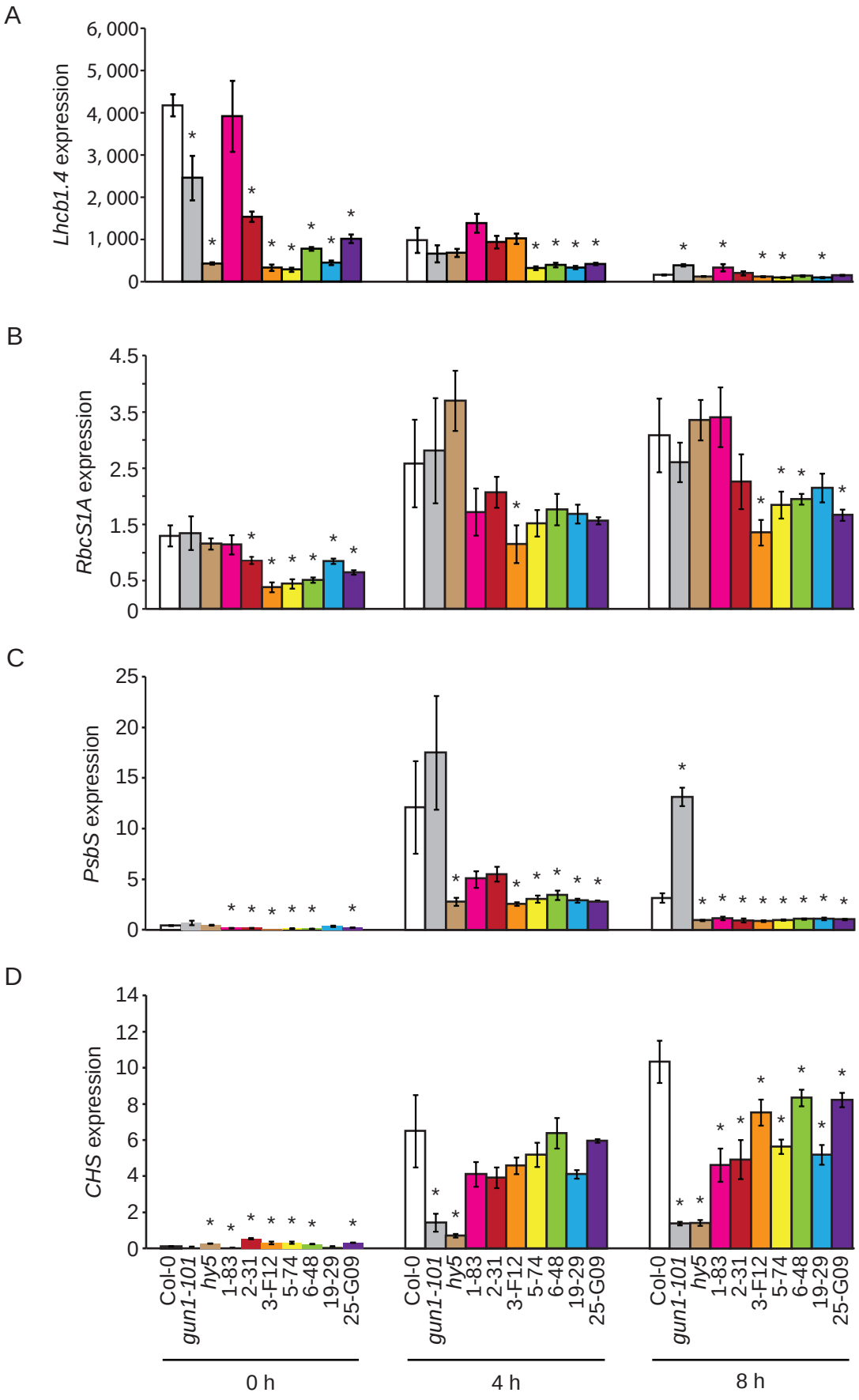
Gene name	AGI code	T-DNA allele	Gene Specific Col-0	Gene Specific T-DNA line	*Ubq10* Col-0	*Ubq10* T-DNA line
AtPP7	At5g63870	Salk_089764				
AtMYC2	At1g32640	Salk_017005				
HFR1	At1g02340	Salk_037727				
GBF1	At4g36730	Salk_096612				
HRB1	At5g49230	Salk_087868				
SPA1	At2g46340	Salk_023840				
ZTL	At5g57360	Salk_012440				
GBF3	At2g46270	Salk_082840				
SPA2	At4g11110	Salk_009832				
PIF1	At2g20180	Salk_131872				
LAF3	At3g55850	SAIL_573_B05				
LAF1	At4g25560	Salk_079609				
FHY3	At3g22170	Salk_002711				
FIN219	At2g46370	Salk_075487				
PAT1	At5g48150	Salk_064220				
FAR1	At4g15090	Salk_031652				
PAPP5	At2g42810	Salk_021153				



Supplemental Figure S10. Characterization of T-DNA insertion alleles of genes that encode light-signaling factors. RNA phenotypes were scored using RT-PCR to detect transcripts from genes that contain T-DNA insertions. RT-PCR detection of transcripts from *UBQ10* was used to test whether equal amounts of total RNA from both T-DNA mutants and wild type were used in each experiment. These genes were at least previously implicated in light signaling: *AtPP7* (Møller et al., 2003); *AtMYC2/ZBF1* (Yadav et al., 2005); *HFR1* (Fairchild et al., 2000); *GBF1* (Schindler et al., 1992); *HRB1* (Kang et al., 2005); *SPA1* (Hoecker et al., 1998); *ZTL* (Kim et al., 2007); *GBF3* (Schindler et al., 1992); *SPA2* (Laubinger et al., 2004); *PIF1* (Huq et al., 2004); *LAF3* (Ballesteros et al., 2001); *LAF1* (Møller et al., 2001); *FHY3* (Wang and Deng, 2002); *FIN219* (Hsieh et al., 2000); *PAT1* (Bolle et al., 2000); *FAR1* (Hudson et al., 1999); *PAPP5* (Ryu et al., 2005); *PIF3* (Ni et al., 1998); *EID1* (Dieterle et al., 2001); *PHYC* (Monte et al., 2003); *PHYE* (Devlin et al., 1998); *PIF4* (Huq and Quail, 2002); *RFI2* (Chen and Ni, 2006); *PIL1* (Salter et al., 2003).



Supplemental Figure S11. Chlorophyll phenotypes of light signaling mutants. De-etiolation was performed and relative chlorophyll levels were quantified for the indicated light-signaling mutants as described in Fig. 7. These alleles were previously generated using either EMS or T-DNA insertional mutagenesis. Names for T-DNA insertion alleles were created from the gene name and the last two numbers of the Salk accession code or the last three digits of the SAIL accession code. For example, the T-DNA insertion allele of *AtPP7* that is derived from Salk_089764 is named *Atpp7-64*. *cry1-92*, *phyA-75*, *phyB-35*, *phot1-58*, *phot2-75*, *nph3-39*, *cry3-30*, and *hy5-51* were previously characterized (Ruckle et al., 2007). The remaining alleles derived from T-DNA insertional mutagenesis are described in Supplemental Fig. S10. The alleles derived from EMS mutagenesis were *cop1-4* (Deng et al., 1992; Deng and Quail, 1992), *det1-1* (Chory et al., 1989), and *phot1-5*, which was formerly known as *nph1-5* (Liscum and Briggs, 1995; Huala et al., 1997). Error bars represent 95% confidence intervals.


