

Table S3B. Detailed lists of genes in the “photosynthesis” module derived from the WGCNA starvation times.

ID	N24	N48	N72	Gene description
slI0504	0.83	0.13	0.13	diaminopimelate decarboxylase
slI0938	1.58	2.53	3.26	aminotransferase, class I
slI0373	1.26	0.71	0.58	probable gamma-glutamyl phosphate reductase
slI0480	0.47	0.16	0.14	aspartate aminotransferase related protein
slI0480	0.47	0.16	0.14	aspartate aminotransferase related protein
slr0260	0.92	1.51	1.06	cob(I)alamin adenosyltransferase
slr0506	0.19	0.13	0.13	protochlorophyllide oxido-reductase
slr1098	2.99	1.83	3.22	phycocyanin alpha phycocyanobilin lyase CpcE
slI1127	0.40	0.54	0.32	naphthoate synthase
slr0426	0.19	0.43	0.44	GTP cyclohydrolase i
slr0969	2.29	1.88	1.98	precorrin-3b c17-methyltransferase
slr1368	2.38	2.67	4.68	precorrin-8w decarboxylase, putative
slr1878	1.22	1.22	1.14	phycocyanobilin lyase alpha subunit
slr1691	1.70	1.43	2.48	NH(3)-dependent NAD(+) synthetase
slI0300	3.56	2.51	6.30	riboflavin synthase alpha chain
slr1098	2.99	1.83	3.22	phycocyanin alpha phycocyanobilin lyase CpcE
slr0646	0.85	0.68	0.73	putative penicillin binding protein precursor, putative
slr1423	0.58	0.27	0.31	udp-n-acetylmuramate--alanine ligase (ec 6.3.2.8)
slr1874	1.39	1.55	1.98	D-alanine--D-alanine ligase
slI0648	0.69	0.77	1.09	undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase, putativ
slI1535	0.09	0.04	0.06	undecaprenyl-phosphate galactosephosphotransferase
slI1694	0.01	0.03	0.02	pilin
slr1693	0.19	0.35	0.44	pilg protein, putative
slr1043	0.69	0.59	0.56	CHEV, putative
slr2024	0.27	0.37	0.31	chemotaxis protein CheY, putative
slr1890	0.08	0.09	0.18	bacterioferritin subunit 2
slI1178	1.14	1.10	0.89	MmcS
slI1566	2.20	1.33	1.65	alpha,alpha-trehalose-phosphate-synthase
slI0690	2.60	2.89	20.93	virulence associated protein C
slI1583	0.07	0.04	0.03	M-protein, putative

slr0488	4.69	2.19	2.41	virulence factor mvn, putative
sll0220	1.29	0.45	0.43	glucosamine--fructose-6-phosphate aminotransferase
sll0643	0.70	0.83	1.01	urease accessory protein UreG
sll1750	1.07	0.44	0.50	urease alpha subunit
sll1079	0.46	0.70	0.44	hydrogenase expression/formation protein B
sll1750	1.07	0.44	0.50	urease alpha subunit
slr1622	0.18	0.13	0.12	inorganic pyrophosphatase (ec 3.6.1.1) (ppase)
slr0662	2.54	0.83	0.89	arginine decarboxylase
sll1193	0.27	0.42	0.28	conserved hypothetical protein
slr1134	1.52	0.99	2.11	8-OXO-dGTPase domain
slr2080	0.20	0.40	0.43	similar to r1t gp26-related
slr0261	0.30	0.35	0.44	NADH-plastoquinone oxidoreductase 49 kDa subunit, chloroplast
slr1329	0.44	0.07	0.06	ATP synthase beta chain
slr0261	0.30	0.35	0.44	NADH-plastoquinone oxidoreductase 49 kDa subunit, chloroplast
slr0600	0.92	1.57	1.57	thioredoxin reductase, putative
ssr0330	0.32	0.64	1.17	ferredoxin-thioredoxin reductase, variable chain
sll1196	0.76	0.32	0.31	Pfk1
sll1085	2.63	2.94	3.81	aerobic glycerol-3-phosphate dehydrogenase, putative
slr1983	0.69	1.11	1.22	icfg protein-related
sll0629	0.63	0.88	1.22	photosystem i reaction centre subunit x (psi-k)
sll0928	0.14	0.22	0.30	allophycocyanin B alpha subunit
sll1577	0.00	0.00	0.00	phycocyanin beta-subunit
sll1578	0.00	0.00	0.00	phycocyanin alpha subunit
sll1580	0.00	0.00	0.00	phycobilisome 32.1 kd linker polypeptide, phycocyanin-associated, rod
slr0012	0.03	0.01	0.00	rubilose-1,5,-bisphosphate carboxylase oxygenase small subunit
slr0335	0.06	0.01	0.01	phycobilisome 100.5 kd core-membrane linker polypeptide (l-cm 100.5)
slr0506	0.19	0.13	0.13	protochlorophyllide oxido-reductase
slr0772	0.08	0.07	0.06	light-independent protochlorophyllide reductase subunit
slr1834	0.05	0.00	0.00	photosystem I p700 chlorophyll a apoprotein a1
slr1878	1.22	1.22	1.14	phycocyanobilin lyase alpha subunit
slr1986	0.04	0.01	0.01	allophycocyanin beta chain
slr2051	0.03	0.02	0.02	phycobilisome rod-core linker polypeptide cpcg
sml0003	0.05	0.05	0.06	photosystem ii reaction centre m protein
smr0004	0.03	0.01	0.01	photosystem I reaction centre subunit viii

