

Table 1S. Differentially expressed genes (DEGs) mapped to Kyoto encyclopedia of genes and genomes (KEGG) pathways related with photosynthesis.

Supplementary material: The list of all differentially expressed genes (DEGs) transcriptional analysis identified 3008 differentially expressed genes (DEGs).

Gene ID	Annotation	FDR	Log2FC	Regulated
A:photosynthesis				
c66228.graph_c0	PsbP-like protein 1	2.84E-08	-1.25418	down
c20544.graph_c0	photosystem I reaction center subunit N	2.17E-08	-1.09801	down
c45444.graph_c0	photosystem II subunit R	1.40E-35	1.986536	up
c79328.graph_c0	photosystem II subunit P-2	5.85E-09	1.487006	up
c45276.graph_c0	photosystem II subunit P-1	9.62E-10	1.008245	up
c79179.graph_c0	--	1.74E-40	2.138073	up
c79427.graph_c0	photosystem II Psb27 protein	3.78E-10	-1.1786	down
c51779.graph_c0	--	1.46E-09	-1.04717	down
B:photosynthesis-antenna proteins				
c32328.graph_c0	light harvesting complex photosystem II subunit 6	2.71E-05	-1.65866	down
c20430.graph_c0	light harvesting complex photosystem II interacting protein Lhcb4.2	5.11E-07	-1.08588	down
c45564.graph_c2	light-harvesting chlorophyll protein complex II subunit B1	1.20E-06	-1.98958	down
c45564.graph_c0	chlorophyll A/B binding protein 3	4.25E-07	-2.16123	down
c62233.graph_c0	photosystem II light harvesting complex protein B1B2	0.000496	-1.0338	down
c70454.graph_c0	light-harvesting chlorophyll B-binding protein 3	2.82E-05	-1.51562	down
c70454.graph_c1	light-harvesting chlorophyll B-binding protein 3	6.03E-07	-1.61896	down
c57685.graph_c0	--	0.001554	-1.49825	down
C:porphyrin and chlorophyll metabolism				
c71347.graph_c0	magnesium-chelatase subunit chlD	3.02E-08	-1.26595	down
c69703.graph_c0	Uroporphyrinogen decarboxylase	4.84E-12	-1.17172	down
c40903.graph_c0	ferritin 2	8.92E-0	1.375799	up
c21659.graph_c0	--	9.12E-12	-2.45469	down
c45265.graph_c0	magnesium-chelatase subunit chlI	1.34E-12	-1.5199	down
c19673.graph_c0	protochlorophyllide reductase A	6.00E-06	-2.18573	down
c67105.graph_c0	protoporphyrinogen oxidase	1.21E-09	-1.23108	down

c60164.graph_c1	ferrochelatase 1		3.43E-11	1.064883	up
c72696.graph_c0	glutamate-1-semialdehyde aminomutase 2	2,1-	1.80E-07	-1.51908	down
c78095.graph_c0	protochlorophyllide reductase C		1.30E-20	-3.29115	down
c63881.graph_c0	pheophorbide A oxygenase		1.11E-17	1.479158	up
c76376.graph_c0	glutamyl-tRNA reductase 1		1.30E-05	-1.14889	down
c20521.graph_c1	--		2.86E-05	-1.84394	down
c76954.graph_c0	cytochrome c oxidase assembly protein COX15		3.25E-08	-1.36171	down
c58660.graph_c0	--		0.000303	-1.59809	down
c56068.graph_c0	--		0.008752	-2.21448	down
c63881.graph_c0	pheophorbide A oxygenase		1.11E-17	1.479158	up
D:carbon fixation in photosynthetic organisms					
c72710.graph_c0	ribose 5-phosphate isomerase		2.19E-25	-2.03829	down
c69498.graph_c1	triosephosphate isomerase		1.22E-07	-1.02283	down
c70530.graph_c0	fructose-1,6-bisphosphatase		2.32E-07	-1.02717	down
c18259.graph_c0	malate dehydrogenase		0.000201	-1.57035	down
c57187.graph_c0	fructose-1,6-bisphosphatase		1.73E-09	-1.68199	down
c55137.graph_c0	malate dehydrogenase 2		1.75E-18	-1.39307	down
c31905.graph_c0	Ribulose bisphosphate carboxylase		9.68E-09	-1.54135	down
c60340.graph_c0	Ribulose bisphosphate carboxylase		0.002516	1.75461	up
c69718.graph_c0	malate dehydrogenase		0.00066	-1.88138	down
