Supplementary Table S1. Functional description of genes upregulated in response to glyphosate shock

Gene name	Gene ID	Functional description	Fold change
Amino acid transport and metabolism			
adiA	b4117	biodegradative arginine decarboxylase	2.45
afuC	b0262	putative ATP-binding component of a transport system	2.02
ansB	b2957	periplasmic L-asparaginase II	2.28
argK	b2918	membrane ATPase/protein kinase	2.12
cadA	b4131	lysine decarboxylase 1	2.60
cadB	b4132	transport of lysine cadaverine	2.83
ddpF	b1483	D,D-dipeptide permease system, ATP-binding component	2.83
ddpX	b1488	D-ala-D-ala dipeptidase, Zn-dependent	2.49
edd	b1851	6-phosphogluconate dehydratase	2.29
elaD	b2269	putative sulfatase phosphatase	2.07
idnD	b4267	L-idonate dehydrogenase	2.31
nikA	b3476	periplasmic binding protein for nickel	2.15
nikB	b3477	transport of nickel, membrane protein	2.17
nikD	b3479	ATP-binding protein of nickel transport system	2.24
oxc	b2373	oxalyl CoA decarboxylase, ThDP-dependent	2.25
pheP	b0576	phenylalanine-specific transport system and proline	2.08
proV	b2677	ATP-binding component of transport system for glycine, betaine and proline	12.96
proW	b2678	high-affinity transport system for glycine betaine and proline	17.69
proX	b2679	high-affinity transport system for glycine betaine and proline	11.66
rspB	b1580	starvation sensing protein	2.47
speF	b0693	ornithine decarboxylase isozyme, inducible	3.04
tdcA	b3118	transcriptional activator of tdc operon	2.56
tdcB	b3117	threonine dehydratase, catabolic	2.89
tdcC	b3116	anaerobically inducible L-threonine, L-serine permease	2.29
tdcF	b3113	predicted L-PSP (mRNA) endoribonuclease	2.18
tdcR	b3119	threonine dehydratase operon activator protein	2.46
tnaA	b3708	tryptophanase	3.91
tnaB	b3709	low affinity tryptophan permease	2.76
tnaC	b3707	tryptophanase leader peptide	3.96
wcaB	b2058	predicted acyl transferase	2.06
wcaD	b2056	putative colanic acid polymerase	2.56
wcaF	b2054	putative transferase	2.70
wzc	b2060	protein-tyrosine kinase	2.68
yagE	b0268	putative lyasesynthase	2.04
yahN	b0328	inner membrane protein, LysE transporter family;overproduction confers sensitivity to L-homoserine	2.38
ydeN	b1498	putative sulfatase	2.46
ydjJ	b1774	putative oxidoreductase	2.10
yedS_3	b1966	putative amino acidamine transport protein	2.09

yfbL	b2271	putative aminopeptidase	2.46
yfcC	b2298	putative S-transferase	2.35
yfiK	b2578	cysteine and O-acetylserine exporter	2.38
ygeW	b2870	putative carbamoyl transferase	2.30
ygeX	b2871	2,3-diaminopropionate ammonia-lyase	2.12
ygeY	b2872	putative deacetylase	2.22
ygfT	b2887	putative oxidoreductase, Fe-S subunit	2.06
yhdX	b3269	putative transport system permease protein	2.14
yhdY	b3270	putative transport system permease protein	2.16
yhfX	b3381	predicted amino acid racemase	2.01
yhiP	b3496	dipeptide and tripeptide permease B	2.30
yjdL	b4130	putative peptide transporter	2.26
yjiM	b4335	predicted 2-hydroxyglutaryl-CoA dehydratase	2.00
yqeA	b2874	putative kinase	2.22
Carbohydrate transport and metabolism			
agaB	b3138	PTS system, cytoplasmic, N-acetylgalactosamine-specific IIB component 1 (EIIB-AGA)	2.15
agaI	b3141	galactosamine-6-phosphate isomerase	2.47
agaV	b3133	PTS system, cytoplasmic, N-acetylgalactosamine-specific IIB component 2 (EIIB-AGA)	2.44