A
Lhcb1.4 expression
6, 000
5, 000
4, 000
3, 000
2, 000
1, 000
0
B
RbcS1A expression
4.5
3.5
2.5
1.5
0.5
0
C
PsbS expression
25
20
15
10
5
0
D
CHS expression
14
12
10
8
6
4
2
0
Col-0
gun1-101
hy5
1-83
2-31
3-F12
5-74
6-48
19-29
25-G09
0 h
4 h
8 h

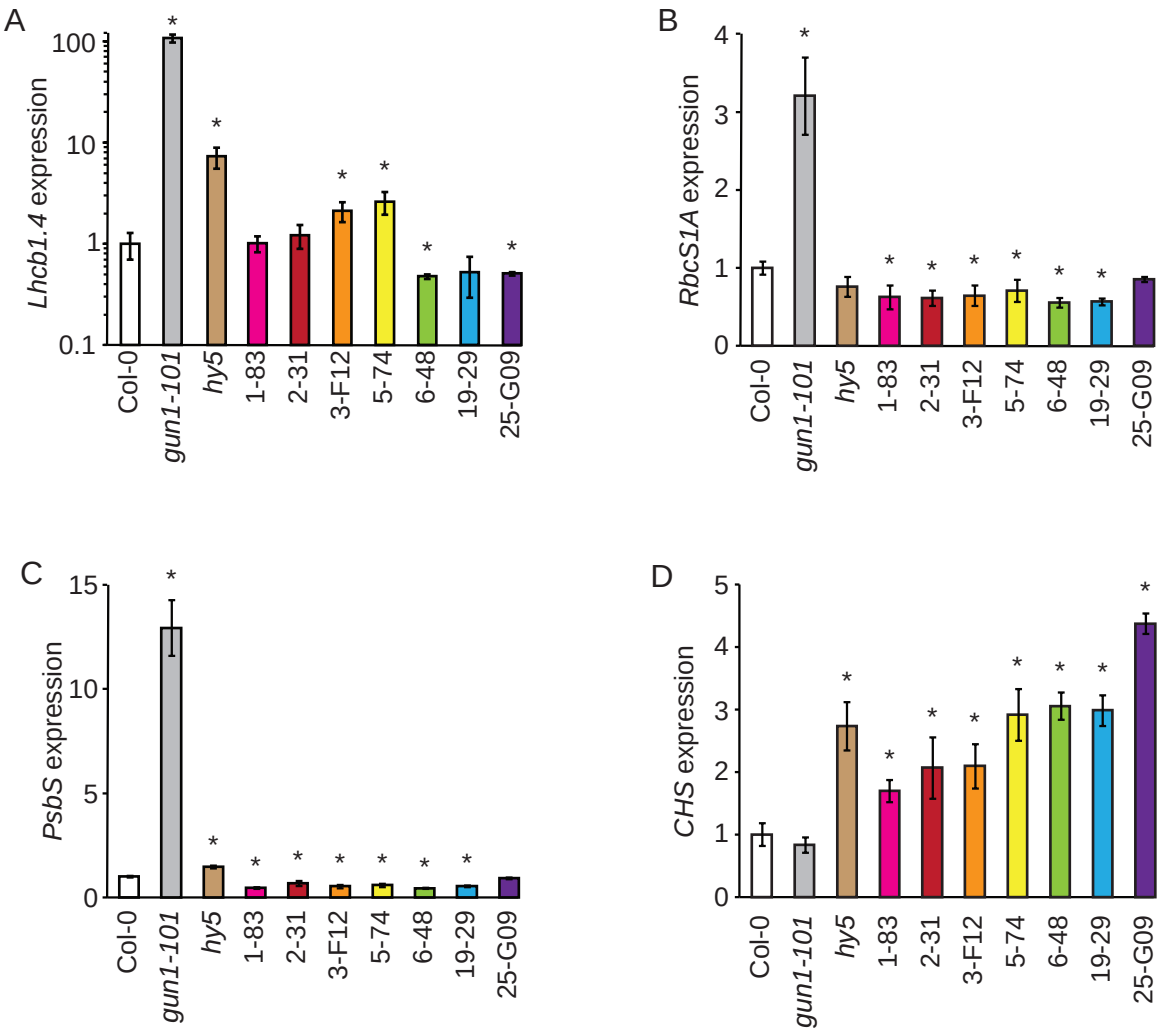
Supplemental Figure S12. *Lhcb1.4*, *RbcS1A*, *PsbS* and *CHS* expression in lincomycin-treated *end* mutants after an increase in fluence rate.

A, *Lhcb1.4* expression in particular *end* mutants after an increase in fluence rate. Wild type (Col-0) and the indicated mutants were grown on media that contained 0.5 mM lincomycin for 6 d in 0.5 μmol m^{-2} s^{-1} BR light, and then transferred to 60 μmol m^{-2} s^{-1} BR light. Seedlings were collected immediately before the fluence-rate shift (0 h), and at 4 h and 8 h following the fluence rate shift. Transcript levels were quantified by qRT-PCR. The order of the lines from left to right: wild type (Col-0, white bars), *gun1-101* (gray bars), *hy5* (brown bars), 1-83 (pink bars), 2-31 (red bars), 3-F12 (orange bars), 5-74 (yellow bars), 6-48 (green bars), 19-29 (blue bars), and 25-G09 (purple bars). Three biological replicates were analyzed for wild type (Col-0) and each mutant in each condition. Error bars indicate standard deviation. * indicates a statistically significant increase ($P=0.0002$ and 0.02) or statistically significant decrease ($P<0.0001$ to 0.03) in the expression of *Lhcb1.4* in a particular mutant relative to wild type.

B, *RbcS1A* expression in particular *end* mutants after an increase in fluence rate. Analysis of *RbcS1A* expression was as described for *Lhcb1.4* expression in A. * indicates a statistically significant decrease ($P=0.002$ to 0.04) in the expression of *RbcS1A* in a particular mutant relative to wild type.

C, *PsbS* expression in particular *end* mutants after an increase in fluence rate. Analysis of *PsbS* expression was as described for *Lhcb1.4* expression in A. * indicates a statistically significant increase ($P<0.0001$) or a statistically significant decrease ($P=0.001$ to 0.03) in the expression of *PsbS* in a particular mutant relative to wild type.

D, *CHS* expression in particular *end* mutants after an increase in fluence rate. Analysis of *CHS* expression was as described for *Lhcb1.4* expression in A. * indicates a statistically significant increase ($P=0.0001$ to 0.007) or a statistically significant decrease ($P=0.0002$ to 0.01) in the expression of *CHS* in a particular mutant relative to wild type.



Supplemental Figure S13. *Lhcb1.4*, *RbcS1A*, *PsbS* and *CHS* expression in particular lincomycin-treated *end* mutants in continuous 60 μmol m^{-2} s^{-1} BR light.

