

**Supplementary Table 1. Identification by tandem mass spectrometry of protein spots from DIGE gels that change in abundance over the diurnal timecourse**

Identities of proteins were determined by tandem mass spectrometry (MS), the predicted molecular weight (MW) and isoelectric point (pI) of the matched protein and the gel sample are shown along with the MOWSE score (p<0.05 when score>38), number of independent, non-redundant peptides matched to tandem mass spectra and the percentage coverage of the matched sequence. The putative subcellular localization of each protein was determined based on the data from SUBA II (<http://www.suba.plantenergy.uwa.edu.au>). Spot numbers correspond to protein spots in Supplementary Figure 1B.

Spot no.	Gene locus	Protein Identity	Functional category	Score <sup>§</sup>	No. of unique peptides matched	% coverage	MM matched	pI matched	MM gel	pI gel	One-way Annona p-value	Known subcellular localization <sup>#</sup>
1	At4g26970	Aconitase (ACON-2)	TCA cycle	633	14	17%	108427	6.71	94000	6.0	0.0412	M
2	At4g26970	Aconitase (ACON-2)	TCA cycle	839	17	21%	108427	6.71	94000	6.1	0.0472	M
3	At4g33010	Glycine decarboxylase P-protein (GDP-1)	Photorespiration	642	15	15%	112853	6.51	94000	6.5	0.0315	M
4	At4g33010	Glycine decarboxylase P-protein (GDP-1)	Photorespiration	322	7	6%	112853	6.51	94000	6.6	0.0004 **	M
5	At4g33010	Glycine decarboxylase P-protein (GDP-1)	Photorespiration	276	6	6%	112853	6.51	94000	6.7	0.0020 **	M
6	At4g33010	Glycine decarboxylase P-protein (GDP-1)	Photorespiration	210	4	4%	112853	6.51	94000	6.8	0.0004 **	M
13	At1g54220	Pyruvate dehydrogenase (E2 subunit)	TCA cycle	367	6	13%	58431	7.95	59000	5.6	0.0015 **	M
14	At1g03090	Methylcrotonyl-CoA carboxylase alpha subunit (MCC-alpha)	Branched-chain amino acid catabolism	488	8	14%	80401	6.42	71000	6.7	0.0304	M
15	At1g03090	Methylcrotonyl-CoA carboxylase alpha subunit (MCC-alpha)	Branched-chain amino acid catabolism	862	13	24%	80401	6.42	71000	6.8	2.76E-05 **	M
16	At1g03090	Methylcrotonyl-CoA carboxylase alpha subunit (MCC-alpha)	Branched-chain amino acid catabolism	602	10	18%	80401	6.42	71000	6.8	0.0001 **	M
17	At1g03090	Methylcrotonyl-CoA carboxylase alpha subunit (MCC-alpha)	Branched-chain amino acid catabolism	361	5	10%	80401	6.42	71000	6.9	3.40E-07 **	M
19	At1g09300	Metallopeptidase M24 family protein	Protein processing	261	5	10%	54947	6.94	51000	6.1	5.65E-09 **	M/C/N
20	At3g48000	Aldehyde dehydrogenase 2	Stress defense	530	9	21%	58552	7.11	53000	6.4	0.0041 **	M
21	At2g43400	Electron-transfer flavoprotein:ubiquinone oxidoreductase (ETFQO)	Branched-chain amino acid catabolism	350	5	9%	70084	7.31	59000	6.7	0.0029 **	M
22	At1g48030	Dihydrolipoamide dehydrogenase (PDC-E3 protein & GDC L-protein)	TCA cycle and photorespiration	580	9	22%	53954	6.96	55000	7.0	0.0029 **	M
23	At4g37930	Serine hydroxymethyltransferase (SHMT1)	Photorespiration	401	7	14%	57364	8.13	55000	7.3	1.35E-05 **	M
24	At4g34030	Methylcrotonyl-CoA carboxylase beta subunit (MCC-beta)	Branched-chain amino acid catabolism	477	9	17%	63972	8.78	58000	8.0	6.74E-05 **	M
25	At4g37930	Serine hydroxymethyltransferase (SHMT1)	Photorespiration	582	11	24%	57364	8.13	55000	7.9	0.0008 **	M
26	At3g06850	Branched chain alpha-ketoacid dehydrogenase complex	Branched-chain amino acid catabolism	543	10	22%	52673	6.29	50000	5.2	0.0030 **	M
29	At2g20420	Succinyl-CoA synthetase beta subunit	TCA cycle	630	11	26%	45317	6.30	44000	5.2	0.0074	M
31	At3g02090	Metallopeptidase beta subunit	Protein processing	195	4	6%	59123	6.30	42000	5.3	0.0457	M
35	At3g59760	O-acetylserine (thiol)-lyase isoform C (OAS-TL-C)	Carbon / nitrogen assimilation	514	11	25%	45786	8.39	40000	5.7	0.0026 **	M
36	At1g53240	Malate dehydrogenase (MDH-2)	TCA cycle	400	5	19%	35782	8.54	38000	6.2	0.0141	M