agaW	b3134	PTS system N-acetylgalactosameine-specific IIC component 2	2.67
agaY	b3137	tagatose-bisphosphate aldolase 2	2.67
agaZ	b3132	tagatose 6-phosphate aldolase 1, kbaZ subunit	2.31
alsA	b4087	fused D-allose transporter subunits of ABC superfamily: ATP-binding components	2.03
alsC	b4086	D-allose transporter subunit	2.13
alsE	b4085	allulose-6-phosphate 3-epimerase	2.06
araA	b0062	L-arabinose isomerase	2.08
araF	b1901	L-arabinose-binding periplasmic protein	2.33
arnF	b2258	undecaprenyl phosphate-alpha-L-ara4N exporter; flippase ArnEF subunit	2.00
bglB	b3721	phospho-beta-glucosidase B; cryptic	2.05
bglF	b3722	PTS system beta-glucosides, enzyme II, cryptic	2.10
citE	b0616	citrate lyase beta chain acyl lyase subunit	2.15
cmtA	b2933	PTS system, mannitol-specific enzyme II component, cryptic	2.24
cmtB	b2934	PTS system, mannitol-specific enzyme II component, cryptic	2.17
dgoT	b3691	D-galactonate transport	2.09
ebgA	b3076	evolved beta-D-galactosidase, alpha subunit; cryptic gene	2.26
ebgC	b3077	evolved beta-D-galactosidase, beta subunit; cryptic gene	2.27
emrB	b2686	multidrug resistance; probably membrane translocase	2.03
frvA	b3900	PTS system, fructose-specific IIA component	2.26
frvB	b3899	PTS system, fructose-like enzyme IIBC component	2.10
frvX	b3898	frv operon protein	2.11
frwB	b3950	PTS system fructose-like IIB component 1	2.84
frwC	b3949	PTS system, fructose-like enzyme II component	2.80

fryB	b2387	predicted enzyme IIB component of PTS	2.24
fryC	b2386	predicted enzyme IIC component of PTS	2.40
fucA	b2800	L-fuculose-1-phosphate aldolase	2.02
fucI	b2802	L-fucose isomerase	2.43
fucK	b2803	L-fuculokinase	2.29
fucP	b2801	fucose permease	2.29
garL	b3126	alpha-dehydro-beta-deoxy-D-glucarate aldolase	2.02
glvB	b3682	PTS system, arbutin-like IIB component	2.00
glvC	b3683	PTS system, arbutin-like IIC component	2.16
glvG	b3681	probable 6-phospho-beta-glucosidase	2.25
gntP	b4321	gluconate transport system permease 3	2.43
gntU	b3436	a gluconate transporter	2.00
gudP	b2789	putative D-glucarate permease (MFS family)	2.52
hcaT	b2536	MFS (major facilitator superfamily) transporter	2.18
hrsA	b0731	protein modification enzyme, induction of ompC	2.05
hycA	b2725	transcriptional repression of hyc and hyp operons	2.00
hyi	b0508	hydroxypyruvate isomerase	2.07
idnT	b4265	L-idonate transporter	2.28
kdgT	b3909	2-keto-3-deoxy-D-gluconate transport system	2.01
lamB	b4036	phage lambda receptor protein; maltose high-affinity receptor	2.01
malF	b4033	part of maltose permease, periplasmic	2.19
malG	b4032	part of maltose permease, inner membrane	2.27
malK	b4035	ATP-binding component of transport system for maltose	2.38
malM	b4037	periplasmic protein of maltose regulon	2.00
maoC	b1387	putative aldehyde dehydrogenase	2.40
melR	b4118	regulator of melibiose operon	2.22
molR_2	b2116	molybdate metabolism regulator, second fragment 2	2.18
nanT	b3224	sialic acid transporter	2.55
otsA	b1896	trehalose-6-phosphate synthase	4.33
otsB	b1897	trehalose-6-phosphate phophatase, biosynthetic	3.78
ptsA	b3947	PEP-protein phosphotransferase system enzyme I	2.17
ptxA	b4195	L-ascorbate-specific enzyme IIA component of PTS	2.03
rhaA	b3903	L-rhamnose isomerase	2.62
rhaB	b3904	rhamnulokinase	2.40
rhaD	b3902	rhamnulose-phosphate aldolase	2.06
