

Supplementary Table 1. Expression data for all genes with significant changes in at least one light condition compared to dark or DCMU compared to white light, respectively.

Description	Functional group	HL/dark	WL/dark	BL/dark	RL/dark	GL/dark	DCMU/WL
PMM0015 Domain of unknown function DUF25	16. Hypothetical	3.7	1.8	2.1	1.3	1.1	-1.3
PMM0041 possible reductase	15. Other categories	2.3	2.6	1.9	1.4	1.3	-1.7
PMM0043 flavoprotein	15. Other categories	4.4	2.1	2.8	1.4	1.0	-1.5
PMM0046 Nucleoside diphosphate kinase	9. Purines, pyrimidines, nucleosides, and nucleotides	1.2	2.0	1.6	1.1	1.5	-1.3
PMM0051 conserved hypothetical protein	16. Hypothetical	-2.5	-1.6	-2.4	-1.4	-1.0	1.5
PMM0061 YGGT family, conserved hypothetical integral membrane protein	15. Other categories	-1.7	-1.5	-2.0	1.0	-1.1	1.3
PMM0065 ABC transporter, ATP binding protein	14. Transport and binding proteins	2.3	1.4	1.2	1.3	1.1	-1.2
PMM0066 conserved hypothetical protein	16. Hypothetical	3.8	1.7	1.9	1.3	1.1	-1.5
PMM0075 conserved hypothetical protein	16. Hypothetical	2.6	2.1	2.8	1.3	1.4	-1.4
PMM0079 bcp putative bacterioferritin comigratory (BCP) protein	14. Transport and binding proteins	-2.3	1.1	-1.4	-1.1	1.3	-1.1
PMM0081 cysH Phosphoadenosine phosphosulfate reductase	1. Amino acid biosynthesis	-2.1	-1.0	-2.1	-1.2	-1.2	-1.2
PMM0082 putative NADH dehydrogenase, transport associated	10. Regulatory functions	2.6	1.5	1.4	1.4	1.1	-1.2
PMM0087 conserved hypothetical protein	16. Hypothetical	-2.5	-1.2	-1.8	-1.4	-1.0	1.1
PMM0092 conserved hypothetical protein	16. Hypothetical	2.5	1.7	1.3	1.2	1.0	-1.4
PMM0110 putative glutathione S-transferase	2. Biosynthesis of cofactors, prosthetic groups, and carriers	3.8	1.8	2.1	1.2	1.1	-1.5
PMM0115 crtQ zeta-carotene desaturase	2. Biosynthesis of cofactors, prosthetic groups, and carriers	3.1	1.7	1.6	1.3	1.0	-1.3
PMM0144 pds,crtD phytoene desaturase	2. Biosynthesis of cofactors, prosthetic groups, and carriers	7.2	2.9	3.9	1.5	1.0	-1.7
PMM0190 conserved hypothetical protein	16. Hypothetical	2.3	1.5	1.4	1.6	1.0	-1.3
PMM0195 pgk, cbbK Phosphoglycerate kinase	15. Other categories	5.9	4.7	5.7	2.9	1.5	-2.2
PMM0200 rnhA possible ribonuclease HI	12. Transcription	1.6	2.2	1.0	1.2	-1.1	-1.5
PMM0215 Delta-aminolevulinic acid dehydratase	7. Fatty acid, phospholipid and sterol metabolism	-3.1	-1.3	-2.3	-1.5	-1.1	1.0
PMM0223 psbA Photosystem II PsbA protein (D1)	8. Photosynthesis and respiration	2.3	1.9	2.0	1.6	1.5	1.0
PMM0226 ftsH2 cell division protein FtsH2	4. Cellular processes	4.1	2.3	2.7	1.5	1.2	-1.4

PMM0227 cysD ATP-sulfurylase	1. Amino acid biosynthesis	-1.1	2.3	-1.1	1.5	1.0	-1.8
PMM0236 crtR	16. Hypothetical	3.6	1.6	1.4	1.7	1.0	-1.3
PMM0239 conserved hypothetical protein	16. Hypothetical	3.9	1.1	-1.2	1.2	1.3	-1.1
PMM0245 cob(I)alamin adenosyltransferase	2. Biosynthesis of cofactors, prosthetic groups, and carriers	-1.0	-1.1	-2.0	-1.2	-1.5	-1.2