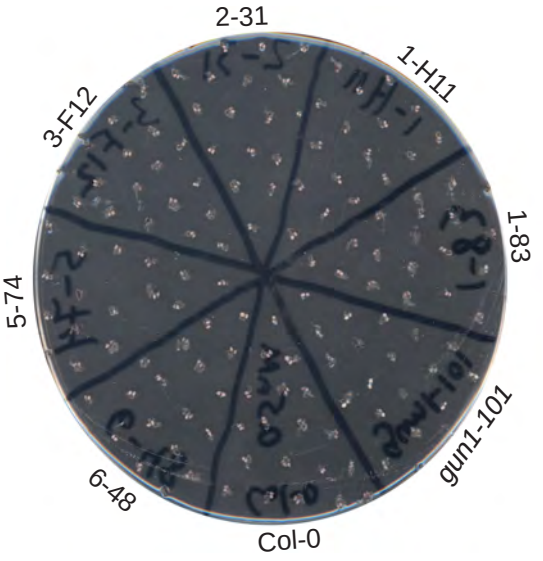
A, *Lhcb1.4* expression in particular *end* mutants grown in continuous 60 μmol m^{-2} s^{-1} BR light. Wild type (Col-0) and the indicated mutants were grown on media that contained 0.5 mM lincomycin for 6 d in continuous 60 μmol m^{-2} s^{-1} BR light. Transcript levels were quantified by qRT-PCR. Three biological replicates were analyzed for wild type (Col-0) and each mutant. Error bars indicate standard deviation. * indicates a statistically significant increase (P<0.0001 to 0.003) or a statistically significant decrease (P=0.04) in the expression of *Lhcb 1.4* in a particular mutant relative to wild type.

B, *RbcS1A* expression in particular *end* mutants. Analysis of *RbcS1A* expression was as described in A. * indicates a statistically significant increase (P=0.002) or statistically significant decrease (0.001 to 0.04) in the expression of *RbcS1A* in a particular mutant relative to wild type .

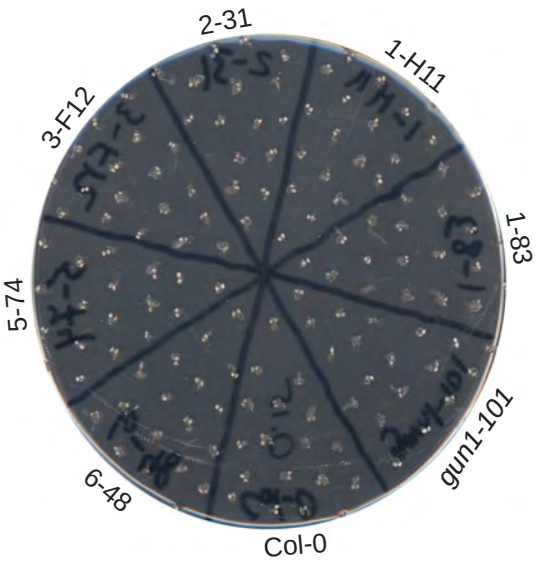
C, *PsbS* expression in particular *end* mutants. Analysis of *PsbS* expression was as described in A. * indicates a statistically significant increase (P=0.0001 and 0.0004) or a statistically significant decrease (P<0.0001 to 0.01) in the expression of *PsbS* in a particular mutant relative to wild type .

D, *CHS* expression in indicated *end* mutants. Analysis of *CHS* expression was as described in A. * indicates a statistically significant increase in the expression of *CHS* in a particular mutant relative to wild type (P<0.0001 to 0.02).