rhaR	b3906	positive regulator for rhaRS operon	2.55
rhaS	b3905	positive regulator for rhaBAD operon	2.05
setB	b2170	lactose/glucose efflux system	2.12
sgaU	b4197	L-xylulose 5-phosphate 3-epimerase	2.22
sgbE	b3583	L-ribulose-5-phosphate 4-epimerase	2.20
sgbH	b3581	3-keto-L-gulonate 6-phosphate decarboxylase	2.03
sgbU	b3582	predicted L-xylulose 5-phosphate 3-epimerase	2.18
sgcX	b4305	KpLE2 phage-like element; predicted endoglucanase with Zn-dependent exopeptidase domain	2.11

srlA	b2702	PTS system, glucitolsorbitol-specific IIC component, one of two	2.05
treB	b4240	PTS system enzyme II, trehalose specific	2.18
treC	b4239	trehalase 6-P hydrolase	2.12
uhpT	b3666	hexose phosphate transport protein	2.13
uxaB	b1521	altronate oxidoreductase	2.06
uxuB	b4323	D-mannonate oxidoreductase	2.08
xylF	b3566	xylose binding protein transport system	2.47
ycjN	b1310	predicted sugar transporter subunit: periplasmic-binding component of ABC superfamily	2.71
ycjU	b1317	beta-phosphoglucomutase	2.16
ycjV	b1318	putative ATP-binding sugar transporter	2.10
ydeZ	b1515	autoinducer 2 import system permease protein	2.03
yeeR	b2001	putative PTS enzyme II	2.44
yeiC	b2166	pseudouridine kinase	2.25
yfeN	b2408	putative sugar hydrolase	2.15
ygbL	b2738	predicted class II aldolase	2.30
ygcE	b2776	putative kinase	2.57
yggF	b2930	glyoxylate-induced protein	2.07
ygiZ	b3027	molybdate metabolism regulator, first fragment	2.25
ygjE	b3063	L-tartrate/succinate antiporte	2.24
ygjK	b3080	alpha-glucosidase	2.16
yhbX	b3173	putative alkaline phosphatase I	2.13
yhfW	b3380	putative mutase	2.01
yiaL	b3576	putative lipase	2.55
yiaM	b3577	L-dehydroascorbate transporter	2.24
yiaN	b3578	L-dehydroascorbate transporter	2.43
yiaO	b3579	L-dehydroascorbate transporter	2.37
yieC	b3720	carbohydrate-specific outer membrane porin, cryptic	2.13
yihO	b3876	putative permease	2.35
yihP	b3877	putative permease	2.62
yihS	b3880	aldose-ketose isomerase; D-mannose isomerase	2.33
yjfR	b4192	L-ascorbate 6-phosphate lactonase	2.08
yjhF	b4296	putative transport system permease	2.06
yjhP	b4306	putative methyltransferase	2.66
yjjN	b4358	L-galactonate oxidoreductase	2.74
yliI	b0837	soluble aldose sugar dehydrogenase	2.05
Cell cycle control, cell division, chromosome partitioning			
dicB	b1575	inhibition of cell division	2.20
dicC	b1569	regulator of dicB	2.14
Cell motility			
fliH	b1940	flagellar assembly protein	2.33
csgC	b1043	curli assembly protein	2.24
ecpD	b0140	probable pilin chaperone similar to PapD	2.44
fhiA	b0229	flagellar biosynthesis	2.05

fimG	b4319	fimbrial morphology	2.06
flgC	b1074	flagellar biosynthesis, cell-proximal portion of basal-body rod	2.83
flgD	b1075	flagellar biosynthesis, initiation of hook assembly	2.08
flgE	b1076	flagellar biosynthesis, hook protein	2.27
flgG	b1078	flagellar biosynthesis, cell-distal portion of basal-body rod	2.23
flgH	b1079	flagellar biosynthesis, basal-body outer-membrane L (lipopolysaccharide layer) ring protein	2.42
flgI	b1080	homolog of Salmonella P-ring of flagella basal body	2.20
flgK	b1082	flagellar biosynthesis, hook-filament junction protein 1	2.32
flhE	b1878	flagellar protein	2.30
fliI	b1941	flagellum-specific ATP synthase	2.07
fliJ	b1942	flagellar fliJ protein	2.32