PMM0252 psbN Photosystem II reaction centre N protein	8. Photosynthesis and respiration	4.9	2.1	2.8	1.5	-1.2	-1.5
PMM0275 pyrE Orotate phosphoribosyltransferase	9. Purines, pyrimidines, nucleosides, and nucleotides	-2.1	-1.2	-2.0	-1.2	-1.2	-1.1
PMM0280 Retinal pigment epithelial membrane protein	15. Other categories	7.9	3.3	5.3	2.0	1.0	-1.8
PMM0283 conserved hypothetical protein	16. Hypothetical	1.7	1.8	2.0	1.2	1.4	-1.3
PMM0286 NUDIX hydrolase	15. Other categories	3.0	2.1	2.5	1.1	1.1	-1.6
PMM0295 rub probable rubredoxin	15. Other categories	3.0	2.3	2.5	1.3	1.2	-1.3
PMM0296 conserved hypothetical protein	16. Hypothetical	2.1	1.9	2.1	1.3	1.2	-1.3
PMM0305 cpeB Phycobilisome protein	8. Photosynthesis and respiration	-3.7	-1.4	-2.5	-1.4	-1.2	-1.0
PMM0307 hypothetical protein	16. Hypothetical	-4.1	-1.2	-2.0	-1.3	-1.0	-1.1
PMM0316 possible ferredoxin	8. Photosynthesis and respiration	12.4	4.7	6.6	2.1	1.1	-1.9
PMM0329 psaE Photosystem I Psae protein	8. Photosynthesis and respiration	-3.7	1.1	-1.9	-1.5	-1.0	-1.3
PMM0330 possible LysM domain	10. Regulatory functions	-2.4	-1.2	-2.1	-1.6	-1.1	-1.1
PMM0336 conserved hypothetical protein	16. Hypothetical	3.0	3.8	2.6	2.5	1.0	-3.6
PMM0340 conserved hypothetical protein	16. Hypothetical	2.4	1.6	2.0	1.3	1.2	1.0
PMM0343 mttA/Hcf106 family	15. Other categories	-1.6	1.1	-2.1	-1.2	-1.1	-1.2
PMM0345 putative bacterioferritin comigratory protein	14. Transport and binding proteins	4.4	1.9	2.5	1.4	1.0	-1.4
PMM0347 conserved hypothetical protein	16. Hypothetical	5.4	2.2	2.6	1.6	1.3	-1.5
PMM0355 conserved hypothetical protein	16. Hypothetical	-2.1	-1.1	-2.0	-1.4	1.0	1.0
PMM0356 Alpha/beta hydrolase fold: Esterase/lipase/thioesterase family	7. Fatty acid, phospholipid and sterol metabolism	-3.1	-1.8	-2.9	-2.0	-1.0	2.0
PMM0364 possible Malic enzyme	15. Other categories	2.2	1.5	2.2	1.5	1.5	1.1
PMM0365 possible DsrE-like protein	15. Other categories	2.5	1.7	2.5	1.0	1.3	-1.2
PMM0366 Type-1 copper (blue) domain	14. Transport and binding proteins	4.3	1.7	2.8	1.4	1.1	-1.1

PMM0367 conserved hypothetical protein	16. Hypothetical	2.0	2.1	2.0	2.0	1.3	-1.4
PMM0380 conserved hypothetical protein	16. Hypothetical	3.1	1.9	2.2	1.2	1.2	-1.3
PMM0400 IrtA light repressed protein A homolog	15. Other categories	-2.6	-1.1	-2.0	-1.6	-1.2	-1.2
PMM0417 hypothetical protein	16. Hypothetical	-2.9	-1.1	-1.8	1.2	-1.0	1.0
PMM0423 conserved hypothetical protein	16. Hypothetical	2.4	1.8	1.5	1.3	-1.1	-1.4
PMM0444 ctaE Cytochrome c oxidase, subunit III	8. Photosynthesis and respiration	-2.1	-1.3	-1.9	-1.2	-1.1	1.1
PMM0446 ctaC (coxB) putative cytochrome c oxidase, subunit 2	8. Photosynthesis and respiration	-2.4	-1.5	-2.3	-1.3	-1.2	-1.0
PMM0452 groEL2, cpn60-2 GroEL2 protein (Chaperonin cpn60 2)	4. Cellular processes	1.3	2.3	1.9	1.1	1.4	-1.6
