

**Table S1.** Microarray analysis of genes differentially transcribed on stool-recovered strain (125RR) compared to wild type strain (125/99).

Gene group/gene*	Known or predicted function	Log <sub>2</sub> FC	p value
<i>Membrane/Transport</i>			
<i>Slp</i>	Outer membrane lipoprotein induced after carbon starvation	1.05	0.022
<i>Metal binding</i>			
<i>zinT</i>	binds divalent metal ions including cadmium, zinc, and nickel	2.24	0.007
<i>fepA</i>	outer membrane porin ferric enterobactin and receptor for colicin B-D	0.80	0.024
<i>Fiu</i>	putative outer membrane receptor for iron complexed with catecholate siderophore receptor	1.06	0.014
<i>cusF</i>	periplasmic binding protein and metallo chaperone. Mediates resistance to copper and silver	1.19	0.067
<i>znuA</i>	periplasmic binding protein. High-affinity zinc uptake system	1.71	0.006
<i>yciF</i>	predicted rubrerythrin/ferritin-like metal-binding protein	0.62	0.063
<i>narK</i>	nitrate:nitrite antiporter NarK	-0.66	0.062
<i>Peptides</i>			
<i>dppB</i>	putative membrane subunit for dipeptide transport system permease protein	-0.62	0.064
<i>Vitamins</i>			
<i>btuC</i>	vitamin B12-transporter permease	-0.64	0.048
<i>chuA</i>	Outer membrane heme/hemoglobin receptor	0.81	0.060
<i>Phosphonate metabolism</i>			
<i>phnP</i>	Phosphoribosyl 1.2-cyclic phosphate phosphodiesterase	0.64	0.063
<i>Amino acid biosynthesis</i>			
<i>asnB</i>	Asparagine synthetase B	-0.71	0.035
<i>pheL</i>	<i>pheA</i> gene leader peptide; Amino acid biosynthesis: Phenylalanine	-0.81	0.022
<i>pheL</i>	leader peptide of chorismate mutase-P-prephenate dehydratase	-0.61	0.065
<i>ilvL</i>	<i>ilvGEDA</i> operon leader peptide; Amino acid biosynthesis: Isoleucine, Valine	-0.93	0.009
<i>Protein metabolism</i>			
<i>c0651</i>	Hypothetical protein <i>ycbY</i> precursor. Methyl transferase activity	0.63	0.054
<i>ykgO</i>	Putative 50S ribosomal protein L36	2.25	0.023
<i>Virulence</i>			
<i>pliG</i>	inhibitor of g-type lysozyme	0.84	0.036
<i>ECs0621/Z0722</i>	Protein HokE. Toxin-antitoxin system	-0.61	0.063
<i>ECs1812/Z6024</i>	unknown protein encoded by cryptic prophage CP-933P	1.33	0.040
<i>espN</i>	Secreted effector protein, cytotoxic necrotizing factor type 2	-0.71	0.043

<i>espX7</i>	Secreted effector protein	-0.66	0.051
<i>ECs1569</i>	Gene immediately downstream of <i>espK</i> effector	-0.95	0.034
<i>espB</i>	Secreted protein <i>EspB</i>	0.94	0.062

---

DNA integration - transposition

<i>intN</i>	partial integrase for prophage CP-933N	-0.88	0.020
<i>xisN</i>	putative excisionase for prophage CP-933N	-0.92	0.030
<i>ECs1527</i>	Hypothetical protein. Putative transposase	-0.74	0.056
<i>ECs1540/Z1356</i>	DNase	-0.86	0.017
<i>ECs1565/Z1826</i>	IS2 transposase	-0.95	0.006
<i>insD</i>	Qin prophage; predicted transposase	-0.93	0.016
<i>insC-1/yaiX</i>	IS2 element protein <i>InsA</i>	-0.91	0.013
<i>c3612</i>	Transposase <i>insC</i> for insertion element IS2A/D/F/H/I/K	-0.69	0.036

---

sRNAs

<i>mcaS-isrA</i>	motility and biofilm regulator	-0.66	0.048
<i>ryhB</i>	iron homeostasis; reduces iron consumption under low-iron conditions	-0.83	0.017
<i>rprA</i>	required for wild-type production of <i>RpoS</i> in response to osmotic shock	-1.03	0.003
<i>arcZ</i>	positive antisense regulator of <i>rpoS</i>	-1.17	0.001
<i>dsrA</i>	riboregulator of <i>RpoS</i> and <i>H-NS</i> production. activates production of <i>RpoS</i>	-0.63	0.055
<i>rybB</i>	antisense regulator of <i>ompC</i> and <i>ompW</i> mRNA instability	-0.77	0.022
<i>omrA</i>	regulates the protein composition of the outer membrane	-0.66	0.045
<i>sibA</i>	antisense regulator of toxic <i>lbsA</i> protein	-1.08	0.005
<i>rydB</i>	regulator of <i>RpoS</i>	-0.85	0.012
<i>micF</i>	negatively regulates translation of the <i>OmpF</i> porin and the stability of <i>OmpF</i> mRNA	-0.88	0.010
<i>omrB</i>	Down regulates OM proteins and curli; positively regulated by <i>OmpR/EnvZ</i>	-1.86	<0.001
<i>spf</i>	Spot 42 small regulatory RNA	-0.83	0.029
<i>sibD</i>	antisense regulator of toxic <i>lbsD</i> protein	-1.40	<0.001
<i>cyaR</i>	promotes degradation of the <i>ompX</i>	-1.52	<0.001
<i>abrB</i>	transport protein; regulator of <i>aidB</i> expression	-0.71	0.035