fliK	b1943	flagellar hook-length control protein	2.17
fliL	b1944	flagellar biosynthesis	2.15
fliP	b1948	flagellar biosynthesis	2.24
fliQ	b1949	flagellar biosynthesis	2.58
fliR	b1950	flagellar biosynthesis	2.55
fliS	b1925	flagellar biosynthesis; repressor of class 3a and 3b operons (RflA activity)	2.05
gspD	b3325	general secretory pathway component, cryptic	2.33
gspE	b3326	general secretory pathway component, cryptic	2.34
gspF	b3327	general secretory pathway component, cryptic	2.02
gspG	b3328	pseudopilin, cryptic, general secretion pathway	2.27
gspH	b3329	general secretory pathway component, cryptic	3.11
gspI	b3330	general secretory pathway component, cryptic	2.57
htrE	b0139	probable outer membrane porin protein involved in fimbrial assembly	2.45
motA	b1890	proton conductor component of motor; no effect on switching	2.39
motB	b1889	enables flagellar motor rotation, linking torque machinery to cell wall	2.19
murP	b2429	flagellar biosynthesis; repressor of class 3a and 3b operons (RflA activity)	2.44
sfmA	b0530	putative fimbrial-like protein	2.48
sfmC	b0531	pilin chaperone, periplasmic	2.54
sfmF	b0534	putative fimbrial-like protein	2.79
sfmH	b0533	involved in fimbrial asembly	3.34
tap	b1885	methyl-accepting chemotaxis protein IV, peptide sensor receptor	2.15
yadN	b0141	putative fimbrial-like protein	2.23
yagZ	b0293	cryptic Mat fimbrillin gene	2.04
ybcW	b0559	putative fimbrial-like protein	2.26
ybgP	b0717	putative chaperone	2.89
ybgQ	b0718	putative outer membrane protein	2.57
ycbF	b0944	putative chaperone	2.17
ycbR	b0939	putative chaperone	2.21
ycbS	b0940	putative outer membrane protein	2.08
ydeQ	b1502	putative adhesin; similar to FimH protein	3.05
ydeS	b1504	putative fimbrial-like protein	2.82
yehB	b2109	putative outer membrane protein	2.49

yehC	b2110	putative chaperone	2.07
yfcR	b2335	putative fimbrial protein	2.23
yfcV	b2339	putative fimbrial-like protein	2.60
yggR	b2950	putative protein transport	2.22
ygiL	b3043	putative fimbrial-like protein	2.45
yodD	b1953	putative curli production protein	2.24
yraK	b3145	putative fimbrial protein	2.10
Cell wall/membrane/envelope biogenesis			
acrE	b3265	transmembrane protein affects septum formation and cell membrane permeability	2.43
agaS	b3136	tagatose-6-phosphate ketose/aldose isomerase	2.23
arnT	b2257	4-amino-4-deoxy-L-arabinose transferase (lipid A modification)	2.07
betT	b0314	high-affinity choline transport	3.77
caiT	b0040	probable carnitine transporter	2.55
cpsB	b2049	mannose-1-phosphate guanyltransferase	2.01
cusC	b0572	copper/silver efflux system, outer membrane component	2.01
fepE	b0587	ferric enterobactin (enterochelin) transport	2.11
gudX	b2788	(D)-glucarate dehydratase 1	2.09
ompN	b1377	outer membrane pore protein N, non-specific	2.32
rspA	b1581	starvation sensing protein	2.63
wcaA	b2059	predicted glycosyl transferase	2.36
wcaC	b2057	predicted glycosyl transferase	2.76
wcaE	b2055	putative colanic acid biosynthesis glycosyl transferase	2.40
wcaG	b2052	putative nucleotide di-P-sugar epimerase or dehydratase	2.30
wcaI	b2050	putative colanic biosynthesis glycosyl transferase	2.21
wcaJ	b2047	putative colanic acid biosynthsis UDP-glucose lipid carrier transferase	2.05
wza	b2062	putative polysaccharide export protein	2.43
yaiU	b0374	putative flagellin structural protein	2.18