PMM0453 fabG 3-oxoacyl-[acyl-carrier protein] reductase	7. Fatty acid, phospholipid and sterol metabolism	-2.0	1.3	-1.6	-1.1	1.2	-1.1
PMM0462 petC Rieske iron-sulfur protein	8. Photosynthesis and respiration	-3.1	-1.2	-1.9	-1.2	1.0	1.0
PMM0468 psaJ Photosystem I PsaJ protein	8. Photosynthesis and respiration	-4.4	-1.2	-2.0	-1.1	-1.0	1.1
PMM0469 psaF Photosystem I PsaF protein	8. Photosynthesis and respiration	-5.3	-1.2	-2.3	-1.8	-1.2	1.1
PMM0481 conserved hypothetical protein	16. Hypothetical	-2.9	-1.0	-2.7	-1.4	-1.0	-1.2
PMM0540 psaM possible photosystem I reaction PsaM protein	8. Photosynthesis and respiration	-3.8	-1.3	-1.5	-1.1	1.1	1.1
PMM0542 por, pcr Light dependent protochlorophyllide oxidoreductase	2. Biosynthesis of cofactors, prosthetic groups, and carriers	-2.0	-1.0	-1.7	1.0	-1.1	-1.2
PMM0543 chlL, frxC Protochlorophyllide reductase iron-sulfur ATP-binding protein	2. Biosynthesis of cofactors, prosthetic groups, and carriers	-3.5	-1.1	-2.1	-1.1	-1.0	1.0
PMM0544 chlB Light-independent protochlorophyllide reductase subunit B	2. Biosynthesis of cofactors, prosthetic groups, and carriers	-6.2	-1.8	-4.1	-1.8	-1.2	1.4
PMM0545 chlN Light-independent protochlorophyllide reductase subunit N	2. Biosynthesis of cofactors, prosthetic groups, and carriers	-5.5	-1.7	-3.6	-1.5	-1.1	1.3
PMM0546 conserved hypothetical protein	16. Hypothetical	-2.9	-1.3	-2.1	-1.9	1.1	1.3
PMM0557 conserved hypothetical protein	16. Hypothetical	-3.0	-1.5	-2.2	-1.7	-1.2	-1.0
PMM0561 putative multidrug efflux ABC transporter	14. Transport and binding proteins	3.3	1.9	1.9	1.6	1.0	-1.4
PMM0577 Putative type II alternative sigma factor, sigma70 family	12. Transcription	-2.0	-1.1	-2.2	-1.5	-1.1	-1.0
PMM0583 hemE Uroporphyrinogen decarboxylase (URO-D)	2. Biosynthesis of cofactors, prosthetic groups, and carriers	-3.6	-1.1	-1.8	-1.2	1.0	1.1

PMM0593 Peptidase family M3	7. Fatty acid, phospholipid and sterol metabolism	3.7	2.4	2.9	1.7	1.1	-1.7
PMM0594 ndhD putative NADH Dehydrogenase (complex I) subunit(chain 4)	15. Other categories	4.3	2.8	2.8	2.2	1.1	-1.7
PMM0600 conserved hypothetical protein	16. Hypothetical	-2.1	-1.2	-2.3	-1.1	-1.2	-1.0
PMM0618 sds polyprenyl synthetase; solanesyl diphosphatesynthase (sds)	2. Biosynthesis of cofactors, prosthetic groups, and carriers	4.1	1.6	1.9	1.3	-1.1	-1.2
PMM0642 cysD putative O-Acetyl homoserine sulfhydrylase	1. Amino acid biosynthesis	-4.4	-1.3	-2.1	-1.5	1.2	1.1
PMM0643 metaA putative homoserine O-succinyltransferase	1. Amino acid biosynthesis	-2.0	-1.2	-1.8	-1.1	-1.1	-1.0
PMM0660 possible RNA recognition motif. (a.k.a. RRM, R	12. Transcription	-4.6	-2.0	-3.2	-1.8	-1.1	1.5
PMM0661 nrdJ, ribonucleotide reductase (Class II)	9. Purines, pyrimidines, nucleosides, and nucleotides	-2.6	1.1	-1.7	-1.2	1.0	-1.1
PMM0680 conserved hypothetical protein	16. Hypothetical	3.8	2.0	2.6	1.5	1.1	-1.5