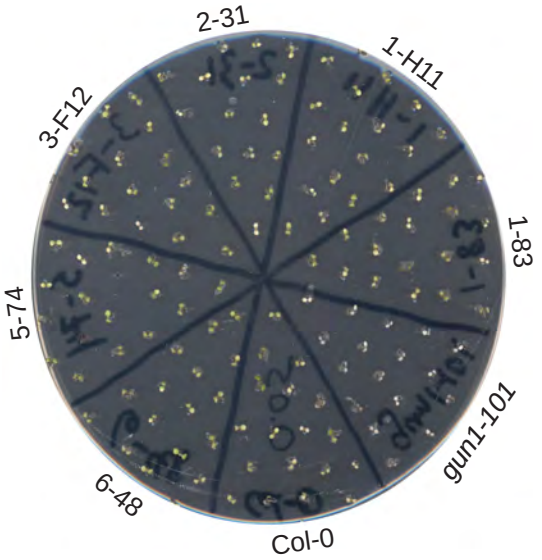
0.5 mM lincomycin



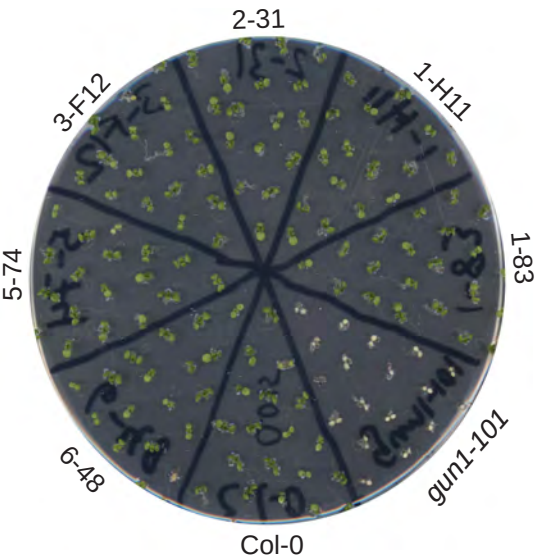
0.15 mM lincomycin



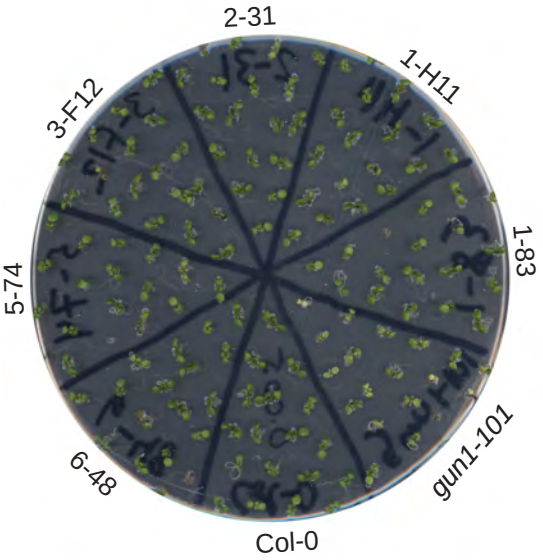
0.05 mM lincomycin



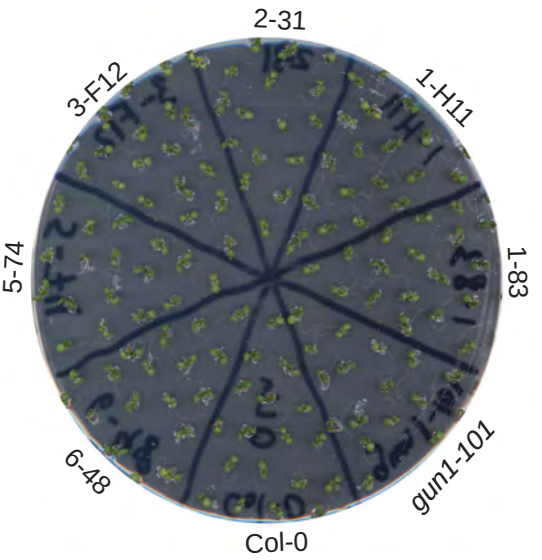
0.015 mM lincomycin



0.005 mM lincomycin

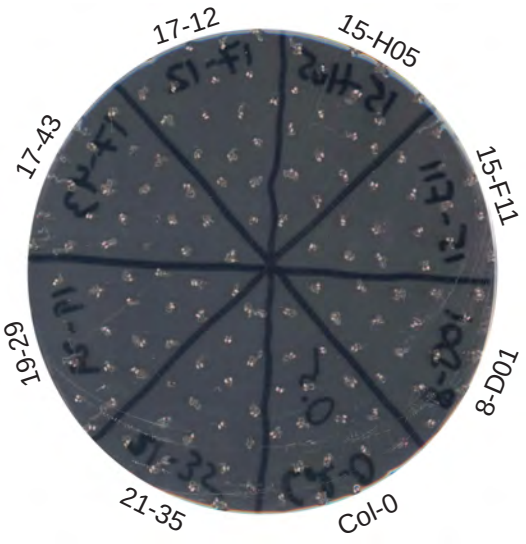


No lincomycin

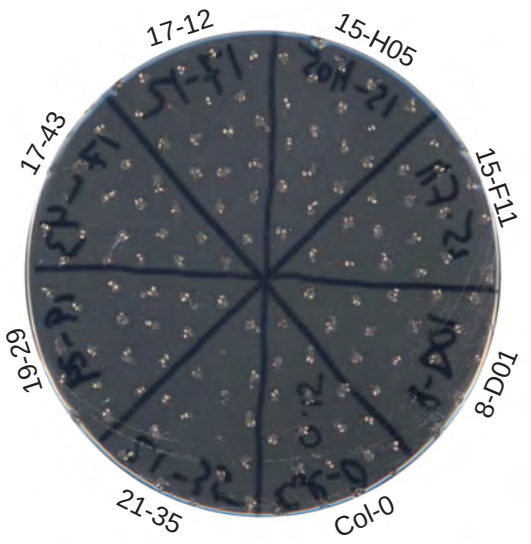


Supplemental Figure S14. *gun1-101*, 1-83, 1-H11, 2-31, 3-F12, 5-74, and 6-48 treated with various concentrations of lincomycin. *gun1-101* and the indicated *end* mutants were grown for 8 d in continuous white light at a fluence rate of 100 μmol m^{-2} s^{-1} on media containing the indicated concentrations of lincomycin.

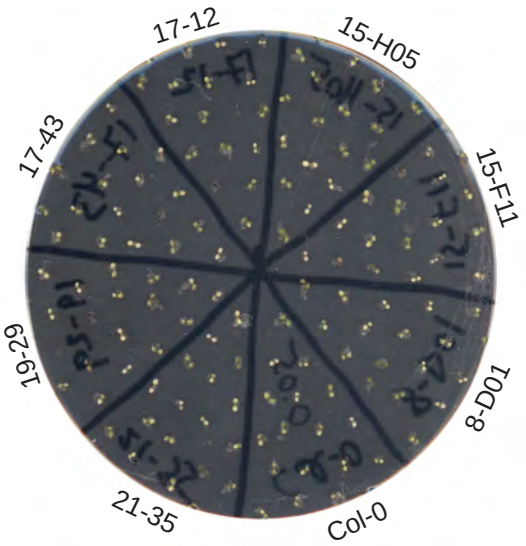
0.5 mM lincomycin



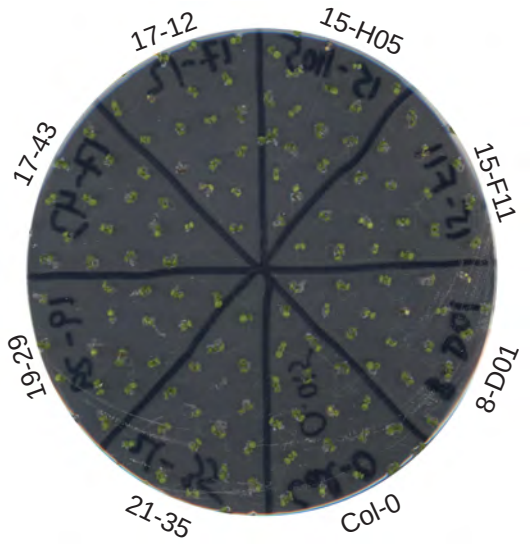
0.15 mM lincomycin



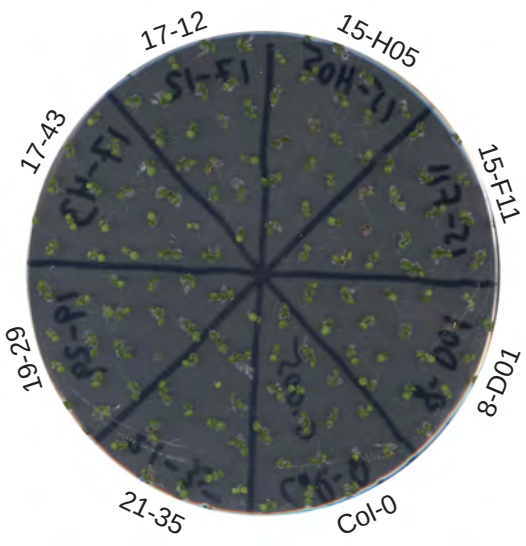
0.05 mM lincomycin



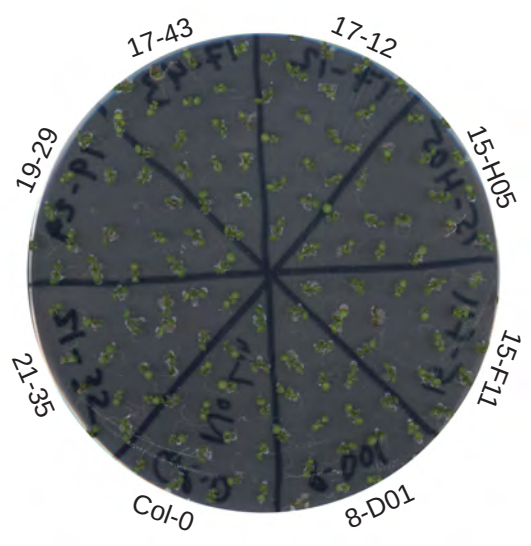
0.015 mM lincomycin



0.005 mM lincomycin

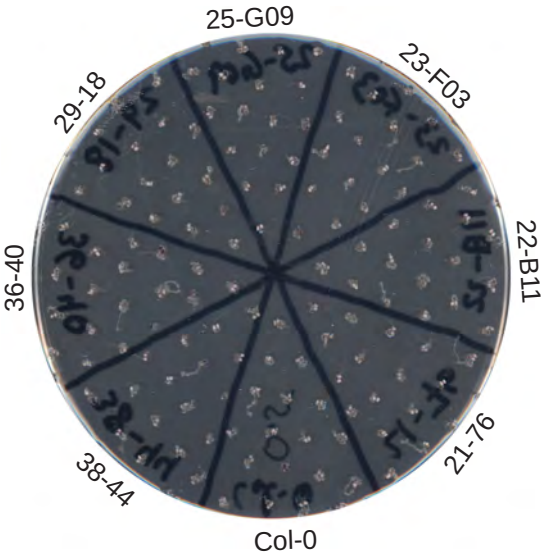


No lincomycin

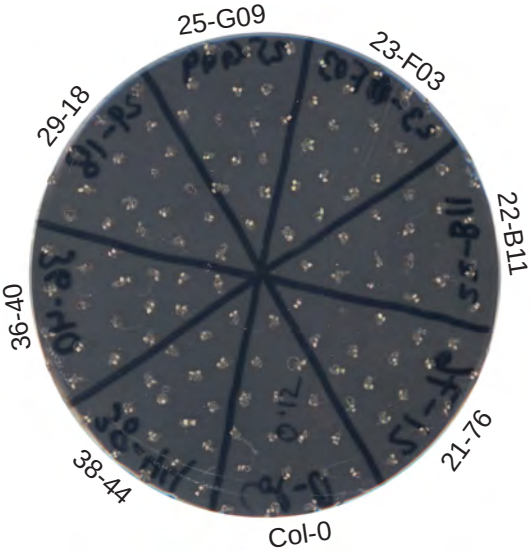


Supplemental Figure S15. 8-D01, 15-F11, 15-H05, 17-12, 17-43, 19-29, and 21-35 treated with various concentrations of lincomycin. The indicated *end* mutants were grown for 8 d in continuous white light at a fluence rate of 100 μmol m^{-2} s^{-1} on media containing the indicated concentrations of lincomycin.