yeaV	b1801	putative transport protein	2.66
yfhD	b2558	putative periplasmic binding transport protein	2.10
yhiU	b3513	putative membrane protein	2.30
yiaD	b3552	putative outer membrane protein	2.46
yjcP	b4080	outer membrane factor of efflux pump	2.19
yohG	b2138	putative channelfilament proteins	2.20
Coenzyme transport and metabolism			
bioA	b0774	7,8-diaminopelargonic acid synthetase	2.01
bioD	b0778	dethiobiotin synthetase	2.11
bioF	b0776	8-amino-7-oxononanoate synthase	2.04
citD	b0617	citrate lyase acyl carrier protein (gamma chain)	2.37
citF	b0615	citrate lyase, citrate-ACP transferase (alpha) subunit	2.10
citG	b0613	2-(5''-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase	2.91
citT	b0612	citrate:succinate antiporter	2.48
citX	b0614	apo-citrate lyase phosphoribosyl-dephospho-CoA transferase	2.68
thiG	b3991	thiamin (thiazole moiety) biosynthesis protein	2.05

thiM	b2104	hydoxyethylthiazole kinase	2.20
Defense mechanisms			
ampC	b4150	beta-lactamase; penicillin resistance	2.09
dinF	b4044	DNA-damage-inducible protein F	2.19
emrK	b2368	multidrug resistance protein K	2.60
emrY	b2367	multidrug resistance protein Y	2.57
mdtC	b2076	multidrug efflux system, subunit C	2.03
mdtF	b3514	multidrug transporter, RpoS-dependent	2.65
mdtJ	b1600	multidrug efflux system transporter	2.34
mdtL	b1599	multidrug efflux system transporter	2.41
ybeR	b0645	putative lambdoid prophage Rac excisionase	2.37
ycfZ	b1121	homolog of virulence factor	2.12
yiaV	b3586	membrane fusion protein (MFP) component of efflux pump, signal anchor	2.21
yibH	b3597	putative membrane protein	2.06
yjcP	b4080	outer membrane factor of efflux pump	2.19
yjcR	b4082	membrane fusion protein of efflux pump	2.19
Energy production and conversion			
aldB	b3588	aldehyde dehydrogenase B (lactaldehyde dehydrogenase)	2.16
allA	b0505	ureidoglycolate hydrolase	2.23
allB	b0512	allantoinase	2.33
allC	b0516	allantoate amidohydrolase	2.47
allD	b0517	ureidoglycolate dehydrogenase	2.60
allS	b0504	DNA-binding transcriptional activator of the allD operon	2.56
araB	b0063	L-ribulokinase	2.12
aslB	b3800	putative arylsulfatase regulator	2.15
betB	b0312	NAD+-dependent betaine aldehyde dehydrogenase	2.74
dcuD	b3227	putative transport protein	2.28
fadH	b3081	2,4-dienoyl-CoA reductase, NADH and FMN-linked	2.17
fadJ	b2341	fused enoyl-CoA hydratase and epimerase and isomerase/3-hydroxyacyl-CoA dehydrogenase	2.31
fadL	b2342	beta-ketoacyl-CoA thiolase, anaerobic, subunit	2.39
fdrA	b0518	involved in protein transport; multicopy suppressor of dominant negative ftsH mutants	2.47
fixA	b0041	predicted electron transfer flavoprotein subunit, required for anaerobic carnitine reduction	3.17
fixC	b0043	predicted oxidoreductase with FAD/NAD(P)-binding domain	2.66
fixX	b0044	predicted 4Fe-4S ferredoxin-type protein	2.57
frc	b2374	formyl-CoA transferase, NAD(P)-binding	2.47
frmA	b0356	alcohol dehydrogenase class III; formaldehyde dehydrogenase, glutathione-dependent	5.45
frmB	b0355	S-formylglutathione hydrolase	12.95
frmR	b0357	repressor of frmRAB	4.75
fucO	b2799	L-1,2-propanediol oxidoreductase	2.02
hcp	b0873	hybrid-cluster	2.40

hycC	b2723	membrane-spanning protein of hydrogenase 3 (part of FHL complex)	2.08
hycD	b2722	membrane-spanning protein of hydrogenase 3 (part of FHL complex)	2.25