PMM0689 hli22 possible high light inducible protein	15. Other categories	10.9	2.0	4.1	1.2	-1.1	-1.3
PMM0690 hli21 possible high light inducible protein	15. Other categories	29.1	4.5	8.9	2.2	1.2	-1.7
PMM0691 conserved hypothetical protein	16. Hypothetical	-2.5	1.4	-1.2	-1.1	1.3	-1.2
PMM0696 hypothetical protein	16. Hypothetical	2.6	1.8	1.4	1.1	1.1	-1.5
PMM0697 possible D12 class N6 adenine-specific DNA met	11. DNA replication, recombination, and repair	2.4	2.0	1.8	1.0	1.0	-1.5
PMM0699 conserved hypothetical protein	16. Hypothetical	3.9	2.7	3.7	1.6	1.3	-1.7
PMM0703 conserved hypothetical protein	16. Hypothetical	11.2	3.2	4.7	1.9	1.0	-1.9
PMM0741 conserved hypothetical protein	16. Hypothetical	1.7	2.2	1.1	1.4	1.0	-1.7
PMM0743 ftsH1 FtsH ATP-dependent protease homolog	4. Cellular processes	3.8	2.2	2.4	1.2	1.1	-1.4
PMM0760 chlP Aromatic-ring hydroxylase (flavoproteinmonooxygenase)	2. Biosynthesis of cofactors, prosthetic groups, and carriers	-3.6	1.1	-2.0	-1.2	-1.1	-1.2
PMM0766 rpe, cbbE Ribulose-phosphate 3-epimerase	15. Other categories	2.1	2.7	2.2	1.4	1.5	-1.5
PMM0781 cbbA, cfxA, fbaA, fda Fructose-bisphosphate/sedoheptulose-1,7-bisphosphate aldolase	7. Fatty acid, phospholipid and sterol metabolism	1.8	2.3	1.6	1.3	1.3	-1.4
PMM0799 conserved hypothetical protein	16. Hypothetical	-2.1	-1.2	-1.9	1.1	1.1	1.0

PMM0808 Rieske iron-sulfur protein 2Fe-2S subunit	5. Central intermediary metabolism	-2.1	-1.1	-1.9	-1.1	-1.2	-1.1
PMM0810 hypothetical protein	16. Hypothetical	4.5	2.2	2.3	1.3	1.1	-1.4
PMM0814 possible Cytochrome oxidase c subunit VIb	15. Other categories	-1.4	-1.2	-2.0	1.1	-1.3	1.0
PMM0817 hli17 possible high light inducible protein	15. Other categories	33.1	6.3	15.0	2.8	1.1	-1.9
PMM0818 hli16 possible high light inducible protein	15. Other categories	41.7	6.6	16.4	2.9	1.2	-2.0
PMM0844 PNIL34,AT103 phytochrome-regulated gene	15. Other categories	-3.3	-1.0	-1.6	-1.1	1.1	-1.0
PMM0861 possible Virion host shutoff protein	14. Transport and binding proteins	1.2	1.3	2.2	-1.1	1.1	-1.1
PMM0881 conserved hypothetical protein	16. Hypothetical	-2.7	-1.7	-2.5	-1.1	-1.2	1.1
PMM0906 psaK Photosystem I PsaK protein	8. Photosynthesis and respiration	-4.3	-1.4	-2.1	-1.1	1.0	1.2
PMM0921 SAM (and some other nucleotide) bindingmotif:Generic methyl-transferase	12. Transcription	3.3	1.8	1.8	1.2	-1.1	-1.6
PMM0953 conserved hypothetical protein	16. Hypothetical	-4.1	-1.0	-1.7	-1.4	1.0	-1.2
PMM0954 ABC transporter, multidrug efflux family	14. Transport and binding proteins	2.8	1.4	1.3	1.2	1.0	-1.3
PMM0962 possible Vng0271c	15. Other categories	2.1	2.1	1.9	1.5	1.2	-1.4
PMM0975 conserved hypothetical protein	16. Hypothetical	2.1	1.3	1.1	1.1	1.0	-1.2
PMM0977 putative multidrug efflux ABC transporter	14. Transport and binding proteins	2.5	1.3	1.4	1.4	1.1	-1.3
PMM0997 possible Protein of unknown function DUF67	16. Hypothetical	3.3	2.9	2.3	2.2	1.2	-1.7