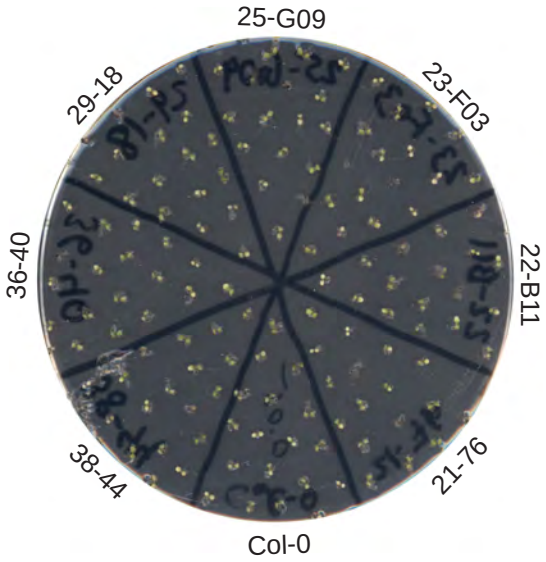
0.5 mM lincomycin



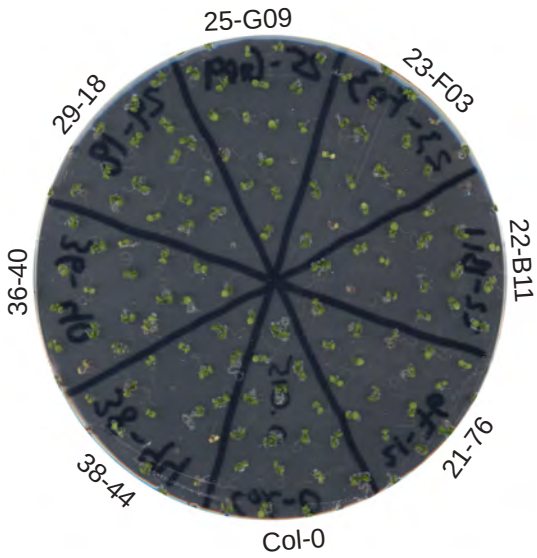
0.15 mM lincomycin



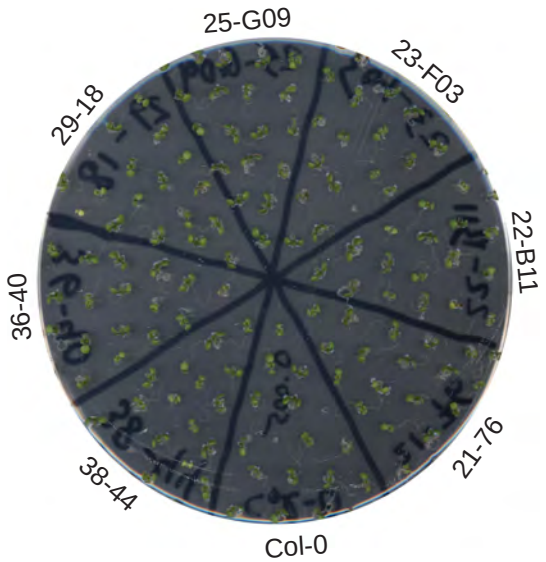
0.05 mM lincomycin



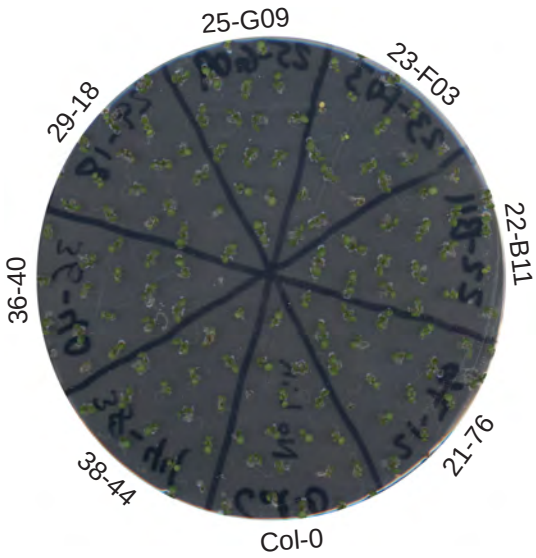
0.015 mM lincomycin



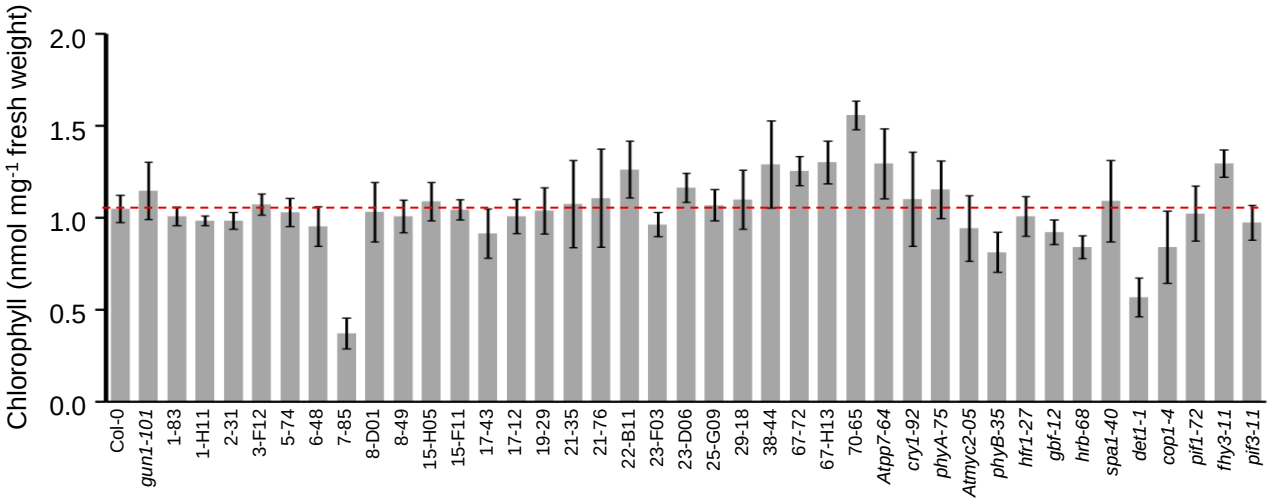
0.005 mM lincomycin



No lincomycin



Supplemental Figure S16. 21-76, 22-B11, 23-F03, 25-G09, 29-18, 36-40, and 38-44 treated with various concentrations of lincomycin. The indicated *end* mutants were grown for 8 d in continuous white light at a fluence rate of 100 μmol m^{-2} s^{-1} on media containing the indicated concentrations of lincomycin.



Supplemental Figure S17. Chlorophyll levels in *end* mutants and light signaling mutants grown in continuous white light. Mutants that accumulated significantly more or less chlorophyll than wild type (Col-0) during de-etiolation experiments (Figs. 7A and B; Figs. 8A and B; Supplemental Fig. S11) were grown for 7 d in continuous 125 μmol m^{-2} s^{-1} broad spectrum white light. Chlorophyll was extracted and quantified from four biological replicates for wild type and each mutant. The mean level of chlorophyll in wild type is indicated with a red-dashed line. Error bars indicate 95% confidence intervals.