37	At2g44350	Citrate synthase	TCA cycle	194	3	6%	52621	6.41	49000	6.3	0.0355	M
38	At2g44350	Citrate synthase	TCA cycle	114	2	6%	52621	6.41	49000	6.4	0.0178	M
39	At5g14780	Formate dehydrogenase	Folate metabolism	212	5	10%	42383	7.12	43000	6.4	0.0468	M
40	At5g14780	Formate dehydrogenase	Folate metabolism	319	7	14%	42383	7.12	43000	6.4	0.0170	M
41	At1g59900	Pyruvate dehydrogenase (E1-alpha subunit)	TCA cycle	616	13	34%	43032	7.16	42000	6.6	0.0065	M
42	At5g07440	Glutamate dehydrogenase - 2	Carbon / nitrogen assimilation	323	6	15%	44671	6.07	45000	6.7	0.0017 **	M
43	At5g14780	Formate dehydrogenase	Folate metabolism	730	16	33%	42383	7.12	45000	6.8	0.0025 **	M
44	At5g14780	Formate dehydrogenase	Folate metabolism	546	11	23%	42383	7.12	45000	6.9	0.0163	M
45	At3g09810	isocitrate dehydrogenase (IDH-3)	TCA cycle	186	3	9%	40550	6.71	39000	6.7	0.0014 **	M
46	At3g22200	Gamma aminobutyrate aminotransferase (GABA-T)	Carbon / nitrogen assimilation	262	5	11%	55152	8.01	39000	6.8	0.0031 **	M
47	At3g61440	L-3-cyanoalanine synthase (CAS) / cysteine synthase	Carbon / nitrogen assimilation	343	7	22%	39902	8.71	39000	7.4	0.0083	M
50	At5g20080	NADH-cytochrome b5 reductase	Respiratory apparatus	109	2	6%	35964	8.76	31000	7.2	0.0106	M
51	At3g01500	Carbonic anhydrase 1	Respiratory apparatus	88	1	5%	29485	5.54	29000	6.1	9.36E-07 **	M
52	At3g06050	Peroxioredoxin IIF	Stress defense	333	5	26%	21432	8.99	23000	6.3	0.0440	M
54	At1g32470	Glycine decarboxylase H-protein subunit 3	Photorespiration	188	4	27%	17886	5.11	19000	3.9	0.0191	M
55	At2g35370	Glycine decarboxylase H-protein subunit 1	Photorespiration	163	3	20%	17936	5.24	19000	4.2	0.0005 **	M
Breakdown products												
9	At2g26080	Glycine decarboxylase P-protein (GDP-2)	Photorespiration	163	3	3%	113703	6.18	67000	5.6	0.0171	M
10	At4g33010	Glycine decarboxylase P-protein (GDP-1)	Photorespiration	289	5	5%	112853	6.51	67000	5.7	0.0029 **	M
11	At4g33010	Glycine decarboxylase P-protein (GDP-1)	Photorespiration	422	8	8%	112853	6.51	67000	5.8	0.0014 **	M
12	At2g26080	Glycine decarboxylase P-protein (GDP-2)	Photorespiration	245	5	5%	113703	6.18	67000	6.0	0.0083	M
30	At5g08670	ATP synthase beta subunit	Respiratory apparatus	536	7	17%	59634	6.18	43000	5.1	0.0013 **	M
53	At5g14780	Formate dehydrogenase	Folate metabolism	249	6	11%	42383	7.12	22000	5.6	0.0467	M
Contaminants												
7	At4g24280	Chloroplast heat shock protein 70-1	Protein processing	204	4	6%	76461	5.07	71000	4.3	0.0002 **	C
8	At2g28000	Chaperonin 60A	Protein processing	681	11	22%	62034	5.09	60000	4.4	6.74E-05 **	C
18	AtCg00490	Rubisco	Photosynthesis	507	10	18%	52922	5.88	51000	6.0	0.01547	C
27	At2g39730	Rubisco activase	Photosynthesis	478	8	23%	51948	5.87	49000	4.8	2.82E-07 **	C
28	At5g35630	Glutamine synthase	Carbon / nitrogen assimilation	142	3	6%	47381	6.43	46000	5.0	2.31E-06 **	M/C
32	At4g13360	3-hydroxyisobutyryl-coenzyme A hydrolase	Branched-chain amino acid catabolism	466	8	20%	46222	6.23	44000	5.4	8.06E-06 **	P
33	At2g21330	Fructose-bisphosphate aldolase	Glycolysis	306	5	12%	42904	6.18	38000	5.3	0.0005 **	C
34	At4g38970	Fructose-bisphosphate aldolase	Glycolysis	262	5	13%	42961	6.78	39000	5.5	0.0018 **	C
48	At5g09660	Peroxisomal malate dehydrogenase 2	Fatty acid metabolism	493	7	29%	34953	7.56	36000	8.1	0.0262	P
49	At2g33150	Acetyl-CoA C-acyltransferase Ketoacyl-CoA thiolase (kat2)	Fatty acid metabolism	366	8	21%	48548	8.62	43000	9.1	0.0007 **	P

<sup>§</sup> Ion score threshold ≥ 38

\*\* values having Bonferroni-corrected significance threshold of ≤ 0.5%

- glycine decarboxylase subunit 1 and 3 match the same set of peptides and hence are distinguishable from one another

<sup>#</sup> M, mitochondrion; P, peroxisome; C, Chloroplast