PMM0998 conserved hypothetical protein	16. Hypothetical	2.7	1.6	1.5	1.2	1.0	-1.4
PMM1001 conserved hypothetical protein	16. Hypothetical	7.7	2.9	3.7	1.6	1.1	-1.8
PMM1003 possible Photosystem II reaction centre N protein	8. Photosynthesis and respiration	-4.0	-1.6	-2.6	-1.0	-1.2	-1.0
PMM1006 Glutathione peroxidase	15. Other categories	7.3	3.0	5.1	1.8	1.2	-1.8
PMM1008 hypothetical protein	16. Hypothetical	2.6	1.4	1.4	1.4	1.0	-1.4
PMM1011 hypothetical protein	16. Hypothetical	-3.3	1.4	-1.1	1.5	1.4	-1.4
PMM1015 conserved hypothetical protein	16. Hypothetical	3.6	1.4	1.9	1.7	1.1	-1.2
PMM1018 hypothetical protein	16. Hypothetical	2.2	2.3	1.6	1.6	1.1	-2.1

PMM1019 possible Integrin alpha cytoplasmic region	15. Other categories	2.0	1.5	1.3	1.0	1.0	-1.3
PMM1022 conserved hypothetical protein	16. Hypothetical	3.5	1.6	1.6	1.2	1.0	-1.3
PMM1026 conserved hypothetical protein	16. Hypothetical	4.0	2.3	3.3	1.8	1.3	-1.5
PMM1028 conserved hypothetical protein	16. Hypothetical	-6.6	-3.5	-3.5	-2.8	1.1	3.4
PMM1055 chl Protoporphyrin IX Magnesium chelatase	2. Biosynthesis of cofactors, prosthetic groups, and carriers	2.3	2.5	2.4	1.6	1.5	-1.5
PMM1058 petG Cytochrome b6/f complex, subunit V	8. Photosynthesis and respiration	-3.1	-1.2	-2.2	-1.1	-1.1	-1.1
PMM1068 conserved hypothetical protein	16. Hypothetical	3.4	1.8	1.9	1.4	1.2	-1.4
PMM1083 possible kinase	15. Other categories	2.6	1.8	1.7	1.2	1.1	-1.4
PMM1118 hli4 possible high light inducible protein	15. Other categories	37.0	12.2	25.4	6.4	1.8	-1.7
PMM1119 som possible porin	3. Cell envelope	1.7	1.7	2.0	1.4	1.4	-1.2
PMM1128 hli15 possible high light inducible protein	15. Other categories	3.9	1.8	2.4	1.3	1.1	-1.2
PMM1131 conserved hypothetical protein	16. Hypothetical	-2.2	-1.1	-2.1	-1.5	-1.1	-1.1
PMM1135 hli14 possible high light inducible protein	15. Other categories	40.8	11.3	23.0	4.9	1.3	-1.7
PMM1148 possible EF-1 guanine nucleotide exchange domain	13. Translation	-11.3	-2.2	-5.0	-2.1	-1.2	1.5
PMM1149 conserved hypothetical	16. Hypothetical	-2.0	1.3	-1.4	-1.0	-1.0	-1.1
PMM1164 futA,sfuA, idiA putative iron ABC transporter, substrate binding protein	14. Transport and binding proteins	1.6	2.3	1.3	1.2	1.4	-1.3
PMM1168 conserved hypothetical protein	16. Hypothetical	5.4	2.3	2.6	1.3	1.0	-1.7
PMM1176 possible Helix-turn-helix protein, copG family	10. Regulatory functions	-2.9	-1.9	-2.6	-1.2	-1.2	1.2
PMM1185 conserved hypothetical protein	16. Hypothetical	2.8	1.8	2.1	1.2	1.0	-1.4
PMM1229 Dehydrogenase, E1 component	6. Energy Metabolism	1.9	2.1	1.5	1.9	1.2	-1.6
PMM1240 methyltransferase	15. Other categories	1.3	2.1	1.3	1.5	1.3	-1.6
PMM1266 conserved hypothetical protein	16. Hypothetical	3.9	2.4	2.6	1.8	1.2	-1.5
PMM1295 putative signal peptidase	10. Regulatory functions	1.8	1.9	1.1	1.3	1.0	-1.3
PMM1314 clpP3 Clp protease proteolytic subunit	13. Translation	2.3	1.7	1.5	-1.1	1.1	1.0
