

Table S1. Primers used in this study

Name	Oligonucleotide sequence (5' to 3') <sup>a</sup>	Purpose	Reference
hdeA_UFP1	aaattgattcgtgacggctctttcactttatagtga ggatattacgatgGTGTAGGCTGGAG CTGCTTC	Deletion of the <i>hdeAB</i> genes	(1)
hdeB_DRP2	gagcagcaagatggctcaactgccactcctttta cttgtaacctcattaATGGGAATTAGCC ATGGTCC	Deletion of the <i>hdeAB</i> genes	(1)
hdeAB_UF	acagcaaccgacgataaac	Screen of the <i>hdeAB</i> deletion mutant	(1)
hdeAB_DR	agatggctcaactgccact	Screen of the <i>hdeAB</i> deletion mutant	(1)
pBBR1MCS-F	gttttcccagtcacgacgtt	Specific to plasmid pBBR1MCS-5, upstream of the MCS site	(1)
pBBR1MCS-R	ggctcgtatgtgtgtggaa	Specific to plasmid pBBR1MCS-5, downstream of the MCS site	(1)
rcsB_FKpnI	gat <b>cggtacc</b> cgctattatgcgctctttg	Cloning the <i>rcsB</i> gene	This study
rcsB_RHind3	gat <b>caagcttt</b> tatatgccgagagggtcagg	Cloning the <i>rcsB</i> gene	This study
rpoS-F1	gagggcaaagtatcgaaac	Sequencing the <i>rpoS</i> gene of curli variants	This study
rpoS-F2	gccggatgatcagagtaac	Sequencing the <i>rpoS</i> gene of curli variants	This study
rpoS-R1	ttgagtgcagaagagcagga	Sequencing the <i>rpoS</i> gene of curli variants	This study
rpoS-R2	ggcttatccagttgctctgc	Sequencing the <i>rpoS</i> gene of curli variants	This study
hns-F1	gcagcgcgatgacaacacctat	Sequencing the <i>hns</i> gene of curli variants	This study
hns-F2	cctggctattgcacaactga	Sequencing the <i>hns</i> gene of curli variants	This study
hns-R1	agcctggcttgaagaagaga	Sequencing the <i>hns</i> gene of curli variants	This study
hns-R2	cgagggatttaccttgctca	Sequencing the <i>hns</i> gene of curli variants	This study
rcsB-UF	gtgaaacgctggaacatctg	Sequencing the <i>rcsB</i> gene of curli variants	This study
rcsB-DR	tatatgccgagagggtcagg	Sequencing the <i>rcsB</i> gene of curli variants	This study
rcsB-F	tctggatatcgaaggatcg	Sequencing the <i>rcsB</i> gene of curli variants	This study
rcsB-R	aacagcgcgagaacttcaact	Sequencing the <i>rcsB</i> gene of curli variants	This study

<sup>a</sup>Nucleotides in upper cases represent the template plasmid pKD4 specific sequence; the first 50 nucleotides in a gene knockout primer are either upstream (UP) or downstream (DR) of the deleting gene; nucleotides in lower cases and bold are the endonuclease restriction sites incorporated in the primers to facilitate the cloning.

Table S2. Up-regulated genes in C<sup>+</sup> variant of *E. coli* O157:H7 strain RM6607

ID	Gene	Product	COG <sup>a</sup>	Fold Change <sup>b</sup>
Z2001	<i>narG</i>	Nitrate reductase 1, alpha subunit	COG5013C	2.0
Z2275	Z2275	Putative aldehyde dehydrogenase	COG1012C	5.4
Z2615	<i>fumA</i>	Fumarase A = fumarate hydratase Class I; aerobic isozyme	COG1951C	3.2
Z2778	Z2778	Putative aldehyde dehydrogenase	COG1012C	5.6
Z3713	<i>cchA</i>	Detox protein	COG4577QC	3.0
Z5008	<i>aldB</i>	Aldehyde dehydrogenase B (lactaldehyde dehydrogenase)	COG1012C	2.0
Z5435	<i>fdoH</i>	Formate dehydrogenase-O, iron-sulfur subunit	COG0437C	2.1
Z5724	<i>fumB</i>	Fumarase B= fumarate hydratase class I; anaerobic isozyme	COG1951C	2.4
Z1936	<i>minE</i>	Cell division topological specificity factor, reverses MinC inhibition of ftsZ ring formation	COG0851D	2.3
Z0671	<i>ylbB</i>	Putative hydantoin utilization protein	COG0624E	2.9
Z0802	<i>gltL</i>	ATP-binding protein of glutamate/aspartate transport system	COG1126E	2.4
Z0803	<i>gltK</i>	Glutamate/aspartate transport system permease	COG0765E	3.0
Z0804	<i>gltJ</i>	Glutamate/aspartate transport system permease	COG0765E	2.5
Z0805	<i>ybeJ</i>	Putative periplasmic binding transport protein	COG0834ET	3.3
Z1033	<i>glnH</i>	Periplasmic glutamine-binding protein; permease	COG0834ET	2.3
Z1952	<i>dada</i>	D-amino acid dehydrogenase subunit	COG0665E	2.1
Z2022	<i>oppD</i>	Homolog of Salmonella ATP-binding protein of oligopeptide ABC transport system	COG0444EP	2.2
Z2223	Z2223	Putative hemin-binding lipoprotein	COG0747E	3.8
Z2224	Z2224	Putative transport system permease protein	COG0601EP	2.4
Z2276	Z2276	Putative transport system permease protein	COG1177E	6.7
Z2277	Z2277	Putative transport system permease protein	COG1176E	3.8
Z2278	Z2278	Putative ATP-binding component of a transport system	COG3842E	5.5
Z2279	Z2279	Putative transport protein	COG0687E	5.7
Z2776	<i>ydjS</i>	Succinylglutamate desuccinylase	COG2988E	4.5
Z2777	Z2777	Succinylarginine dihydrolase	COG3724E	6.0
Z2779	Z2779	Arginine succinyltransferase	COG3138E	5.8
Z2780	<i>cstC</i>	Acetylornithine delta-aminotransferase	COG4992E	4.9
Z3010	<i>fliY</i>	Putative periplasmic binding transport protein	COG0834ET	6.4
Z3568	<i>hisP</i>	Histidine/lysine/arginine/ornithine transporter subunit	COG4598E	4.2
Z3569	<i>hisM</i>	Histidine transport, membrane protein M	COG4160E	2.1
Z3570	<i>hisQ</i>	Histidine transport system permease protein	COG4215E	2.7
Z3571	<i>hisJ</i>	Histidine-binding periplasmic protein of high-affinity histidine transport system	COG0834ET	2.8
Z3572	<i>argT</i>	Lysine-, arginine-, ornithine-binding periplasmic protein	COG0834ET	3.9
Z3717	Z3717	Hypothetical protein	COG4917E	2.6
Z4241	<i>gcvH</i>	Glycine cleavage system protein H	COG0509E	2.2
Z4242	<i>gcvT</i>	Glycine cleavage system aminomethyltransferase T	COG0404E	2.2
Z4961	<i>dppA</i>	Dipeptide transport protein	COG0747E	2.4

