

Supplementary Table S2. Functional description of genes downregulated in response to glyphosate shock

Gene name	Gene ID	Functional description	Fold change
Amino acid transport and metabolism			
<i>aroA</i>	b0908	high-affinity leucine-specific transport system; periplasmic binding protein	-2.10
<i>aroB</i>	b3389	serine hydroxymethyltransferase	-2.33
<i>aroD</i>	b1693	in glycine cleavage complex, carrier of aminomethyl moiety via covalently bound lipoyl cofactor	-2.81
<i>aroG</i>	b0754	3-deoxy-D-arabino-heptulosonate-7-phosphate synthase, phenylalanine repressible	-3.28
<i>aroH</i>	b1704	2-isopropylmalate synthase	-2.19
<i>aroK</i>	b3390	ATP-binding component of putrescine transport system	-2.13
<i>asd</i>	b3433	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase (DAHP synthetase, phenylalanine repressible)	-2.35
<i>aspC</i>	b0928	glycine decarboxylase, P protein of glycine cleavage system	-2.60
<i>cvpA</i>	b2313	histidine transport, membrane protein M	-2.34
<i>cysD</i>	b2752	acetolactate synthase III, valine sensitive, large subunit	-2.31
<i>cysH</i>	b2762	3-phosphoadenosine 5-phosphosulfate reductase	-3.75
<i>cysM</i>	b2421	ATP:sulfurylase (ATP:sulfate adenylyltransferase), subunit 2	-2.65
<i>dadA</i>	b1189	D-amino acid dehydrogenase	-2.05
<i>dosC</i>	b1490	cysteine synthase B, O-acetylserine sulphydrolase B	-2.67
<i>dppA</i>	b3544	dipeptide transporter	-5.26
<i>dppB</i>	b3543	dipeptide/heme transporter	-3.35
<i>dppC</i>	b3542	dipeptide/heme transporter	-2.75
<i>dppD</i>	b3541	dipeptide/heme transporter	-3.65
<i>dppF</i>	b3540	dipeptide ABC transporter	-3.04
<i>fliY</i>	b1920	cell division inhibitor, a membrane ATPase, activates minC	-2.35
<i>gcvB</i>	b4443	putative outer membrane protein	-2.04
<i>gcvH</i>	b2904	peptidoglycan-associated lipoprotein	-3.81
<i>gcvP</i>	b2903	carboxy-terminal protease for penicillin-binding protein 3	-3.25
<i>gcvR</i>	b2479	DNA-binding transcriptional repressor, regulatory protein accessory to GcvA	-2.58
<i>gcvT</i>	b2905	aminomethyltransferase, tetrahydrofolate-dependent, subunit (T protein) of glycine cleavage complex	-5.58
<i>gdhA</i>	b1761	a minor lipoprotein	-2.72
<i>glgS</i>	b3049	alanine racemase 2, catabolic	-3.03
<i>gltB</i>	b3212	glutamate synthase, large subunit	-4.68
<i>gltD</i>	b3213	glutamate synthase, 4Fe-4S protein, small subunit	-6.06
<i>glyA</i>	b2551	riboflavin synthase, alpha chain	-3.97
<i>gnsB</i>	b1550	tyrosine aminotransferase, tyrosine repressible	-4.36
<i>gsiA</i>	b0829	glutathione transporter ATP-binding protein, ABC super family	-2.71
<i>gsiB</i>	b0830	glutathione periplasmic binding protein, ABC superfamily transporter	-2.79
<i>gsiC</i>	b0831	glutathione transporter, permease component, ABC superfamily	-3.26
<i>gsiD</i>	b0832	glutathione transporter, permease component, ABC superfamily	-2.47

