Supplementary Table S3 Summary of regulated pathways in response to expressing EPSP synthase

Locus	Locus Tag	Product Name	Fold [a]
Shikimate pathway			
aroA	b0908	5-enolpyruvylshikimate-3-phosphate synthetase	0.92±0.12
aroB	b3389	3-dehydroquinate synthase	0.81±0.12
aroC	b2329	chorismate synthase	0.86±0.11
aroD	b1693	3-dehydroquinate dehydratase	0.82±0.08
aroE	b3281	dehydroshikimate reductase	0.90±0.10
aroF	b2601	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase (DAHP synthetase, tyrosine repressible)	-1.15±0.15
aroG	b0754	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase (DAHP synthetase, phenylalanine repressible)	0.91±0.09
aroH	b1704	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase (DAHP synthetase, tryptophan repressible)	-1.06±0.14
aroK	b3390	shikimate kinase I	0.91±0.11
aroL	b0388	shikimate kinase II	0.93±0.14
aroM	b0390	protein of *aro* operon, regulated by *aroR*	-1.14±0.13
aroP	b0112	aromatic amino acid transport protein	0.87±0.10
ydiB	b1692	putative oxidoreductase	-1.40±0.17
Aromatic acids biosynthesis			
tyrA	b2600	chorismate mutase-T and prephenate dehydrogenase	0.99±0.13
tyrB	b4054	tyrosine aminotransferase, tyrosine repressible	0.80±0.09
tyrP	b1907	tyrosine-specific transport system	-1.28±0.18
tyrR	b1323	transcriptional regulation of *aroF*, *aroG*, *tyrA* and aromatic amino acid transport	-1.08±0.15
tyrS	b1637	tyrosine tRNA synthetase	-0.96±0.13
pheA	b2599	chorismate mutase-P and prephenate dehydratase	-1.14±0.16
aspC	b0928	aspartate aminotransferase	1.20±0.17
ilvE	b3770	branched-chain amino-acid aminotransferase	1.32±0.19
trpA	b1260	tryptophan synthase, alpha protein	-1.10±0.15
trpB	b1261	tryptophan synthase, beta protein	-1.10±0.14
trpC	b1262	N-(5-phosphoribosyl)anthranilate isomerase and indole-3-glycerolphosphate synthetase	-1.03±0.09
trpD	b1263	anthranilate synthase component II, glutamine amidotransferase and phosphoribosylanthranilate transferase	-1.38±0.18
trpE	b1264	anthranilate synthase component I	-1.20±0.13
trpL	b1265	*trp* operon leader peptide	-1.08±0.15
trpR	b4393	regulator for *trp* operon and *aroH*; *trp* operon repressor	0.90±0.07
trpS	b3384	tryptophan tRNA synthetase	0.99±0.08
***tdc* operon**			
dsdA	b2366	D-serine dehydratase	-1.95±0.25
dsdC	b3464	DNA-binding transcriptional dual regulator	-1.90±0.12
tdcR	b3119	DNA-binding transcriptional activator	-2.89±0.33

tdcA	b3118	DNA-binding activator	-2.12±0.29
tdcB	b3117	threonine dehydratase	-1.58±0.20
tdcC	b3116	threonine/serine transporter	-1.41±0.19
tdcD	b3115	propionate kinase	-1.41±0.18
tdcE	b3114	2-ketobutyrate formate-lyase/pyruvate formate-lyase 4, inactive	-3.26±0.30
tdcF	b3113	predicted enamine/imine deaminase	-1.02±0.15
tdcG	b3112	L-serine deaminase III	0.97±0.14
***sfm* operon**			
sfmA	b0530	predicted fimbrial-like adhesin protein	-1.88±0.27
sfmC	b0531	predicted pilin chaperone, periplasmic	-2.33±0.30
sfmD	b0532	putative outer membrane protein, export function	-1.76±0.19
sfmF	b0534	putative fimbrial-like adhesin protein	-1.81±0.26
sfmH	b0533	predicted fimbrial-like adhesin protein	-2.37±0.31
fimZ	b0535	transcriptional regulator	-2.18±0.30

[a] **Changes in expression of genes were represented by mean expression ratios ($P<0.05$)**