

Supplementary Table S1 Upregulated genes in heterologous EPSP synthase-expressing strain.

Locus	Locus_Tag	Product Name	Fold ^a
Transcription			
<i>ybcM</i>	b0546	predicted DNA-binding transcriptional regulator	3.22 ± 0.32
<i>yahB</i>	b0316	predicted transcriptional regulator, LysR-type	2.92 ± 0.29
Replication, recombination and repair			
<i>yagL</i>	b0278	DNA-binding protein	2.45 ± 0.24
Cell motility			
<i>fimA</i>	b4314	major type 1 subunit fimbrin (pilin)	2.29 ± 0.14
Energy production and conversion			
<i>tdcE</i>	b3114	2-ketobutyrate formate-lyase/pyruvate formate-lyase 4, inactive	2.34 ± 0.22
<i>betB</i>	b0312	betaine aldehyde dehydrogenase	5.13 ± 0.39
Amino acid transport and metabolism			
<i>yahI</i>	b0323	predicted carbamate kinase-like protein	2.25 ± 0.08
<i>yahN</i>	b0328	predicted neutral amino acid efflux system	2.90 ± 0.22
<i>mmuM</i>	b0261	homocysteine S-methyltransferase	3.16 ± 0.17
Nucleotide transport and metabolism			
<i>Coda</i>	b0337	cytosine deaminase	2.34 ± 0.19
Inorganic ion transport and metabolism			
<i>nikD</i>	b3479	nickel ABC transporter - ATP binding subunit	2.33 ± 0.20
<i>fhuA</i>	b0150	ferrichrome / phage / antibiotic outer membrane porin FhuA	2.05 ± 0.04
<i>feoA</i>	b3408	ferrous iron transport protein A	2.48 ± 0.13
General function prediction only			
<i>ygbD</i>	b2711	flavorubredoxin reductase	2.04 ± 0.11
Function unknown			
<i>Yagp</i>	b0282	predicted transcriptional regulator LYSR-type	2.27 ± 0.05
<i>intF</i>	b0281	CP4-6 prophage; predicted phage integrase	3.48 ± 0.13
<i>ykgK</i>	b0294	MatA DNA-binding transcriptional dual regulator	2.52 ± 0.09
Not in COGs			
<i>ykgI</i>	b0303	predicted protein, hypochlorite stress response	2.68 ± 1.00
<i>yffM</i>	b2444	predicted protein	6.31 ± 0.45

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