<i>hisA</i>	b2024	pantothenate synthetase	-2.31
<i>hisF</i>	b2025	D-3-phosphoglycerate dehydrogenase	-2.46
<i>hisH</i>	b2023	3-phosphoserine aminotransferase	-2.36
<i>hisI</i>	b2026	cytochrome b(561)	-2.01
<i>hisM</i>	b2307	pyridine nucleotide transhydrogenase, alpha subunit	-2.03
<i>ilvC</i>	b3774	ketol-acid reductoisomerase, NAD(P)-binding	-7.78
<i>ilvD</i>	b3771	dihydroxyacid dehydratase	-2.10
<i>ilvE</i>	b3770	branched-chain amino-acid aminotransferase	-2.96
<i>ilvG_1</i>	b3767	membrane-bound ATP synthase, F1 sector, delta-subunit	-4.25
<i>ilvG_2</i>	b3768	malate dehydrogenase	-3.59
<i>ilvH</i>	b0078	succinate dehydrogenase, cytochrome b556	-2.94
<i>ilvI</i>	b0077	succinate dehydrogenase, hydrophobic subunit	-4.03
<i>ilvL</i>	b3766	2-oxoglutarate dehydrogenase (decarboxylase component)	-2.67
<i>ilvM</i>	b3769	NADH dehydrogenase I chain F	-3.68
<i>ilvN</i>	b3670	D-lactate dehydrogenase, FAD protein, NADH independent	-2.98
<i>leuA</i>	b0074	succinate dehydrogenase, flavoprotein subunit	-3.71
<i>leuC</i>	b0072	NADH dehydrogenase I chain I	-3.19
<i>leuD</i>	b0071	3-isopropylmalate dehydrogenase	-3.11
<i>leuL</i>	b0075	leu operon leader peptide	-3.60
<i>livG</i>	b3455	acetolactate synthase II, valine insensitive, small subunit	-2.96
<i>livH</i>	b3457	leucine/isoleucine/valine transporter subunit	-2.20
<i>livK</i>	b3458	leucine transporter subunit	-4.05
<i>livM</i>	b3456	leucine/isoleucine/valine transporter subunit	-2.02
<i>metA</i>	b4013	Subunit composition of homoserine O-succinyltransferase	-2.52
<i>metC</i>	b3008	cystathionine beta-lyase, PLP-dependent	-2.51
<i>metE</i>	b3829	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase	-2.15
<i>mtr</i>	b3161	tryptophan transporter of high affinity	-2.46
<i>potF</i>	b0854	sulfite reductase (NADPH), flavoprotein beta subunit	-4.55
<i>potG</i>	b0855	periplasmic sulfate-binding protein	-3.39
<i>potH</i>	b0856	sulfate transport system permease W protein	-2.05
<i>speC</i>	b2965	DNA-binding protein HU-alpha (HU-2)	-2.31
<i>thrA</i>	b0002	fused aspartokinase I and homoserine dehydrogenase I	-3.09
<i>thrB</i>	b0003	homoserine kinase	-3.20
<i>thrC</i>	b0004	threonine synthase	-3.16
<i>thrL</i>	b0001	transcriptional regulator cys regulon; accessory regulatory circuit affecting cysM	-4.33
<i>tyrB</i>	b4054	replication initiation inhibitor, binds to 13-mers at oriC	-2.61
<i>yacL</i>	b0119	regulator for leucine (or lrp) regulon and high-affinity branched-chain amino acid transport system	-2.07
<i>ybiB</i>	b0800	thr operon leader peptide	-2.43
<i>ybiK</i>	b0828	asparaginase III α - β complex	-3.00
<i>ydjN</i>	b1729	homoserine transsuccinylase	-2.93
<i>yeaC</i>	b1777	cystathionine beta-lyase (beta-cystathionase)	-2.16
<i>yecC</i>	b1917	transporter subunit: ATP-binding component of ABC superfamily	-2.68
<i>yecS</i>	b1918	glycogen biosynthesis, rpoS dependent	-2.72

