Supplementary Table 1. Identification of the proteins differentially expressed during carbon starvation.

Protein name	Gene name	Ro no.	Genetic context	MASCOT score [a]	Peptides matched	Normalized signal intensity (NV)[b]						
						ML	TP	PTP	ES	MS	LS	LLS
benzoate 1,2-dioxygenase alpha subunit	*benA*	02384	*ben* cluster	163	14	1.70	1.30	0.61	0.43	0.15	0.11	0.07
benzoate 1,2-dioxygenase beta subunit	*benB*	02385	*ben* cluster	87	5	1.09	0.97	0.59	0.46	0.18	0.17	0.18
benzoate 1,2-dioxygenase reductase subunit	*benC*	02386	*ben* cluster	113	11	0.98	0.81	0.35	0.21	0.02	N	N
cis-1,6-dihydroxycyclohexa-3,5-diene-1-carboxylate dehydrogenase	*benD*	02387	*ben* cluster	102	8	0.56	0.50	0.33	0.20	0.02	0.04	0.01
catechol 1,2-dioxygenase	*catA*	02373	*cat* cluster	84	9	3.50	3.28	2.40	1.82	0.67	0.36	0.19
muconate cycloisomerase	*catB*	02372	*cat* cluster	60	7	0.42	0.35	0.23	0.11	0.02	0.01	0.01
3-oxoacid CoA-transferase, subunit A	*pcaI*	01334	*pca* cluster	80	8	0.35	0.32	0.30	0.27	0.10	0.04	0.02
protocatechuate dioxygenase alpha subunit	*pcaG*	01336	*pca* cluster	60	4	0.26	0.28	0.25	0.18	0.04	0.05	0.05
3-oxoacid CoA-transferase	*pcaJ*	01333	*pca* cluster	119	7	0.10	0.12	0.10	0.02	0.02	0.02	0.02
Acetyl-CoA C-acyltransferase	*pcaF*	01340	*pca* cluster	151	13	0.28	0.39	0.42	0.39	0.30	0.20	0.02
3-carboxy-cis,cis-muconate cycloisomerase	*pcaB*	01337	*pca* cluster	211	5	0.10	0.11	0.07	0.08	0.08	0.07	N
protocatechuate dioxygenase beta subunit	*pcaH*	01335	*pca* cluster	349	7	0.14	0.20	0.08	0.08	0.02	0.01	0.01
3-oxoadipate enol-lactone hydrolase/4-carboxymuconolactone decarboxylase	*pcaL*	01338	*pca* cluster	27	4	0.21	0.20	0.10	0.06	0.08	0.06	0.03
transcriptional regulator, IclR family	*pcaR*	01339	*pca* cluster	95	7	0.03	0.04	0.05	0.06	0.05	0.03	0.02
biphenyl 2,3-dioxygenase alpha subunit	*bphAa*	08060	*bph* cluster	64	6	N	N	N	N	0.48	0.54	0.15
cis-3-phenylcyclohexa	*bphB2*	10126	*bph/etb* cluster	184	14	N	N	N	N	0.03	0.03	0.13

-3,5-diene-1,2-diol dehydrogenase												
2,6-dioxo-6-phenylhexa-3-enoate hydrolase	*bphD1*	10136	*bph/etb* cluster	93	13	N	N	N	N	0.10	0.08	0.03
ethylbenzene dioxygenase alpha subunit	*etbAa1*	10133	*bph/etb* cluster	71	13	N	N	N	N	0.47	0.45	0.26
2-hydroxy-6-oxohepta-2,4-dienoate hydrolase	*etbD1*	*08044*	*bph/etb* cluster	97	7	0.01	0.01	0.02	0.01	0.24	0.29	0.18
2,6-dioxo-6-phenylhexa-3-enoate hydrolase	*etbD2*	10146	*bph/etb* cluster	132	9	0.01	0.01	0.02	0.02	0.27	0.26	0.10
phthalate 3,4-dioxygenase, ferredoxin reductase subunit	*padAd1*	*08162/ 12013*	*pad* clusters	52	11	0.02	0.05	0.07	0.09	0.03	0.02	N
phthalate ester hydrolase	*patE*	*08169*	*pat* cluster	66	9	0.04	0.04	0.09	0.12	0.07	0.06	0.03
propane monooxygenase hydroxylase large subunit		00441	large cluster with phenol gydroxylase and GroEL	69	12	0.02	0.03	0.03	0.04	0.13	0.68	0.38
probable 1,3-propanediol dehydrogenase		06057	ATP-dependent protease	160	14	0.05	0.03	0.15	0.24	0.24	0.56	0.29
CO dehydrogenase, medium subunit		04975	CODH	85	7	0.09	0.13	0.08	0.12	0.22	0.20	0.19
^{c}CO dehydrogenase, maturation factor		05229	CODH	71	11	N	N	N	N	0.17	0.38	0.49
^{c}CO dehydrogenase, medium subunit		05230	CODH	89	12	0.04	0.07	0.03	0.04	0.18	0.20	0.43
^{c}CO dehydrogenase, large subunit		05232	CODH	147	26	N	N	0.05	0.04	0.17	0.20	0.46
5,10-methylene tetrahydromethanopterin reductase		03459	single gene	145	9	0.02	0.05	0.12	0.20	0.32	0.35	0.39
5,10-methylene tetrahydromethanopterin reductase		02204	not clear	58	6	0.23	0.24	0.28	0.31	0.34	0.4	0.28
5,10-methylene tetrahydromethanopterin reductase		02495	monooxygenase	75	12	0.02	0.01	0.03	0.02	0.07	N	N
citrate synthase	*citA4*	04993, 08812	phosphoserine transamina	44	9	0.09	0.1	0.03	0.01	0.02	0.01	0.004