hydN	b2713	involved in electron transport from formate to hydrogen, Fe-S centers	2.03
hyfA	b2481	hydrogenase 4 Fe-S subunit	2.71
hyfB	b2482	hydrogenase 4 membrane subunit	2.76
hyfC	b2483	hydrogenase 4 membrane subunit	2.45
hyfD	b2484	hydrogenase 4 membrane subunit	2.23
hyfE	b2485	hydrogenase 4 membrane subunit	2.07
hyfG	b2487	hydrogenase 4 subunit	2.62
napG	b2205	ferredoxin-type protein: electron transfer	2.01
narG	b1224	nitrate reductase 1, alpha subunit	3.47
narH	b1225	nitrate reductase 1, beta subunit	2.22
narJ	b1226	nitrate reductase 1, delta subunit, assembly function	2.25
ndh	b1109	respiratory NADH dehydrogenase	2.34
norV	b2710	citrate lyase alpha chain	2.10
nrfC	b4072	formate-dependent nitrite reductase; Fe-S centers	2.60
paaA	b1388	ring 1,2-phenylacetyl-CoA epoxidase subunit	2.57
paaB	b1389	ring 1,2-phenylacetyl-CoA epoxidase possible subunit, not required for in vitro activity	2.54
paaC	b1390	ring 1,2-phenylacetyl-CoA epoxidase subunit	2.75
paaD	b1391	ring 1,2-phenylacetyl-CoA epoxidase subunit	2.57
paaE	b1392	ring 1,2-phenylacetyl-CoA epoxidase, NAD(P)H oxidoreductase component	2.04
rutA	b1012	pyrimidine oxygenase, FMN-dependent	2.47
rutB	b1011	ureidoacrylate amidohydrolase	2.53
rutC	b1010	putative aminoacrylate peracid reductase	2.04
rutD	b1009	putative aminoacrylate hydrolase	2.32
rutF	b1007	flavin:NADH reductase	2.02
torC	b0996	trimethylamine N-oxide reductase, cytochrome c-type subunit	2.06
torD	b0998	part of trimethylamine-N-oxide oxidoreductase	2.54
torR	b0995	DNA-binding response regulator in two-component regulatory system with TorS	2.10
torS	b0993	hybrid sensory histidine kinase in two-component regulatory system with TorR	2.24
ttdA	b3061	L-tartrate dehydratase, subunit A	2.07
ttdB	b3062	L-tartrate dehydratase, subunit B	2.14
xdhA	b2866	xanthine dehydrogenase, molybdenum binding subunit	2.28
yagS	b0285	PaoABC aldehyde oxidoreductase, FAD-containing subunit	2.13
yahF	b0320	putative oxidoreductase subunit	2.02
yccM	b0992	predicted 4Fe-4S membrane protein	2.28
ycgH_1	b1169	putative ATP-binding component of a transport system	3.04
ycgH_2	b1170	putative part of putative ATP-binding component of a transport system	2.31
ydbK	b1378	putative oxidoreductase, Fe-S subunit	3.52
yddA	b1496	putative ATP-binding component of a transport system	2.30
yeaW	b1802	predicted 2Fe-2S cluster-containing protein	2.36

yfdE	b2371	predicted CoA-transferase, NAD(P)-binding	2.23
ygcN	b2766	predicted oxidoreductase with FAD/NAD(P)-binding domain	2.20
ygcR	b2770	putative transport protein	2.18
ygcU	b2773	putative oxidoreductase subunit	2.03
yhiD	b3508	putative Mg(2+)transport ATPase	2.11
yiaK	b3575	putative dehydrogenase	2.17
yiaY	b3589	putative oxidoreductase	2.41
yjiL	b4334	putative ATPase, activator of(R)-hydroxyglutaryl-CoA dehydartase	2.14
ykgD	b0305	putative ARAC-type regulatory protein	2.03
ykgE	b0306	putative dehydrogenase subunit	2.09
ylbF	b0520	response transcriptional regulator for torA (sensor TorS)	2.10
ynbB	b1409	putative phosphatidate cytidiltransferase	2.56
yodB	b1974	cytochrome b561 homolog 1	2.05
yqhD	b3011	putative oxidoreductase	3.92
Inorganic ion transport and metabolism			
arsB	b3502	arsenical pump membrane protein	2.39
