Electronic Supplementary Material (ESI) for Molecular BioSystems.
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Supplementary Table S2 Downregulated genes in heterologous EPSP synthase-expressing strain.

Locus	Locus_Tag	Product Name	Fold [a]
Translation			
ykgM	b0296	predicted ribosomal protein	-151.27±7.33
cspF	b1558	cold shock protein	-2.33±0.25
marR	b1530	DNA-binding transcriptional repressor	-2.14±0.23
pspA	b1304	regulatory protein for the phage shock protein operon	-2.05±0.20
tdcA	b3118	DNA-binding transcriptional activator	-2.12±0.21
yagI	b0272	predicted DNA-binding transcriptional regulator	-5.58±0.64
ybdO	b0603	predicted DNA-binding transcriptional regulator LYSR-type	-2.17±0.18
ydeO	b1499	DNA-binding transcriptional dual regulator	-2.24±0.20
yhiF	b3507	predicted DNA-binding transcriptional regulator	-2.22±0.24
Transcription			
yqeI	b2847	predicted transcriptional regulator	-2.19±0.12
Signal transduction mechanisms			
evgA	b2369	transcriptional regulator	-2.06±0.09
fimZ	b0535	transcriptional regulator	-2.18±0.23
yahA	b0315	phosphodiesterase, c-di-GMP-specific	-11.00±0.89
ycgG	b1168	conserved inner membrane protein	-2.24±0.07
Replication, recombination and repair			
fimE	b4313	regulator for fimA	-2.23±0.24
pine	b1158	site-specific DNA recombinase	-3.12±0.25
pinR	b1374	predicted site-specific recombinase	-2.03±0.22
Yncl	b1458	small membrane protein	-2.27±0.16
Cell wall/membrane/envelope biogenesis			
betT	b0314	Transporter: choline:H^+ symporter	-2.47±0.21
Pbl	b2854	predicted peptidoglycan-binding enzyme	-2.27±0.17
rfaL	b3622	O-antigen ligase	-2.31±0.25
ycgH_1	b1169	conserved protein;	-2.58±0.09
ycgH_2	b1170	conserved protein;	-2.08±0.19
yeel_1	b1980	predicted protein, N-terminal fragment	-2.12±0.20
yibJ	b3595	predicted Rhs-family protein	-2.03±0.14
Cell motility			
cpxP	b3913	regulator of the Cpx response and possible chaperone involved in resistance to extracytoplasmic stress	-2.46±0.11
sfmC	b0531	predicted pilin chaperone, periplasmic	-2.33±0.22
sfmH	b0533	predicted fimbrial-like adhesin protein	-2.37±0.17
ydeR	b1503	predicted fimbrial-like adhesin protein	-2.34±0.28
ydeS	b1504	predicted fimbrial-like adhesin protein	-2.14±0.20
yehC	b2110	putative fimbrial chaperone	-2.34±0.10