Supplemental Table S1. Significance of enriched biological process and cellular component GO terms in particular expression patterns

		GO Term	GO ID	Enrich-ment in all genes	Expressed genes / Total genes in GO term	Light pattern of expression with the highest enrichment		Light cluster of expression with the highest enrichment		Plastid pattern of expression with the highest enrichment		Plastid cluster of expression with the highest enrichment	
				p-value		Pattern number	p-value	Cluster letter	p-value	Pattern number	p-value	Cluster letter	p-value
Plastid													
1	P	Photosyntheisis	GO:0015979	$8x10^{-29}$	74/90	12	$4x10^{-15}$	B	$4x10^{-21}$	25	$3x10^{-34}$	Q	$2x10^{-35}$
2	C	Thylakoid lumen	GO:0031977	$5x10^{-17}$	45/48	12	$2x10^{-17}$	B	$1x10^{-27}$	23	$4x10^{-33}$	Q	$2x10^{-23}$
3	C	Photosystem II	GO:0009523	$8x10^{-14}$	14/15	12	$8x10^{-5}$	B	$1x10^{-6}$	25	$1x10^{-27}$	Q	$3x10^{-23}$
4	C	Thylakoid membrane	GO:0042651	$9x10^{-20}$	48/64	12	$8x10^{-17}$	B	$4x10^{-20}$	23	$3x10^{-26}$	Q	$3x10^{-26}$
5	C	Plastid stroma	GO:0009532	$1x10^{-16}$	80/117	34	$2x10^{-11}$	B	$5x10^{-21}$	23	$7x10^{-17}$	N	$7x10^{-13}$
6	C	Plastoglobule	GO:0010287	$3x10^{-15}$	49/56	12	$6x10^{-8}$	B	$4x10^{-13}$	21	$1x10^{-13}$	Q	$5x10^{-20}$
7	C	Photosystem I	GO:0009522	$1x10^{-5}$	8/9	32	$1.20x10^{-4}$	B	$4x10^{-5}$	22	$7x10^{-14}$	Q	$4x10^{-15}$
8	C	Stromule	GO:0010319	$5x10^{-5}$	22/33	12	$1x10^{-9}$	B	$2x10^{-13}$	21	$7x10^{-9}$	Q	$2x10^{-6}$
9	C	NAD(P)H dehydro-genase complex	GO:0010598	$8x10^{-5}$	9/9	12	$2x10^{-7}$	Y	$1x10^{-9}$	22	$1x10^{-10}$	Q	$2x10^{-11}$
10	P	Tetrapyrrole metabolic process	GO:0033013	$6x10^{-6}$	38/61	12	$5x10^{-6}$	B	$2x10^{-10}$	23	$1x10^{-6}$	P	$3x10^{-6}$
11	P	Plastid organization	GO:0009657	$5x10^{-6}$	49/84	30	$2x10^{-7}$	Z	$7x10^{-10}$	21	$1.66x10^{-4}$	N	$7x10^{-9}$
12	P	Carotenoid metabolic process	GO:0016116	$7.41x10^{-4}$	16/24	N/A	N/A	B	$1x10^{-7}$	N/A	N/A	N	$9x10^{-5}$
13	C	Plastid ribosome	GO:0009547	$3.55x10^{-4}$	16/24	N/A	N/A	EE	$2x10^{-7}$	N/A	N/A	J	$4x10^{-5}$
14	C	Plastid chromosome	GO:0009508	$1.95x10^{-4}$	13/16	10	$1x10^{-6}$	Y	$1x10^{-5}$	25	$1.26x10^{-2}$	N	$1x10^{-5}$
15	C	Plastid membrane	GO:0042170	$2.82x10^{-3}$	57/104	N/A	N/A	Z	$2x10^{-6}$	N/A	N/A	P	$2x10^{-6}$
Translation													
1	P	Translation	GO:0006412	$2x10^{-6}$	32/59	32	$5x10^{-24}$	E	$1x10^{-19}$	23	$7.08x10^{-3}$	N	$9x10^{-23}$
2	C	Cytosolic ribosome	GO:0022626	$1.91x10^{-1}$	70/181	32	$1x10^{-21}$	E	$6x10^{-18}$	24	$4.57x10^{-1}$	N	$3x10^{-12}$
3	P	Ribosome biogenesis	GO:0042254	$2x10^{-5}$	8/10	32	1x10-12	E	$8x10^{-8}$	23	$3.72x10^{-4}$	N	$2x10^{-8}$
Growth and development													
1	P	Cell cycle	GO:0007049	$7.41x10^{-1}$	39/123	N/A	N/A	EE	$9x10^{-7}$	N/A	N/A	K	$4.79x10^{-3}$
2	P	Embryonic development	GO:0009790	$1.62x10^{-1}$	123/326	N/A	N/A	Z	$1x10^{-5}$	N/A	N/A	N	$2.88x10^{-1}$
3	C	Cell wall	GO:0005618	$1.05x10^{-1}$	64/123	31	$2.57x10^{-4}$	N/A	N/A	18	$2x10^{-6}$	N/A	N/A
4	P	Cell wall modification	GO:0042545	$1.23x10^{-1}$	27/61	N/A	N/A	CC	$1.66x10^{-3}$	N/A	N/A	K	$7x10^{-6}$
5	P	DNA replication	GO:0006260	$6.31x10^{-2}$	21/43	27	$4x10^{-6}$	DD	$9x10^{-5}$	28	$7x10^{-7}$	K	$4x10^{-6}$
6	P	Regulation of post-embryonic development	GO:0048580	$1.58x10^{-2}$	57/135	N/A	N/A	GG	$1x10^{-5}$	N/A	N/A	M	$3.31x10^{-4}$
Regulation of gene expression													
1	P	Regulation of transcription	GO:0045449	$9.33x10^{-1}$	206/558	4	$9x10^{-7}$	R	$4x10^{-10}$	21	$3.16x10^{-1}$	M	$2x10^{-5}$
2	P	Cellular protein catabolic process	GO:0044257	$3.02x10^{-1}$	56/134	33	$4x10^{-7}$	GG	$3x10^{-7}$	20	$7.94x10^{-4}$	L	$1.86x10^{-4}$
2	C	Ubiquitin ligase complex	GO:0000151	$1.66x10^{-2}$	19/42	16	$2x10^{-5}$	GG	$1.12x10^{-2}$	20	$1x10^{-7}$	L	$3x10^{-6}$
3	P	RNA processing	GO:0006396	$7x10^{-6}$	47/96	6	$7x10^{-6}$	GG	$6x10^{-7}$	21	$5.25x10^{-1}$	O	$3x10^{-5}$
Metabolism													
1	P	Carbon utilization	GO:0015976	$3.31x10^{-4}$	11/13	12	$1.05x10^{-3}$	Y	$6.31x10^{-4}$	21	$8x10^{-8}$	Q	$3x10^{-6}$
3	P	Cellular amino acid metabolism	GO:0006520	$3x10^{-7}$	59/113	34	$1x10^{-6}$	E	$3x10^{-6}$	22	$2.10x10^{-3}$	N	$4x10^{-5}$
4	P	Lipid transport	GO:0006869	$4.79x10^{-4}$	9/16	N/A	N/A	F	$3x10^{-7}$	N/A	N/A	J	$9x10^{-7}$
5	P	Starch metabolic process	GO:005982	$1.23x10^{-3}$	21/33	32	$2.45x10^{-4}$	N/A	N/A	23	$3x10^{-6}$	N/A	N/A
6	P	Monosaccharide metabolic process	GO:0005996	$6.61x10^{-4}$	22/45	30	$4x10^{-6}$	B	$8x10^{-6}$	21	$3.72x10^{-4}$	P	$1.82x10^{-3}$
Other cellular components													
1	C	Endoplasmic reticulum	GO:0005783	$2.00x10^{-1}$	103/267	N/A	N/A	H	$1x10^{-5}$	N/A	N/A	J	$2.88x10^{-2}$
2	C	Mitochondrion	GO:0005739	$8x10^{-5}$	232/551	32	$2x10^{-9}$	Z	$6x10^{-16}$	29	$4.72x10^{-2}$	J	$2x10^{-5}$

