

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

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

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

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

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

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

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

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

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

Significant expression ratios ( $\geq 2$ -fold and 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.