smr0008	0.36	0.49	0.77	photosystem ii reaction centre j protein
ssr2831	0.15	0.20	0.35	photosystem i reaction centre subunit iv (photosystem i 8.1 kd protein)
ssr3383	0.07	0.03	0.03	phycobilisome 7.8 kd linker polypeptide, allophycocyanin-associated, c
sll1709	1.65	0.98	0.55	3-ketoacyl-acyl carrier protein reductase, putative
ssl2084	0.16	0.10	0.09	acyl carrier protein
slr1916	0.42	0.71	0.79	carboxylesterase, putative
sll1329	0.59	0.38	0.49	26.5 kda protein, putative
slr1622	0.18	0.13	0.12	inorganic pyrophosphatase (ec 3.6.1.1) (ppase)
slr1764	0.67	1.56	1.32	phage inhibition protein terE
sll0666	2.43	6.91	2.89	putative transposase
sll0667	0.25	0.50	0.22	probable transposase for insertion sequence element is701-related
sll1474	2.42	4.90	4.26	putative transposase for insertion sequence element is5377, putative
slr0265	7.82	5.66	7.88	putative transposase
slr1246	2.01	2.71	3.81	transposase
slr2096	1.87	1.54	2.35	insertion element iso-is1n protein insb, putative
sll0236	1.25	1.18	0.95	carboxypeptidase (EC 3.4.17.-) - Streptomyces griseus, putative
sll0535	0.82	0.45	0.66	atp-dependent clp protease atp-binding subunit clpx
sll1679	2.73	0.48	0.36	periplasmic serine protease
slr1924	0.32	0.47	0.49	Alkaline D-peptidase
sll0533	0.45	0.44	0.28	trigger factor, putative
sll0415	1.31	1.45	1.48	hypothetical abc transporter ATP-binding protein sll0415
slr2076	0.66	0.03	0.03	60 kd chaperonin 1 (protein cpn60 1) (groel homolog 1)
sll1743	0.06	0.03	0.02	L11 protein
sll1745	0.01	0.00	0.00	ribosomal protein L10
sll1746	0.04	0.02	0.02	50s ribosomal protein l7/l12
sll1805	0.71	0.04	0.04	cyanelle ribosomal protein L16
sll1807	0.05	0.02	0.02	50s ribosomal protein l24
sll1808	0.08	0.02	0.03	50s ribosomal protein l5
slr0853	0.70	1.42	1.04	ribosomal-protein-alanine acetyltransferase, putative
slr1678	0.08	0.07	0.06	50S ribosomal protein L21
slr0958	2.43	1.22	1.23	cysteinyI-tRNA synthetase, putative
slr1720	0.39	0.20	0.17	aspartyl-tRNA synthetase
ssr1720	3.40	6.54	3.54	tyrosyl-tRNA synthetase
sll0467	2.77	2.77	2.77	S-adenosylmethionine tRNA ribosyltransferase

slr0591	0.25	0.33	0.29	ribonucleoside-diphosphate reductase 1 beta chain
slr0600	0.92	1.57	1.57	thioredoxin reductase, putative
sll1059	0.40	0.55	0.49	adenylate kinase (ec 2.7.4.3) (atp-amp transphosphorylase)
sll1056	3.48	2.22	2.91	phosphoribosylformylglycinamide synthase II
sll0370	1.04	0.66	0.49	carbamoyl-phosphate synthase, large (or ammonia) subunit
sll0698	0.53	0.38	0.36	sensor-like histidine kinase ycf26, putative
sll0779	2.25	2.61	2.93	utilizing regulatory protein tutC
sll1205	4.78	4.97	4.69	yersiniabactin/pesticin receptor regulator, putative
sll1365	0.95	1.92	1.98	regulatory protein, putative
sll1672	0.59	0.63	0.58	sensory transduction histidine kinase
slr1212	2.25	1.41	1.28	sensory transduction histidine kinase
slr1693	0.19	0.35	0.44	pilg protein, putative
slr2024	0.27	0.37	0.31	chemotaxis protein CheY, putative
sll1689	0.81	0.21	0.17	RpoD2 sigma factor
slr0949	2.95	4.75	30.30	conserved hypothetical protein
sll0683	1.77	0.95	1.04	phosphate ABC transporter, ATP-binding protein
slr1248	10.17	3.99	12.78	peripheral membrane protein C
slr1249	4.80	4.56	10.97	phosphate ABC transporter, permease protein
sll0108	0.25	0.30	0.44	ammonium transporter
sll0671	33.75	21.04	29.20	divalent cation transport-related protein
sll1920	5.64	1.24	1.22	cation-transporting ATPase pacs
slr1890	0.08	0.09	0.18	bacterioferritin subunit 2
sll0163	2.03	0.48	0.44	putative WD-repeat containing protein, putative
ssr2595	1.19	2.09	1.23	hliA protein

l analysis. N24, N48, N72 indicate the nitrogen

[illegible]