PMM1357 Steroid 5-alpha reductase, C-terminal domain	10. Regulatory functions	8.8	3.0	3.8	2.0	1.0	-1.6
PMM1358 conserved hypothetical protein	16. Hypothetical	2.6	1.6	1.4	1.2	1.0	-1.4

PMM1359 conserved hypothetical protein	16. Hypothetical	61.2	17.4	37.2	5.9	1.1	-4.2
PMM1360 similar to DNA photolyase	11. DNA replication, recombination, and repair	2.4	1.5	1.7	1.2	1.1	-1.4
PMM1361 Short-chain dehydrogenase/reductase (SDR) superfamily	15. Other categories	6.4	2.4	4.3	1.5	1.1	-1.6
PMM1368 conserved hypothetical protein	16. Hypothetical	3.2	1.6	2.0	1.3	1.2	-1.2
PMM1369 GAF domain	10. Regulatory functions	-3.4	-1.8	-3.2	-1.2	-1.4	1.3
PMM1372 conserved hypothetical protein	16. Hypothetical	-2.1	-1.1	-1.6	-1.3	-1.0	-1.0
PMM1374 possible Type I restriction modification DNA s	14. Transport and binding proteins	-1.6	-1.7	-2.0	-1.5	-1.0	1.6
PMM1379 putative dape gene and orf2	10. Regulatory functions	-4.8	-1.9	-3.5	-1.4	1.1	1.9
PMM1384 hli12 possible high light inducible protein	15. Other categories	13.4	6.6	9.4	3.6	1.6	-1.5
PMM1385 hli11 possible high light inducible protein	15. Other categories	9.5	5.4	8.1	3.3	1.4	-1.4
PMM1387 hypothetical protein	16. Hypothetical	6.1	2.6	3.5	1.6	1.0	-1.7
PMM1395 hypothetical protein	16. Hypothetical	2.9	1.4	1.5	1.7	1.1	-1.1
PMM1396 hli9 possible high light inducible protein	15. Other categories	41.3	6.8	16.7	2.5	1.1	-2.0
PMM1397 hli8 possible high light inducible protein	15. Other categories	42.2	8.1	19.2	2.2	1.2	-2.0
PMM1400 possible Hemagglutinin-neuraminidase	15. Other categories	-3.5	-2.0	-1.7	-2.9	-1.1	1.5
PMM1402 hypothetical protein	16. Hypothetical	-2.0	-1.2	-2.2	-1.8	1.3	1.5
PMM1404 hli5 possible high light inducible protein	15. Other categories	39.5	4.6	20.0	3.2	1.3	-1.5
PMM1421 possible Gibberellin regulated protein	15. Other categories	2.9	1.7	2.1	1.4	1.0	-1.3
PMM1422 conserved hypothetical protein	16. Hypothetical	3.8	2.0	2.9	1.0	1.1	-1.4
PMM1429 conserved hypothetical protein	16. Hypothetical	1.9	2.0	1.5	1.5	1.3	-1.3
PMM1442 pepP putative aminopeptidase P	10. Regulatory functions	2.6	1.6	1.5	1.4	1.1	-1.3
PMM1456 atpI ATP synthase A subunit	8. Photosynthesis and respiration	2.4	2.7	2.1	2.5	1.4	-1.5
PMM1457 atp1 possible ATP synthase subunit 1	16. Hypothetical	2.4	2.7	2.3	2.4	1.4	-1.6
PMM1462 conserved hypothetical protein	16. Hypothetical	-3.6	-1.3	-1.7	-2.8	-2.9	-2.1
PMM1477 conserved hypothetical protein	16. Hypothetical	2.8	1.8	1.3	1.5	1.0	-1.6
PMM1478 conserved hypothetical protein	16. Hypothetical	3.1	2.2	1.8	1.5	-1.1	-1.7

PMM1482 hli3 possible high light inducible protein	15. Other categories	2.9	1.9	2.2	1.7	1.1	-1.4
PMM1490 Serine proteases, trypsin family:Chymotrypsin-serine protease	13. Translation	4.1	2.0	2.6	1.6	1.0	-1.4
PMM1498 conserved hypothetical protein	16. Hypothetical	3.5	1.8	2.3	1.5	1.0	-1.4