<i>yfbQ</i>	b2290	haemolysin expression modulating protein	-3.13
<i>ygbE</i>	b2749	ilvGEDA operon leader peptide	-2.72
<i>ygiU</i>	b3089	sodium:serine/threonine symporter	-3.80
<i>ynfN</i>	b1551	aspartate aminotransferase	-4.07
<i>yoaC</i>	b1810	tryptophan-specific transport protein	-3.60

Carbohydrate transport and metabolism

<i>celA</i>	b1738	N-(5-phospho-L-ribosyl-formimino)-5-amino-1-(5-phosphoribosyl)-4-imidazolecarboxamide isomerase	-2.03
<i>gatZ</i>	b2095	outer membrane protein 3b (a), protease VII	-2.28
<i>lpcA</i>	b0222	bifunctional: aspartokinase I (N-terminal); homoserine dehydrogenase I (C-terminal)	-2.01
<i>rpe</i>	b3386	phosphoribosylaminoimidazolecarboxamideformyltransferase	-2.00
<i>rybA</i>	b4416	phosphoribosylglycinamide formyltransferase 2	-2.34
<i>rygD</i>	b4447	phosphoribosylformyl-glycineamide synthetase	-2.02
<i>ybhE</i>	b0767	6-phosphogluconolactonase	-2.17
<i>ycdL</i>	b1431	NADP-specific glutamate dehydrogenase	-2.29
<i>yhjS</i>	b3536	cellulose production protein	-2.60
<i>yibO</i>	b3612	phosphoglycero mutase III, cofactor-independent	-2.15
<i>zwf</i>	b1852	glucose-6-phosphate dehydrogenase	-2.67

Cell cycle control, cell division, chromosome partitioning

<i>damX</i>	b3388	cell division protein that binds to the septal ring	-2.04
<i>fhuF</i>	b4367	cell division protein; ingrowth of wall at septum	-2.92
<i>ftsL</i>	b0083	periplasmic molecular chaperone for outer membrane proteins	-2.26
<i>minC</i>	b1176	cell division inhibitor	-2.04
<i>minD</i>	b1175	membrane ATPase of the MinC-MinD-MinE system	-2.04

Cell wall/membrane/envelope biogenesis

<i>dadX</i>	b1190	dipeptide transport system permease protein 2	-2.10
<i>ddg</i>	b2378	palmitoleoyl-acyl carrier protein (ACP)-dependent acyltransferase	-2.84
<i>hlpA</i>	b0178	pyridine nucleotide transhydrogenase, beta subunit	-3.50
<i>mscL</i>	b3291	mechanosensitive channel protein, high conductance	-2.04
<i>nlpC</i>	b1708	C40 clan, lipoprotein	-2.07
<i>nmpC</i>	b0553	orf, hypothetical protein	-5.14
<i>ompF</i>	b0929	taurine ATP-binding component of a transport system	-11.07
<i>ompT</i>	b0565	taurine transport system periplasmic protein	-2.57
<i>pal</i>	b0741	lipoprotein-28	-2.52
<i>prc</i>	b1830	carboxy-terminal protease for penicillin-binding protein 3	-2.51
<i>rlpB</i>	b0641	phosphoribosylaminoimidazole synthetase	-2.17
<i>yabC</i>	b0082	cold shock protein	-2.21
<i>yciD</i>	b1256	outer membrane protein W	-2.52
<i>yncA</i>	b1448	predicted acyltransferase with acyl-CoA N-acyltransferase domain	-2.38

Coenzyme transport and metabolism

<i>cobT</i>	b1991	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase (DAHP synthetase, tryptophan repressible)	-2.51
<i>folE</i>	b2153	cell division inhibitor, inhibits ftsZ ring formation	-2.56