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Purines, pyrimidines, nucleosides, and nucleotides
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Purines, pyrimidines, nucleosides, and nucleotides
Regulatory functions
Regulatory functions
Regulatory functions
Regulatory functions
Regulatory functions
Regulatory functions
Regulatory functions
Regulatory functions
Transcription
Transport and binding proteins
Transport and binding proteins
Transport and binding proteins
Transport and binding proteins
Transport and binding proteins
Transport and binding proteins
Transport and binding proteins
Transport and binding proteins
Unclassified
Unknown function

Table S3. Detailed lists of genes in the “hypothetic” module derived from the V the nitrogen starvation times.

Gene	N24	N48	N72	Gene description
slI0207	0.89	1.13	1.06	glucose-1-phosphate thymidyltransferase
slr2102	3.92	1.81	2.43	probable signal recognition particle protein (docking pr
slI0474	1.43	3.37	3.71	sensor kinase rtpA, putative
slI0420	0.62	1.41	0.79	urease beta subunit
slr1899	0.41	0.49	0.80	urease accessory protein UreF
slI0420	0.62	1.41	0.79	urease beta subunit
slI1078	0.32	0.73	0.28	hydrogenase expression/formation protein hypa, putativ
slI1234	1.85	0.42	0.35	S-adenosylhomocysteine hydrolase
slr1239	0.18	0.07	0.07	nad(p) transhydrogenase subunit alpha
slI0459	1.98	2.09	2.58	excinuclease abc subunit b
slI0459	1.98	2.09	2.58	excinuclease abc subunit b
slr0214	1.66	2.03	2.89	modification methylase xorii
slI1393	0.28	0.31	0.26	bacterial glycogen synthase
slI1226	0.66	1.30	1.20	hoxH
slr1239	0.18	0.07	0.07	nad(p) transhydrogenase subunit alpha
slr2007	1.65	1.42	1.29	NADH dehydrogenase, putative-related
ssr1386	0.51	0.61	1.14	NADH dehydrogenase subunit L
slI1019	0.69	0.56	0.53	probable hydroxyacylglutathione hydrolase
slI0807	0.28	0.31	0.31	ribulose-phosphate 3-epimerase (ec 5.1.3.1) (ppe) (r5p
slI0549	1.61	1.24	1.51	conserved hypothetical protein
slr0099	0.52	0.90	0.68	probable transposase
slr0704	1.45	2.70	2.90	putative transposase
slI0241	1.01	1.12	2.43	hypothetical protein
slI0058	1.80	1.60	2.06	DnaK
ssl3436	0.10	0.03	0.03	50s ribosomal protein l29
slI1099	0.07	0.01	0.01	elongation factor tu
slI0362	3.76	1.90	2.02	alanyl-tRNA synthetase
slr1031	1.01	2.22	2.30	tyrosyl-tRNA synthetase
slr1226	2.22	1.49	1.31	phosphoribosylaminoimidazole-succinocarboxamide sy
slI0649	2.13	2.02	1.38	DNA-binding response regulator
slI0790	1.61	3.30	3.09	histidine protein kinase
slr1140	0.75	1.00	1.00	pleiotropic regulatory protein DegT, putative
slI0649	2.13	2.02	1.38	DNA-binding response regulator
slI0754	0.80	0.53	0.49	ribosome-binding factor a
slI0384	0.45	0.36	0.33	putative
slr2057	0.45	0.13	0.15	aquaporin Z
slr1919	1.53	4.33	1.71	predicted protein-related
slI0040	0.39	0.16	0.15	CheW-related

WGCNA analysis. N24, N48, N72 indicate

Main-role
Cell envelope
Cellular processes
Cellular processes
Central intermediary metabolism
Central intermediary metabolism
Central intermediary metabolism
Central intermediary metabolism
Central intermediary metabolism
Central intermediary metabolism
DNA metabolism
DNA metabolism
DNA metabolism
Energy metabolism
Energy metabolism
Energy metabolism
Energy metabolism
Energy metabolism
Energy metabolism
Energy metabolism
Hypothetical proteins
Mobile and extrachromosomal element functions
Mobile and extrachromosomal element functions
19No Data
Protein fate
Protein synthesis
Protein synthesis
Protein synthesis
Protein synthesis
Purines, pyrimidines, nucleosides, and nucleotides
Regulatory functions
Regulatory functions
Regulatory functions
Transcription
Transcription
Transport and binding proteins
Transport and binding proteins
Transport and binding proteins
23 Unclassified