---

Bacteriophage/prophage related

<i>ECs1504/Z1768</i>	unknown protein encoded by prophage CP-933N	-1.08	0.008
<i>ECs1508/Z1772</i>	Transcriptional regulator	-1.27	0.003
<i>ECs1511/Z1775</i>	unknown protein encoded by prophage CP-933N	-0.75	0.033
<i>ECs1512/Z1776</i>	unknown protein encoded by prophage CP-933N	-0.66	0.061
<i>ECs1515/Z1779</i>	unknown protein encoded by prophage CP-933N	-0.73	0.041
<i>ECs1516/Z1780</i>	unknown protein encoded by prophage CP-933N	-0.77	0.029
<i>ECs1518/Z1781</i>	unknown protein encoded by prophage CP-933N	-0.72	0.029
<i>ECs1528</i>	unknown protein encoded by prophage CP-933N	-0.95	0.017
<i>ECs1535</i>	Phage murein endopeptidase; host cell lysis	-0.85	0.017
<i>ECs1541/Z1357</i>	Phage terminase small subunit	-0.69	0.058

<i>ECs1543/Z1360</i>	<i>major head protein/prohead proteinase</i>	-0.82	0.036
<i>ECs1557/Z1818</i>	<i>Antirepressor protein</i>	-0.79	0.034
<i>Z1816</i>	<i>unknown protein encoded by prophage CP-933N</i>	-1.02	0.057
<i>Z1821</i>	<i>unknown protein encoded by prophage CP-933N</i>	-1.15	0.009
<i>ECs5417/Z3334</i>	<i>unknown protein encoded within prophage CP-933V</i>	-1.07	0.005
<i>yfdH</i>	<i>Prophage bactoprenol glucosyltransferase</i>	0.60	0.070
<i>ECs2243/Z1811</i>	<i>Major tail subunit Bacteriophage</i>	-0.88	0.036
<i>ycaQ</i>	<i>Probable phage tail protein</i>	0.67	0.058

---

*Hypothetical*

<i>ECs1400</i>	<i>Hypothetical protein</i>	-0.73	0.060
<i>ECs1517</i>	<i>Hypothetical protein</i>	-0.80	0.018
<i>ECs1529</i>	<i>Hypothetical protein</i>	-0.87	0.041
<i>ECs1537</i>	<i>Hypothetical protein</i>	-0.85	0.020
<i>Ecs1538</i>	<i>Hypothetical protein</i>	-1.21	0.002
<i>ECs1539</i>	<i>Hypothetical protein</i>	-1.02	0.007
<i>ECs2253</i>	<i>Hypothetical protein</i>	-0.70	0.035
<i>ECs2270</i>	<i>Hypothetical protein</i>	-0.72	0.041
<i>c0670</i>	<i>Hypothetical protein</i>	0.82	0.030
<i>c0869</i>	<i>Hypothetical protein</i>	-0.75	0.040
<i>c1020</i>	<i>Hypothetical protein</i>	-0.60	0.065
<i>c1036</i>	<i>Hypothetical protein</i>	-0.68	0.055
<i>c1089</i>	<i>Hypothetical protein</i>	-0.73	0.041
<i>c1111</i>	<i>Hypothetical protein</i>	-1.17	0.001
<i>c3104</i>	<i>Hypothetical protein</i>	-1.23	0.048
<i>c3194</i>	<i>Hypothetical protein</i>	0.77	0.031
<i>c4363</i>	<i>Hypothetical protein</i>	-0.67	0.044
<i>c4376</i>	<i>Hypothetical protein</i>	-0.78	0.041
<i>c3644</i>	<i>Hypothetical protein</i>	-0.62	0.054
<i>c3902</i>	<i>Hypothetical protein</i>	-0.59	0.070
<i>Z1038</i>	<i>Hypothetical protein</i>	-1.37	<0.001
<i>Z1184</i>	<i>Hypothetical protein</i>	-0.64	0.059
<i>Z3066</i>	<i>Hypothetical protein</i>	2.07	0.025
<i>Z4320</i>	<i>Hypothetical protein</i>	-0.86	0.029
<i>ECs5328</i>	<i>Hypothetical protein</i>	0.90	0.023
<i>Ecs5328</i>	<i>Hypothetical protein</i>	0.84	0.023

---

\* Gene denomination is the following: prefix *Z* indicates genes belonging to EDL933 strain, prefix *ECs* to Sakai strain, prefix *b* to MG1655 and prefix *c* to CFT073.