<i>panC</i>	b0133	taurine transport system permease protein	-2.07
<i>panD</i>	b0131	cytoplasmic ferritin (an iron storage protein)	-2.57
<i>pdxJ</i>	b2564	adenosine 5-phosphosulfate kinase	-2.55
<i>ribC</i>	b1662	transcriptional regulation of gcv operon	-2.62
<i>serA</i>	b2913	thioredoxin reductase	-4.20
<i>serC</i>	b0907	survival protein	-3.47

Energy production and conversion

<i>isrB</i>	b4434	NADH dehydrogenase I chain C, D	-4.04
<i>acnB</i>	b0118	dipeptide transport protein	-2.12
<i>atpB</i>	b3738	F0 sector of membrane-bound ATP synthase, subunit a	-2.13
<i>atpE</i>	b3737	F0 sector of membrane-bound ATP synthase, subunit c	-2.07
<i>atpF</i>	b3736	F0 sector of membrane-bound ATP synthase, subunit b	-2.63
<i>atpH</i>	b3735	F1 sector of membrane-bound ATP synthase, delta subunit	-2.38
<i>cybB</i>	b1418	high-affinity branched-chain amino acid transport	-3.49
<i>dld</i>	b2133	glucose-6-phosphate dehydrogenase	-2.20
<i>hdeA</i>	b3510	GTP cyclohydrolase I	-3.15
<i>hdeB</i>	b3509	pyridoxine biosynthesis	-2.30
<i>ivbL</i>	b3672	membrane-bound ATP synthase, F0 sector, subunit a	-3.62
<i>leuB</i>	b0073	membrane-bound ATP synthase, F0 sector, subunit c	-3.43
<i>mdh</i>	b3236	Malate dehydrogenase	-2.35
<i>mviM</i>	b1068	putative structural protein	-2.65
<i>nuoA</i>	b2288	NADH:ubiquinone oxidoreductase, membrane subunit A	-2.09
<i>nuoB</i>	b2287	NADH:ubiquinone oxidoreductase, chain B	-2.52
<i>nuoC</i>	b2286	NADH:ubiquinone oxidoreductase, fused CD subunit	-2.19
<i>nuoE</i>	b2285	NADH:ubiquinone oxidoreductase, chain E	-2.41
<i>nuoF</i>	b2284	NADH:ubiquinone oxidoreductase, chain F	-2.21
<i>nuoG</i>	b2283	NADH:ubiquinone oxidoreductase, chain G	-2.41
<i>nuoI</i>	b2281	NADH:ubiquinone oxidoreductase, chain I	-2.04
<i>pntA</i>	b1603	sulfite reductase, alpha subunit	-3.23
<i>pntB</i>	b1602	ATP-binding component of sulfate permease A protein; chromate resistance	-2.98
<i>ryeA</i>	b4432	AMP nucleosidase	-2.42
<i>sdhA</i>	b0723	succinate dehydrogenase, flavoprotein subunit	-2.08
<i>sdhC</i>	b0721	succinate dehydrogenase, membrane subunit, binds cytochrome b556	-2.34
<i>sdhD</i>	b0722	succinate dehydrogenase, membrane subunit, binds cytochrome b556	-2.34
<i>sucA</i>	b0726	excinuclease ABC, subunit C; repair of UV damage to DNA	-2.30
<i>tas</i>	b2834	glutamine amidotransferase subunit of heterodimer with HisF	-2.91
<i>udhA</i>	b3962	homolog of Salmonella cold shock protein	-2.45
<i>ybiC</i>	b0801	predicted dehydrogenase	-2.53

Inorganic ion transport and metabolism

<i>cysA</i>	b2422	dihydroxyacid dehydratase	-2.82
<i>cysC</i>	b2750	acetolactate synthase II, large subunit, cryptic, interrupted	-3.59
<i>cysI</i>	b2763	acetolactate synthase II, valine insensitive, large subunit, silent in K-12	-3.57
<i>cysJ</i>	b2764	branched-chain amino-acid aminotransferase	-2.62
<i>cysN</i>	b2751	glutamate synthase, small subunit	-2.39