Testing for the enrichment of GO terms was described in Materials and Methods, Fig. 2, Supplemental Figs. S2, S3, S4, and S5. Enrichment in all genes refers to the significance of enrichment of a particular GO term in the entire dataset of 7104 genes. Ontologizer 2.0 was used to calculate the indicated p-values. The ratio of genes in our dataset that are associated with a particular GO term to the total number of genes that are associated with that same GO term is presented for each GO term. The most significantly enriched light- and plastid-regulated expression pattern and cluster is indicated for each GO term. If a particular pattern or cluster was not significantly enriched ($p<0.01$), a p-value is not presented (N/A).

Supplemental Table S2. Significance of enriched biological process and response to stimulus GO terms in particular expression patterns

		GO Term	GO ID	Enrich-ment in all genes	Expressed genes / Total genes in GO term	Light pattern of expression with the highest enrichment		Light cluster of expression with the highest enrichment		Plastid pattern of expression with the highest enrichment		Plastid cluster of expression with the highest enrichment	
				p-value		Pattern number	p-value	Cluster letter	p-value	Pattern number	p-value	Cluster letter	p-value
Oxidative Stress and ROS scavenging													
1	R	Oxidative stress	GO:0006979	$6x10^{-10}$	102/173	34	$3.16x10^{-4}$	I	$1x10^{-5}$	21	$8x10^{-6}$	O	$5.13x10^{-4}$
2	P	Phenyl propanoid Metabolic process	GO:0009698	$4x10^{-5}$	43/82	N/A	N/A	AA	$1x10^{-9}$	N/A	N/A	J	$2.45x10^{-6}$
3	P	Glycoside metabolic process	GO:0016137	$3x10^{-4}$	30/48	16	$1x10^{-6}$	AA	$1x10^{-6}$	18	$1x10^{-7}$	K	$3x10^{-6}$
4	P	Cell death	GO:0008219	$1.86x10^{-3}$	44/80	N/A	N/A	FF	$4x10^{-7}$	N/A	N/A	M	$2.09x10^{-2}$
Biotic and Abiotic stress													
1	R	Heat	GO:0009408	$4x10^{-8}$	57/99	6	$1x10^{-6}$	C	$8x10^{-25}$	20	$3.16x10^{-3}$	M	$1.82x10^{-3}$
2	R	Cold	GO:0009409	$1x10^{-13}$	128/216	34	$1x10^{-7}$	S	$4x10^{-5}$	22	$5x10^{-5}$	J	$2x10^{-6}$
3	R	Water deprivation	GO:0009414	$2x10^{-13}$	97/145	34	$6x10^{-9}$	H	$2x10^{-8}$	20	$6x10^{-10}$	J	$2x10^{-8}$
4	R	Salt stress	GO:0009651	$6x10^{-12}$	117/202	33	$5x10^{-6}$	H	$3x10^{-8}$	20	$8x10^{-5}$	M	$2x10^{-7}$
5	R	Wounding	GO:0009611	$1x10^{-7}$	67/114	15	$6x10^{-5}$	CC	$3.24x10^{-3}$	22	$2.69x10^{-3}$	J	$6.76x10^{-4}$
6	R	Carbohydrate stimulus	GO:0009743	$4x10^{-7}$	93/174	15	$2x10^{-6}$	D	$1x10^{-5}$	20	$3.02x10^{-2}$	M	$7x10^{-6}$
7	R	Metal ion	GO:0010038	$9x10^{-6}$	44/70	11	$2.24x10^{-3}$	D	$6x10^{-5}$	25	$2.14x10^{-2}$	M	$1.26x10^{-3}$
Light													
1	R	UV light	GO:0009411	$5x10^{-7}$	38/55	4	$2x10^{-6}$	AA	$4x10^{-16}$	20	$4x10^{-5}$	K	$3.02x10^{-2}$
2	R	High light intensity	GO:0009644	$3x10^{-10}$	34/41	4	$8x10^{-5}$	C	$1x10^{-9}$	21	$9x10^{-6}$	P	$1x10^{-7}$
3	R	Red and far-red light	GO:0009639	$6x10^{-6}$	77/129	4	$2x10^{-6}$	R	$2x10^{-7}$	21	$3x10^{-8}$	M	$9x10^{-6}$
4	R	Blue light	GO:0009637	$1x10^{-6}$	30/44	4	$8.71x10^{-4}$	U	$1.38x10^{-3}$	21	$3.98x10^{-4}$	Q	$8x10^{-5}$
5	P	Circadian rhythm	GO:0007623	$6x10^{-6}$	30/43	33	$1.66x10^{-4}$	BB	$1.51x10^{-4}$	21	$8x10^{-5}$	L	$4.37x10^{-4}$
Hormones													
1	R	Abscisic acid stimulus	GO:0009737	$4x10^{-12}$	137/245	17	$2x10^{-6}$	H	$9x10^{-9}$	20	$6x10^{-8}$	J	$9x10^{-9}$
2	R	Auxin stimulus	GO:0009733	$3.02x10^{-3}$	76/169	3	$2x10^{-6}$	X	$7x10^{-11}$	21	$1.95x10^{-3}$	M	$2x10^{-9}$
3	R	Jasmonic acid stimulus	GO:0009753	$1x10^{-8}$	80/140	2	$1.10x10^{-4}$	T	$1x10^{-5}$	23	$1.86x10^{-3}$	J	$1.51x10^{-4}$
5	R	Gibberellin stimulus	GO:0009739	$3x10^{-8}$	59/99	11	$9x10^{-6}$	H	$4x10^{-7}$	20	$2.35x10^{-3}$	L	$2.00x10^{-3}$

Testing for the enrichment of GO terms was described in Materials and Methods, Fig. 2, Supplemental Figs. S2, S3,S4, and S5. Enrichment in all genes refers to the significance of enrichment of a particular GO term in the entire dataset of 7104 genes. Ontologizer 2.0 was used to calculate the indicated p-values. The ratio of genes in our dataset that are associated with a particular GO term to the total number of genes that are associated with that same GO term is presented for each GO term. The most significantly enriched light- and plastid-regulated expression pattern and cluster is presented for each GO term. If a particular pattern or cluster was not significantly enriched ($p<0.01$), a p-value is not presented (N/A).