aslA	b3801	arylsulfatase	2.33
clcB	b1592	chloride channel, voltage-gated	2.01
cynS	b0340	cyanate aminohydrolase	2.31
cynT	b0339	carbonic anhydrase	2.07
cynX	b0341	cyanate transport	2.17
focB	b2492	probable formate transporter (formate channel 2)	2.36
katE	b1732	catalase; hydroperoxidase HPII(III)	2.84
mgtA	b4242	Mg2+ transport ATPase, P-type 1	3.86
narK	b1223	nitrite extrusion protein	2.54
nrfD	b4073	formate-dependent nitrate reductase complex; transmembrane protein	2.26
phnD	b4105	periplasmic binding protein component of Pn transporter	2.11
phnE	b4104	membrane channel protein component of Pn transporter	2.17
phnG	b4101	phosphonate metabolism	2.13
phnH	b4100	phosphonate metabolism	2.02
phnI	b4099	phosphonate metabolism	2.07
phnJ	b4098	phosphonate metabolism	2.09
pitB	b2987	low-affinity phosphate transport	2.03
zinT	b1973	zinc and cadmium binding protein, periplasmic	3.78
znuA	b1857	cyanate aminohydrolase, cyanase	2.31
Intracellular trafficking, secretion, and vesicular transport			
gspC	b3324	general secretory pathway component, cryptic	2.24
gspJ	b3331	general secretory pathway component, cryptic	2.29
gspK	b3332	general secretory pathway component, cryptic	2.40
gspL	b3333	general secretory pathway component, cryptic	2.02
spy	b1743	periplasmic protein related to spheroblast formation	2.68
yghE	b2969	putative general secretion pathway for protein export (GSP)	2.46
Lipid transport and metabolism			
aes	b0476	acetyl esterase	2.05

atoA	b2222	acetyl-CoA:acetoacetyl-CoA transferase beta subunit	2.22
atoD	b2221	acetyl-CoA:acetoacetyl-CoA transferase alpha subunit	2.40
caiD	b0036	carnitine racemase	2.89
caiE	b0035	stimulator of CaiD and CaiB enzyme activities	2.41
glxR	b0509	tartronate semialdehyde reductase, NADH-dependent	2.16
idnO	b4266	5-keto-D-gluconate 5-reductase	2.05
prpD	b0334	2-methylcitrate dehydratase	2.09
prpE	b0335	propionyl-CoA synthetase	2.34
srlD	b2705	glucitol (sorbitol)-6-phosphate dehydrogenase	2.16
ygbJ	b2736	putative dehydrogenase	2.19
yihU	b3882	putative dehydrogenase	2.25
Nucleotide transport and metabolism			
hyuA	b2873	D-stereospecific phenylhydantoinase	2.40
rihB	b2162	ribonucleoside hydrolase 2	2.48
rihc	b0030	ribonucleoside hydrolase 3	2.00
ssnA	b2879	predicted chlorohydrolase/aminohydrolase	2.30
stpA	b2669	DNA binding protein, nucleoid-associated	2.07
xapA	b2407	xanthosine phosphorylase	2.70
ybbY	b0513	putative transport	2.19
yeiJ	b2161	nucleoside permease	2.42
ygfO	b2882	xanthine permease	2.00
ygfU	b2888	putative permease	2.22
Posttranslational modification, protein turnover, chaperones			
hscC	b0650	DnaK-like protein	2.40
hslJ	b1379	heat shock protein hslJ	2.06
htpG	b0473	chaperone Hsp90, heat shock protein C 62.5	2.08
nrfF	b4075	part of formate-dependent nitrite reductase complex	2.21
nrfG	b4076	part of formate-dependent nitrite reductase complex	2.32
osmB	b1283	osmotically inducible lipoprotein	4.38
osmC	b1482	osmotically inducible protein	3.15
osmE	b1739	activator of ntrL gene	3.99
osmY	b4376	periplasmic protein	2.61
ycaL	b0909	putative heat shock protein	2.36
yhbU	b3158	putative collagenase	2.03
Replication, recombination and repair			
endA	b2945	DNA-specific endonuclease I	2.21
fimE	b4313	recombinase involved in phase variation; regulator for fimA	2.59