<i>cysW</i>	b2423	dipeptide transport system permease protein 1	-2.47
<i>ftn</i>	b1905	outer membrane porin protein; locus of qsr prophage	-3.69
<i>katG</i>	b3942	aconitate hydratase B	-2.13
<i>nlpA</i>	b3661	stationary-phase protein, cell division	-4.89
<i>pstB</i>	b3725	catalase; hydroperoxidase HPI(I)	-2.20
<i>sbp</i>	b3917	sulfate transporter subunit	-2.55
<i>tauA</i>	b0365	taurine transporter subunit	-5.59
<i>tauB</i>	b0366	taurine transporter subunit	-6.09
<i>tauC</i>	b0367	taurine transporter subunit	-4.62
<i>yibN</i>	b3611	predicted rhodanese-related sulfurtransferase	-2.27
Intracellular trafficking, secretion, and vesicular transport			
<i>secG</i>	b3175	preprotein translocase membrane subunit	-2.21
Lipid transport and metabolism			
<i>accD</i>	b2316	aminomethyltransferase (T protein; tetrahydrofolate-dependent) of glycine cleavage system	-2.27
<i>acpS</i>	b2563	glutamate synthase, large subunit	-2.30
<i>cdh</i>	b3918	ornithine decarboxylase isozyme	-2.21
<i>fabB</i>	b2323	D-ribulose-5-phosphate 3-epimerase	-2.23
<i>kduD</i>	b2842	NADH dehydrogenase I chain A	-2.02
Nucleotide transport and metabolism (11)			
<i>amn</i>	b1982	periplasmic putrescine-binding protein; permease protein	-2.54
<i>guaC</i>	b0104	aspartate 1-decarboxylase	-2.76
<i>purC</i>	b2476	protein export - membrane protein	-2.98
<i>purD</i>	b4005	CoA:apo-(acyl-carrier-protein) pantetheinephosphotransferase	-2.87
<i>purH</i>	b4006	acetylCoA carboxylase, carboxytransferase component, beta subunit	-2.62
<i>purL</i>	b2557	CDP-diacylglycerol phosphatidylhydrolase	-2.40
<i>purM</i>	b2499	3-oxoacyl-(acyl-carrier-protein) synthase I	-2.94
<i>purT</i>	b1849	2-deoxy-D-gluconate 3-dehydrogenase	-2.56
<i>pyrB</i>	b4245	uracil phosphoribosyltransferase	-2.60
<i>upp</i>	b2498	CspB	-3.90
<i>yefF</i>	b1103	ilvB operon leader peptide	-2.38
Posttranslational modification, protein turnover, chaperones			
<i>bcp</i>	b2480	aspartate-semialdehyde dehydrogenase	-3.22
<i>cyoE</i>	b0428	phosphoribosyl-amp cyclohydrolase; phosphoribosyl-ATP pyrophosphatase	-2.01
<i>cysU</i>	b2424	sulfate/thiosulfate transporter subunit	-2.28
<i>fkpB</i>	b0028	isopropylmalate isomerase subunit	-2.20
<i>ppiB</i>	b0525	ATP-sulfurylase (ATP:sulfate adenylyltransferase), subunit 1, probably a GTPase	-2.12
<i>sohB</i>	b1272	multicopy suppressor of htrA(degP)	-2.12
<i>surA</i>	b0053	peptidyl-prolyl cis-trans isomerase (PPIase)	-2.16
<i>trxB</i>	b0888	cold shock protein	-2.18
<i>yaiB</i>	b0382	anti-RssB factor, RpoS stabilizer during Pi starvation;	-2.36
<i>yjiD</i>	b4326	RpoS stabilizer after DNA damage, anti-RssB factor	-2.27
<i>yliJ</i>	b0838	glutathione S-transferase homolog	-3.04
Replication, recombination and repair			