PMM1505 SAM (and some other nucleotide) binding motif	12. Transcription	2.9	1.5	1.5	1.3	-1.1	-1.3
PMM1506 ATP-dependent protease La (LON) domain	10. Regulatory functions	3.2	2.0	1.8	1.6	1.0	-1.3
PMM1519 psaL Photosystem I protein PsaL	8. Photosynthesis and respiration	-4.2	-1.2	-1.8	-1.2	1.1	1.1
PMM1520 psal photosystem I protein Psal	8. Photosynthesis and respiration	-4.0	-1.2	-1.8	-1.3	1.1	1.0
PMM1547 rpl24, rplX 50S ribosomal protein L24	13. Translation	1.8	2.2	1.4	-1.1	1.0	-1.6
PMM1548 rpl14, rplN 50S Ribosomal protein L14	13. Translation	2.0	2.5	1.5	1.1	1.0	-1.7
PMM1549 rps17, rpsQ 30S Ribosomal protein S17	13. Translation	1.9	2.1	1.2	1.0	-1.1	-1.5
PMM1550 rpl29, rpmC 50S ribosomal protein L29	13. Translation	1.9	2.3	1.2	1.0	1.0	-1.7
PMM1551 rpl16, rplP 50S ribosomal protein L16	13. Translation	1.9	2.2	1.4	1.1	1.0	-1.6
PMM1578 psaD Photosystem I protein PsaD	8. Photosynthesis and respiration	-4.3	-1.0	-1.7	-1.6	1.0	-1.1
PMM1589 purM,purG phosphoribosyl formylglycinamide cyclo-ligase	9. Purines, pyrimidines, nucleosides, and nucleotides	-2.5	-1.3	-1.7	-1.5	-1.1	1.0
PMM1599 conserved hypothetical protein	16. Hypothetical	3.2	1.7	1.8	1.5	1.0	-1.2
PMM1618 lysS Lysyl-tRNA synthetase	13. Translation	1.8	2.0	1.6	1.4	1.3	-1.4
PMM1628 possible alpha/beta hydrolase superfamily	15. Other categories	3.8	2.0	2.5	1.7	1.2	-1.4
PMM1629 Type II alternative RNA polymerase sigma factor,sigma-70 family	14. Transport and binding proteins	12.5	11.4	10.3	4.3	2.3	-1.3
PMM1657 clpX Clp protease ATP-binding subunit	13. Translation	-3.8	-1.7	-3.2	-1.7	-1.3	1.2
PMM1663 putative photosystem I assembly related proteinYcf37	10. Regulatory functions	2.1	2.0	1.2	1.2	-1.1	-1.4
PMM1669 gcsH, gcvH putative Glycine cleavage H-protein	10. Regulatory functions	3.7	1.7	1.5	1.6	1.0	-1.3
PMM1670 conserved hypothetical protein	16. Hypothetical	6.2	1.3	-1.4	2.6	-1.2	-1.3
PMM1671 conserved hypothetical protein	16. Hypothetical	9.6	1.5	-1.7	4.2	-1.6	-1.5

PMM1672 des9 Fatty acid desaturase, type 1	7. Fatty acid, phospholipid and sterol metabolism	18.9	2.1	-2.1	6.4	-2.2	-1.8
PMM1697 Type II alternative RNA polymerase sigma factor, sigma-70 family	12. Transcription	-3.5	-1.6	-3.0	-1.6	-1.2	1.2
PMM1704 dnaK2 Molecular chaperone DnaK2, heat shock protein hsp70-2	4. Cellular processes	1.6	2.0	2.7	1.4	1.7	-1.2
PMM1712 uvrA Excinuclease ABC, A subunit, ATP/GTP-binding site motif A (P-loop)	14. Transport and binding proteins	2.7	1.5	1.6	1.3	1.0	-1.2
PMM1714 possible protein kinase: ABC1 family	15. Other categories	2.5	1.7	1.5	1.4	1.0	-1.3

Significant expression ratios (≥ 2 -fold and $\text{FDR} \leq 0.05$) are given in blue bold numbers. Positive values indicate induction and negative values reduction of gene expression upon transfer to the respective light treatment. HL – high white light; WL – white light, BL – blue light; RL – red light; GL – green light; DCMU – DCMU + white light.