yqiH	b3047	predicted periplasmic pilin chaperone	-2.13±0.18
Energy production and conversion			
yodB	b1974	predicted cytochrome	-2.07±0.17
yagT	b0286	aldehyde dehydrogenase, Fe-S subunit	-3.12±0.21
yfdE	b2371	acetyl-CoA:oxalate CoA-transferase	-2.31±0.14
Carbohydrate transport and metabolism			
agaI	b3141	predicted galactosamine-6-phosphate isomerase	-2.02±0.11
ygaR	b2655	predicted protein	-2.61±0.08
ygaR	b2656	predicted protein	-3.10±0.25
yqaC	b2657	conserved protein	-2.78±0.38
Amino acid transport and metabolism			
ygiS	b3020	predicted transporter subunit	-2.02±0.09
evgS	b2370	EvgS sensory histidine kinase	-3.55±0.42
ybdL	b0600	methionine-oxo-acid transaminase, PLP-dependent	-2.12±0.17
Inorganic ion transport and metabolism			
ydeN	b1498	putative sulfatase	-2.16±0.16
General function prediction only			
arpA	b4017	regulator of acetyl CoA synthetase	-2.11±0.19
arpB_1	b1720	predicted protein, N-ter fragment	-2.58±0.30
arpB_2	b1721	predicted protein, C-ter fragment	-2.05±0.25
ybcV	b0558	predicted protein	-2.68±0.33
ycgX	b1161	predicted protein	-2.87±0.26
yddA	b1496	predicted multidrug transporter subunits of ABC superfamily: membrane component, ATP-binding component	-2.70±0.13
ydeM	b1497	predicted anaerobic sulfatase maturation enzyme	-2.41±0.26
ydfO	b1549	Qin prophage; predicted protein	-3.84±0.29
yfdR	b2361	deoxyribonucleoside 5'-monophosphate phosphatase	-2.47±0.16
yfdV	b2372	YfdV AEC Transporter	-2.52±0.27
ygeG	b2851	predicted chaperone	-2.23±0.23
ygeH	b2852	predicted transcriptional regulator	-2.35±0.19
Function unknown			
emrY	b2367	EmrKY putative multidrug efflux transporter - membrane subunit	-2.74±0.26
ydaQ	b1346	conserved protein	-2.48±0.16
yddB	b1495	predicted porin protein	-2.15±0.10
yddK	b1471	predicted protein	-2.72±0.29
yedM	b1935	conserved protein	-2.65±0.31
yedN	b1934	predicted protein, C-ter fragment	-2.78±0.33
yedN	b1933	predicted protein, N-ter fragment	-2.90±0.30
yedS	b1966	predicted protein, C-ter fragment	-2.00±0.14
yedV	b1968	predicted sensory kinase in two-component regulatory system with YedW	-2.25±0.10
yfjZ	b2645	CP4-57 prophage; predicted antitoxin of the YpjF-	-2.07±0.27

		YfjZ toxin-antitoxin system	
ygeL	b2856	predicted protein	-2.07±0.16
yibG	b3596	conserved protein	-2.28±0.26
yjbI	b4038	conserved protein	-2.06±0.21
yjcF	b4066	conserved protein	-2.07±0.09
yjhB	b4279	YjhB MFS transporter	-2.64±0.10
yqeG	b2845	YqeG STP transporter	-2.34±0.25
Not in COGs			
ais	b2252	protein induced by aluminum	-2.07±0.16
dsrA	b1954	RNA: DsrA small regulatory RNA; riboregulator of RpoS and H-NS production	-2.02±0.22
eaeH	b0297	attaching and effacing protein homolog, pathogenesis factor	-51.66±0.93
elaD	b2269	Enzyme: deubiquitinase	-2.09±0.18
emrK	b2368	EmrKY-TolC multidrug efflux transport system - membrane fusion protein	-2.48±0.28
intS	b2349	CPS-53 (KpLE1) prophage; prophage CPS-53 integrase	-2.07±0.26
intZ	b2442	CPZ-55 prophage; predicted integrase	-2.94±0.15
kilR	b1352	Rac prophage; inhibitor of FtsZ, killing protein	-2.00±0.22
lit	b1139	Lit, cell death peptidase; phage exclusion	-2.13±0.16
pinH	b2648	predicted invertase fragment	-2.74±0.22
rzpR	b1362	predicted defective peptidase	-2.14±0.12
sfa	b0991	predicted regulator of phosphatidylethanolamine synthesis	-2.12±0.12
stfE	b1157	e14 prophage; predicted side tail fiber protein fragment	-2.17±0.11
tdcR	b3119	TdcR DNA-binding transcriptional activator	-2.89±0.23
tfaE	b1156	e14 prophage; predicted tail fiber assembly protein	-2.00±0.20
tpr	b1229	predicted protamine-like protein	-2.28±0.23
yagY	b0292	*E. coli* common pilus chaperone - cryptic	-2.15±0.10
ybcN	b0547	DLP12 prophage; DNA base-flipping protein	-2.24±0.12
yccE	b1001	predicted protein	-2.26±0.16
ycgW	b1160	inhibitor of σ^S proteolysis	-2.59±0.22
yddJ	b1470	hypothetical protein	-3.15±0.24
yddK	b1741	predicted protein	-2.00±0.11
yddL	b1472	predicted lipoprotein	-2.21±0.21
ydeQ	b1502	predicted fimbrial-like adhesin protein	-2.91±0.29
ydeW	b1567	Qin prophage; predicted protein	-2.02±0.24
ydfN	b1547	predicted side tail fibre assembly protein	-2.30±0.14
ydfP	b1553	Qin prophage; conserved protein	-2.71±0.27
ydfU	b1560	Qin prophage; predicted protein	-2.15±0.23
ydfX	b1568	Qin prophage; predicted protein	-2.44±0.22
yehD	b2111	predicted fimbrial-like adhesin protein	-2.01±0.23