<i>hupA</i>	b4000	HU, DNA-binding transcriptional regulator, alpha subunit	-4.37
<i>hupB</i>	b0440	membrane-bound ATP synthase, F0 sector, subunit b	-2.70
<i>pinR</i>	b1374	Rac prophage; predicted site-specific recombinase	-2.34
<i>smf</i>	b4473	peptidyl-prolyl cis-trans isomerase B (rotamase B)	-2.08
<i>uvrC</i>	b1913	positive transcriptional regulator for cysteine regulon	-2.44
<i>yabP</i>	b0056	repressor of aceBA operon	-3.34
<i>yabQ</i>	b0057	RNase II, mRNA degradation	-3.11

Secondary metabolites biosynthesis, transport and catabolism

<i>mhpF</i>	b0351	acetaldehyde-CoA dehydrogenase II, NAD-binding	-2.02
<i>ycgM</i>	b1180	3-dehydroquinone dehydratase	-3.38

Signal transduction mechanisms

<i>chpR</i>	b2783	high-affinity branched-chain amino acid transport system; membrane component	-2.04
<i>ycgF</i>	b1163	acetolactate synthase III, valine sensitive, small subunit	-2.14
<i>yiiT</i>	b3923	stress-induced protein	-2.25

Transcription

<i>cbl</i>	b1987	3-dehydroquinone synthase	-5.91
<i>cspB</i>	b1557	tetrahydropteroyltryptophan methyltransferase	-3.00
<i>cspC</i>	b1823	shikimate kinase I	-3.36
<i>cspE</i>	b0623	5-enolpyruvylshikimate-3-phosphate synthetase	-2.62
<i>cspG</i>	b0990	D-amino acid dehydrogenase subunit	-3.00
<i>cspI</i>	b1552	cold shock protein	-3.76
<i>cysB</i>	b1275	ketol-acid reductoisomerase	-2.87
<i>gadX</i>	b3516	DNA-binding transcriptional dual regulator	-2.18
<i>hha</i>	b0460	nicotinate-nucleotide dimethylbenzimidazole-P phosphoribosyl transferase	-2.00
<i>iciA</i>	b2916	DNA-binding transcriptional activator, replication initiation inhibitor	-3.05
<i>iclR</i>	b4018	NADH dehydrogenase I chain B	-2.37
<i>lrp</i>	b0889	DNA-binding transcriptional dual regulator, leucine-binding	-2.20
<i>pspF</i>	b1303	ATP-binding component of high-affinity phosphate-specific transport system	-2.33
<i>rnb</i>	b1286	GMP reductase	-2.29
<i>sdiA</i>	b1916	sulfate, thiosulfate transport system permease T protein	-2.72
<i>spf</i>	b3864	DNA-binding protein HU-beta, NS1 (HU-1)	-2.72
<i>uvrY</i>	b1914	transcriptional regulator of ftsQAZ gene cluster	-2.54
<i>ycbW</i>	b0946	cold shock-like protein	-3.11
<i>ycgE</i>	b1162	leu operon leader peptide	-2.04
<i>ydfH</i>	b1540	predicted DNA-binding transcriptional regulator	-2.16
<i>yfeC</i>	b2398	predicted DNA-binding protein, DUF1323 family	-2.23
<i>yhiW</i>	b3515	transcriptional activator of gadA and gadBC in absence of GadX	-2.05
<i>yjeB</i>	b4178	nitric oxide-sensitive repressor for NO regulon	-2.04

Translation, ribosomal structure and biogenesis

<i>frr</i>	b0172	outer membrane protein 1a (Ia;b;F)	-2.07
<i>rimJ</i>	b1066	phosphoribosylaminoimidazole-succinocarboxamide synthetase	-2.92
<i>rmf</i>	b0953	phosphoribosylglycinamide synthetase	-2.96
<i>rplY</i>	b2185	aspartate carbamoyltransferase, catalytic subunit	-2.04