mutM	b3635	formamidopyrimidine DNA glycosylase	2.38
nohB	b0560	bacteriophage DNA packaging protein	2.39
polB	b0060	DNA polymerase II	2.02
radC	b3638	DNA repair protein	2.38
recE	b1350	exonuclease VIII, ds DNA exonuclease, 5 --> 3 specific	2.60
recX	b2698	regulator, OraA protein	2.15
wcaH	b2051	GDP-mannose mannosyl hydrolase	2.10

yaiC	b0385	diguanylate cyclase of cellulose, biofilm, motility regulation	2.41
ybeS	b0646	putative enzyme of polynucleotide modification	2.18
ydaV	b1360	putative DNA replication factor	2.34
ydeO	b1499	transcriptional activator for mdtEF	2.66
yeeS	b2002	putative DNA repair protein, RADC family	2.21
yfdL	b2355	putative RNA polymerase beta	2.75
yfjY	b2644	putative DNA repair protein	2.66
yghG	b2971	restriction alleviation and modification enhancement	2.05
yhdJ	b3262	DNA adenine methyltransferase	2.21
yicF	b3647	putative enzyme	2.08
ykfG	b0247	putative DNA repair protein	2.43
Secondary metabolites biosynthesis, transport and catabolism			
cchB	b2456	detox protein	2.29
Signal transduction mechanisms			
adrB	b1815	predicted phosphodiesterase	2.08
fimZ	b0535	fimbrial Z protein; probable signal transducer	2.19
glnG	b3868	response regulator for gln (sensor glnL) (nitrogen regulator I, NRI)	2.21
glnL	b3869	histidine protein kinase sensor for GlnG regulator (nitrogen regulator II, NRII)	3.02
uhpB	b3668	sensor histidine protein kinase phosphorylates UhpA	2.01
ycgG	b1168	predicted cyclic-di-GMP phosphodiesterase	2.18
yjiY	b4354	putative carbon starvation protein	2.14
Transcription			
adiY	b4116	DNA-binding transcriptional activator	2.15
alpA	b2624	prophage CP4-57 regulatory protein alpA	2.19
arsR	b3501	transcriptional repressor of chromosomal ars operon	2.07
betI	b0313	probably transcriptional repressor of bet genes	3.42
bglG	b3723	positive regulation of bgl operon	2.29
dsdC	b2364	D-serine dehydratase (deaminase) transcriptional activator	2.39
envR	b3264	DNA-binding transcriptional regulator	2.29
fhlA	b2731	formate hydrogen-lyase transcriptional activator for fdhF, hyc and hyp operons	2.05
fliA	b1922	flagellar biosynthesis; alternative sigma factor 28; regulation of flagellar operons	3.25
frvR	b3897	putative frv operon regulatory protein	2.64
gatR	b2087	split galactitol utilization operon repressor, interrupted	2.41
htgA	b0012	positive regulator for sigma 32 heat shock promoters	2.42
hyfR	b2491	DNA-binding transcriptional activator, formate sensing	2.40
lysR	b2839	positive regulator for lys	2.04
rcsA	b1951	positive regulator for ctr capsule biosynthesis, positive transcription factor	3.46
rhmR	b2248	putative regulator	2.39
rtcR	b3422	sigma54-dependent regulator of rtcBA expression	2.08
ybeF	b0629	putative transcriptional regulator LYSR-type	2.37
ybhD	b0768	putative transcriptional regulator LYSR-type	2.36

ybiH	b0796	putative transcriptional regulator	2.29
ycgW	b1160	Rpos stabilzer during Mg starvation, anti-RssB factor	3.80
ygeK	b2855	putative 2-component transcriptional regulator	2.22
yidP	b3684	putative transcriptional regulator	2.32
Translation, ribosomal structure and biogenesis			
lysU	b4129	lysine tRNA synthetase, inducible; heat shock protein	2.00
prfH	b0236	probable peptide chain release factor	2.35
micF	b4439	antisense regulator of the translation of OmpF porin	3.16