Supplemental Table S3. Genes that exhibit enhanced light-induced expression in lincomycin-treated seedlings and that lack publicly available T-DNA alleles

Number	Arabidopsis Genome Initiative (AGI) Identifier	Light Induction	Plastid regulation	Name/Description	Biological function, process, and location
4	At1g14345	2.45	-5.92	Aldo/keto reductase domain	Oxidation reduction[IEA], Chloroplast thylakoid membrane[a]
9	At1g11380	2.06	-1.80	Cys-rich domain	Unknown
12	At3g49580	1.98	-1.67	LSU1, RESPONSE TO LOW SULFUR 1	Unknown
18	At2g30520	1.87	-1.21	RPT2, ROOT PHOTOTROPISM 2[b]	Phototropism[b], Nucleus[ISS]
24	At5g47610	1.76	-3.56	Zinc finger (C3HC4-type RING finger)	Protein binding[ISS]
26	At2g42540	1.73	5.80	COR15A, COLD-REGULATED 15A	Cold acclimation[c], Chloroplast[d]
27	At1g12250	1.73	-2.48	Expressed protein	Chloroplast thylakoid membrane[a]
30	At1g16720	1.68	-2.19	HCF173, HIGH CHLOROPHYLL FLUORESCENCE 173[e]	Translational initiation[e], Photosystem II assembly[e], Chloroplast[f]
31	At1g42550	1.65	-3.08	PMI1, PLASTID MOVEMENT IMPAIRED1[g]	Chloroplast relocation[g], Plasma membrane[h]
32	At1g79270	1.65	-1.68	ECT8, EVOLUTIONARILY CONSERVED C-TERMINAL REGION 8	Unknown
33	At1g32080	1.64	-6.56	LrgB-like domain protein	Chloroplast inner membrane[i]
34	At5g49330	1.57	1.38	ATMYB111, MYB DOMAIN PROTEIN 111	Transcription factor activity[ISS]
37	At2g02950	1.52	1.17	PKS1, PHYTOCHROME KINASE SUBSTRATE 1	Phototropism[j], Red-far red light signaling[k], Ctytoplasm[k], Plasma membrane[j]

Thirteen genes are ranked by their light induction. Light induction is defined as the ratio of light-induced expression in lincomycin-treated seedlings to light-induced expression in untreated seedlings at 1 h following the BR-fluence-rate shift. Plastid regulation is represented as the ratio of induced or repressed (-) expression in lincomycin-treated seedlings to expression in untreated seedlings at 0 h relative to the BR-fluence-rate shift. Gene names and descriptions are based on available literature or on TIGR gene annotation records. Biological function, process, and location are based on the current literature or the gene ontology with evidence codes as described in Materials and Methods. References: a (Peltier et al., 2004); b (Sakai et al., 2000); c (Lin and Thomashow, 1992); d (Kleffmann et al., 2004); e (Schult et al., 2007); f (Zybailov et al., 2008); g (DeBlasio et al., 2005); h (Nühse et al., 2003); i (Ferro et al., 2003); j (Lariguet et al., 2006); k (Fankhauser et al., 1999).

Supplemental Table S4. Alleles of genes that exhibit similar light-induced expression in lincomycin-treated and untreated seedlings that cause *end* phenotypes

No.	AGI code	Light Induction	Plastid regulation	Name/Description	Biological function, process, and location	T-DNA line(s)	Transcript phenotype in the homozygote
67	At5g59220	1.20	-0.10	HAI1, HIGHLY ABA-INDUCED PP2C GENE 1	Chloroplast[IEA], protein serine/threonine phosphatase activity[ISS], ABA signaling[a-c]	Salk_142672 SAIL_520_H12	Null Upregulated
70	At5g23730	0.83	-0.64	RUP2/EFO2, WD-40 repeat family protein	UV-B signaling[d], vegetative development and flowering[e], CUL4 RING ubiquitin ligase complex[ISS]	Salk_015765	Knockdown

The light induction and the plastid regulation were calculated as described in Supplemental Table S3. Gene names and descriptions are based on available literature or on TIGR gene annotation records. Biological function, process, and location are based on the current literature or the gene ontology with evidence codes as described in Materials and Methods. References: a(Fujita et al., 2009); b(Guo et al., 2010); c(Antoni et al., 2012); d(Gruber et al., 2010); e(Wang et al., 2011).

Supplemental Table S5. The diverse regulators of genes that exhibit enhanced light-induced expression in lincomycin-treated seedlings

Number	AGI Code	Regulators of gene expression
1	At5g24120	Far-red light[E, 1], Red light[E, 1], UV-B[M, 2], Plastid signals[SS, 3], Blue light[E, 4]
2	At3g56290	UV-B[M ,2]
3	At2g30040	Nitrogen[E, 5], Far-red light[E, 1], Red light[E, 1], Brassinosteroid[E, 6], Auxin[E, 6], Cold[E, 7]
5	At5g08050	NA
6	At5g24660	Sulfur[M, L, 8]
7	At3g17040	Red light[E, 9]
8	At1g44000	NA
10	At2g24540	Salt[M, 10], Osmotic[M, 10], Cold[M, 10], Circadian clock[11], UV-B[E, 12]
11	At5g35970	High light[M,13], UV-B[E,12]
13	At4g11360	Phenylglycosides[E, 14], Sucrose starvation[L, 15, Immune response to flg22E[16] , Sucrose addition[E, 17], Chitin[E, 18]
14	At5g14970	NA
15	At5g58650	NA
16	At2g41660	UV-B[E, 12]
17	At5g13770	NA
19	At2g16365	NA
20	At5g52780	NA
21	At3g54990	Photoperiod[19], Nitrogen[E, 5]
22	At5g62430	Circadian clock[20]
23	At3g02380	Reactive oxygen[SS, 21], Far-red light[E, 1], Red light[E, 1]
25	At1g43160	Wounding[E, 22], Intense light[E, 23], Brassinosteroid[E, 6], Auxin[E, 6], Drought[L, 24], Cytokinin[E, 25], Cold[M, 26], Blue light[E, 27], Far-red light[E, 28], Red light[E, 28]
28	At5g52250	Far-red light[E, 1], Red light[E, 1], UV-B[E, 29], High light[M, 13]
29	At1g04770	Sulfur[M, L, 8]
35	At2g33250	NA
36	At2g46340	Far-red light[E, 1], Red light[E, 1], Blue light[E, 30], Green light[E, 31]
38	At4g28740	NA

Only signals that both regulate the expression of these genes and are indicated in the text (including embedded tables) of the indicated references were considered. Large datasets provided in the supplemental material online were not considered. The kinetics of regulated expression is also provided: E, Early, 0-2 h; M, Mid, 2-8 h; L, Late, 8-24 h; SS, Steady State. References: 1 (Khanna et al., 2006); 2 (Brown et al., 2005); 3 (Ankele et al., 2007); 4 (Onda et al., 2008); 5 (Scheible et al., 2004); 6 (Goda et al., 2004); 7 (Lee et al., 2005); 8 (Maruyama-Nakashita et al., 2005); 9 (Monte et al., 2004); 10 (Kreps et al., 2002); 11 (Harmon and Kay, 2003); 12 (Oravecz et al., 2006); 13 (Kleine et al., 2007); 14 (Guan and Nothnagel, 2004); 15 (Contento et al., 2004); 16 (Navarro et al., 2004); 17 (Osuna et al., 2007); 18 (Libault et al., 2007); 19 (Schmid et al., 2003); 20 (Imaizumi et al., 2005); 21 (Charron et al., 2008); 22 (Yan et al., 2007); 23 (Rossel et al., 2007); 24 (Catala et al., 2007); 25 (Rashotte et al., 2003); 26 (Fowler and Thomashow, 2002); 27 (Folta et al., 2003); 28 (Tepperman et al., 2004); 29 (Ulm et al., 2004); 30 (Fittinghoff et al., 2006); 31 (Dhingra et al., 2006).

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