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citrate synthase		04998	peptidylprolyl isomerase	117	11	0.03	0.05	0.05	0.05	0.03	0.02	N
isocitrate dehydrogenase		06238	Arabinose efflux permease	95	11	0.16	0.10	0.02	N	N	N	N
succinate-CoA ligase, alpha subunit	*sucD*	05573	*suc* cluster	77	9	1.00	0.85	0.85	0.80	0.67	0.58	0.42
succinate-CoA ligase, beta subunit	*sucC*	05574	*suc* cluster	139	12	1.07	0.82	0.79	1.03	0.92	0.58	0.50
succinate dehydrogenase	*sdhA2*	06246	*sdh* cluster	71	12	0.60	0.45	0.33	0.31	0.32	0.19	0.27
fumarate hydratase		08824	succinate dehydrogenase	206	10	N	N	0.01	0.01	0.01	0.02	0.02
malate dehydrogenase	*fabF*	*06000*	single gene	95	7	0.20	0.24	0.25	0.16	0.06	0.02	0.06
dihydrolipoyl dehydrogenase	*dldH1*	02140	Hypothetical	74	10	0.09	0.04	N	N	N	N	N
isocitrate lyase		02122	lipid metabolism	132	15	0.20	0.22	0.74	0.75	0.59	0.38	0.46
glucose-6-phosphate 1-dehydrogenase	zwf4	07184	pentose phosphate pathway	120	12	0.03	0.02	0.03	0.04	0.05	0.05	0.11
phosphogluconate dehydrogenase	gnd3	07246	RNA helicase	126	14	0.08	0.06	0.15	0.23	0.39	0.43	0.50
6-phosphofructokinase	pfkA	06479	Amidotransferase *gat*	84	13	0.02	0.04	0.03	0.03	0.01	N	N
pyruvate kinase	pyk1	01007	glutamate synthase	63	10	0.29	0.29	0.29	0.27	0.30	0.18	0.19
glucose-6-phosphate isomerase		05567	Hypothetical	159	15	0.08	0.09	0.10	0.11	0.10	0.12	0.11
phosphoglycerate mutase	gpmA	02070	long-chain-fatty-acid-CoA ligase	93	7	0.02	0.05	0.13	0.09	0.09	0.12	0.36
glycosyltransferase		05974	single gene	84	12	N	0.02	0.05	0.06	0.10	0.09	0.08
glycosyltransferase		05764	glycosyltransferase	56	6	0.02	0.02	0.03	0.05	0.15	0.18	0.24
[c]nucleoside-diphosphate-sugar epimerase		00180	transcriptional regulator	81	8	0.01	0.03	0.05	0.03	0.09	0.07	0.11
1,4-alpha-glucan branching enzyme	*glgB*	01449	glycosidase	250	25	0.03	0.03	0.04	0.05	0.07	0.11	0.04
glycoside hydrolase		04568	hypothetical genes	75	10	N	N	0.01	0.02	0.03	0.03	0.04
carboxyvinyl-	*prpB*	02162	Single	47	4	0.06	0.07	0.12	0.22	0.23	0.24	0.23