yfdF	b2345	predicted protein	-2.79±0.24
yfdL	b2355	CPS-53 (KpLE1) prophage; conserved protein	-2.20±0.16
yfdI	b2352	CPS-53 (KpLE1) prophage; predicted inner membrane protein	-3.04±0.26
yfdM	b2356	CPS-53 (KpLE1) prophage; predicted methyltransferase	-2.05±0.20
yfdN	b2357	CPS-53 (KpLE1) prophage; predicted protein	-2.16±0.10
yfdO	b2358	CPS-53 (KpLE1) prophage; predicted defective phage replication protein	-2.41±0.12
yfdS	b2362	CPS-53 (KpLE1) prophage; predicted protein	-2.11±0.17
yfdX	b2375	predicted protein	-2.24±0.26
yfjI	b2625	CP4-57 prophage; predicted protein	-2.45±0.24
yfjJ	b2626	CP4-57 prophage; predicted protein	-2.62±0.16
yfjM	b2629	CP4-57 prophage; predicted protein	-2.48±0.21
yfjW	b2642	CP4-57 prophage; predicted inner membrane protein	-2.65±0.22
ygaQ	b2654	predicted protein	-3.28±0.26
ygeF	b2850	predicted protein	-2.36±0.21
ygeK	b2855	predicted DNA-binding transcriptional regulator	-2.47±0.24
ygeL	b2853	predicted protein	-3.00±0.25
ygeM	b2857	predicted protein	-3.40±0.30
ygeN	b2858	predicted protein	-2.99±0.15
yhaB	b3120	predicted protein	-2.08±0.30
yhaC	b3121	predicted protein	-2.59±0.23
yhiK	b3489	predicted protein	-2.41±0.25
yhiL	b3490	predicted protein	-2.28±0.13
yjbL	b4047	predicted protein	-2.44±0.20
yjbM	b4048	predicted protein	-2.23±0.10
yjhA	b4311	Transporter: N-acetylneuraminic acid outer membrane channel	-2.18±0.23
ykgH	b0310	predicted inner membrane protein	-3.75±0.30
ykgL	b0295	predicted protein	-1017.36±1.20
ykiB	b0370	Phantom Gene	-2.26±0.11
ylcE	b0563	DLP12 prophage; predicted protein	-2.00±0.14
ymdE	b1028	predicted protein	-2.12±0.17
ymfD	b1137	e14 prophage; predicted SAM-dependent methyltransferase	-2.02±0.19
ymfE	b1138	e14 prophage; predicted inner membrane protein	-2.00±0.19
ymfJ	b1144	e14 prophage; predicted protein	-2.07±0.16
ymfT	b1146	e14 prophage; predicted DNA-binding transcriptional regulator	-2.04±0.27
yncH	b1455	hypothetical protein	-3.59±0.23
yneL	b1506	predicted transcriptional regulator	-2.47±0.27
yneN	b1500	two-component system connector protein	-3.05±0.29
ynfN	b1551	Qin prophage; predicted protein	-2.72±0.26

ypjB	b2649	predicted protein	-3.04±0.19
ypjC	b2650	predicted protein	-3.23±0.35
yqaD	b2658	conserved protein	-3.11±0.21
yqeK	b2849	predicted protein	-3.36±0.26

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