carboxyphosphonate phosphorylmutase			gene										
succinate-semialdehyde dehydrogenase (NAD(P)+)	*gabD4*	05568	Single gene		111	15	0.06	0.07	0.1	0.14	0.23	0.23	0.42
succinate-semialdehyde dehydrogenase (NAD(P)+)	*gabD3*	04543	*gabT2*		110	7	0.05	0.16	0.34	0.29	0.17	0.19	0.21
60kDa chaperonin GroEL	*groL2*	02146	universal stress protein	143		12	0.83	0.69	0.60	0.60	0.65	0.63	N
chaperone protein	*groEL*	06190	10 kDa chaperonin	138		12	0.81	0.67	1.20	0.93	0.71	0.63	0.34
60 kDa chaperonin GroEL	*groL1*	00448	propane monooxygenase	81		7	N	N	0.61	0.37	0.11	1.45	N
heat shock protein Hsp70	dnaK1	05497	chaperones: grpE1, dnaJ2	80		15	1.01	1.10	0.71	0.72	1.07	1.99	1.36
universal stress protein		02263	universal stress protein, oxidoreductase	278		8	0.03	0.03	0.05	0.05	0.04	0.03	0.03
universal stress protein		04893	pseudouridylate synthase	71		6	0.08	0.06	0.06	0.12	0.12	0.19	0.18
type I restriction-modification system, methyltransferase	*hsdM*	11151	restriction-modification system	60		13	N	N	N	N	0.01	0.07	N
thiocyanate hydrolase gamma subunit		04428	thiocyanate hydrolase subunits	85		7	N	N	N	0.08	0.23	0.21	0.11
epoxide hydrolase		08833	hypothetical genes	98		11	0.17	0.16	0.19	0.23	0.25	0.27	0.27
superoxide dismutase	*sodA*	04009	amidotransferase	62		6	1.08	0.90	1.10	1.19	1.40	1.38	1.62
[c]heme superoxide dismutase		06860	Heme biosynthesis, oxidoreductase	73		6	0.19	0.19	0.18	0.26	0.25	0.31	0.39
catalase	*katE*	04309	Fe(3+) uptake regulator	77		14	0.02	0.05	0.05	0.07	0.04	0.01	0.02
ATP-dependent Clp protease		01371	clpX , FKBP-type	59		7	0.25	0.25	0.40	0.41	0.30	0.43	0.50

			bacterial trigger factor									
prolyl aminopeptidase		01171	*panB,* coenzyme metabolism	8	74	7	0.01	0.03	0.03	0.02	0.01	0.09
FeS assembly ATPase	*sufC*	07198	*suf* cluster	76	8	0.21	0.17	0.17	0.14	0.11	0.09	0.09
bacterioferritin		04043	Bacterioferritin-associated ferredoxin	80	6	0.002	0.02	0.11	0.18	0.37	0.28	0.41
bacterioferritin		04028	transcriptional regulator, LytR	40	5	0.03	0.04	0.02	0.04	0.07	0.04	0.09
cell division initiation protein		01080	cell division	135	11	0.002	0.005	0.01	0.07	0.11	0.08	0.03
sensor kinase, two-component system		02255	single gene	51	8	0.11	0.11	0.08	0.04	N	N	N
transcriptional activator TenA		01597	ABC-type nitrate/sulfonate/bicarbonate transport	60	5	0.16	0.18	0.14	0.10	0.04	0.04	0.06
transcriptional regulator; TetR family		08719	hypothetical genes	31	5	0.06	0.09	0.09	0.12	0.06	0.06	0.07
transcriptional regulator, TetR family		10228	single gene (carveol dehydrogenase)	53	7	0.03	0.04	0.03	0.06	0.04	0.02	0.01
conserved hypothetical protein		00906	transcriptional regulator	81	8	0.04	0.04	0.13	0.09	0.18	0.21	0.23
RNA polymerase sigma factor G	*sigG*	05361	ArsR	122	12	0.07	0.07	0.11	0.13	0.17	0.14	0.18
transcriptional regulator, GntR family		03232	probable multidrug resistance transporter	51	5	0.02	0.04	0.05	0.13	0.06	0.03	0.04
iron dependent transcription repressor		06652	single gene	62	6	0.02	0.06	0.07	0.12	0.17	0.12	0.06
transcriptional regulator; IclR family		02458	carbohydrate kinase, PfkB family	52	4	N	N	N	N	N	0.01	N

[a]MASCOT generated Probability Based Mowse Score. The scores greater than 55 are significant ($p<0.05$); [b]spot signal intensities were normalized and averaged over three replica gels (each from independent experiment). [c]Protein annotation was edited. N, not detected.