Z5744	<i>aspA</i>	Aspartate ammonia-lyase	COG1027E	5.3
Z0801	<i>ybeK</i>	Putative tRNA synthetase	COG1957F	3.0
<b>Z3196</b>	<i>wbdQ</i>	GDP-mannose mannosylhydrolase	COG1051F	2.1
Z0826	<i>nagE</i>	PTS system, N-acetylglucosamine-specific enzyme IIABC	COG1263G	2.5
Z1109	<i>aqpZ</i>	Transmembrane water channel	COG0580G	2.6
Z1314	<i>mgsA</i>	Methylglyoxal synthase	COG1803G	2.4
Z2188	<i>yneB</i>	Aldolase	COG1830G	2.6
Z2189	<i>Z2189</i>	Putative LACI-type transcriptional regulator	COG1879G	2.7
Z2192	<i>Z2192</i>	Putative ATP-binding component of a transport system	COG1129G	2.5
Z2194	<i>ydeV</i>	Autoinducer-2 (AI-2) kinase	COG1070G	2.9
Z2463	<i>ycjV</i>	Putative ATP-binding component of a transport system	COG3839G	2.1
<b>Z3194</b>	<i>manB</i>	Phosphomannomutase	COG1109G	2.0
Z3431	<i>yeiQ</i>	Putative oxidoreductase	COG0246G	3.5
Z4819	<i>ugpE</i>	Glycerol-3-phosphate transporter membrane protein	COG0395G	2.4
Z4820	<i>ugpA</i>	Glycerol-3-phosphate transporter permease	COG1175G	3.1
Z4822	<i>ugpB</i>	Glycerol-3-phosphate transporter periplasmic binding protein	COG1653G	3.2
Z4991	<i>xylF</i>	D-xylose transporter subunit XylF	COG4213G	2.0
Z5252	<i>rbsB</i>	D-ribose transporter subunit RbsB	COG1879G	2.3
Z5409	<i>yihM</i>	Hypothetical protein	COG1082G	2.6
<b>Z5691</b>	<i>Z5691</i>	Putative ATP-binding protein of ribose ABC transport system	COG1129G	2.1
Z5838	<i>ytfQ</i>	Putative LACI-type transcriptional regulator	COG1879G	2.7
Z5839	<i>Z5839</i>	Putative ATP-binding component of ABC transporter	COG1129G	2.2
Z0278	<i>yafH</i> ( <i>fadE</i> )	Putative acyl-CoA dehydrogenase, functions in fatty acid oxidation	COG1960I	5.7
Z2624	<i>hdhA</i>	NAD-dependent 7alpha-hydroxysteroid dehydrogenase, dehydroxylation of bile acids	COG1028IQR	2.0
Z2848	<i>fadD</i>	Acyl-CoA synthetase, long-chain-fatty-acid--CoA ligase	COG0318IQ	5.4
Z3604	<i>Z3604</i>	Multifunctional fatty acid oxidation complex subunit alpha	COG1250I	3.6
Z3605	<i>Z3605</i>	3-ketoacyl-CoA thiolase	COG0183I	3.1
Z3608	<i>fadL</i>	Long-chain fatty acid outer membrane transporter	COG2067I	4.4
Z3691	<i>ucpA</i>	Short chain dehydrogenase	COG1028IQR	4.3
Z5366	<i>fadA</i>	3-ketoacyl-CoA thiolase	COG0183I	4.2
Z5367	<i>fadB</i>	Multifunctional fatty acid oxidation complex subunit alpha	COG1250I	5.9
Z5668	<i>acs</i>	Acetyl-CoA synthetase	COG0365I	5.0
<b>Z0463<sup>c</sup></b>	<i>Z0463</i>	Putative response regulator; hexosephosphate transport	COG2197TK	2.5
Z1117	<i>cspD</i>	Cold shock protein	COG1278K	3.0
<b>Z1531<sup>c</sup></b>	<i>Z1531</i>	Putative regulator; Not classified	COG3710K	2.8
Z1673	<i>csgD</i>	Putative 2-component transcriptional regulator for 2nd curli operon	COG2197TK	13.4
Z2269	<i>Z2269</i>	DNA-binding transcriptional regulator	COG1802K	2.4
Z2299	<i>Z2299</i>	Putative transcriptional regulator LYSR-type	COG0583K	2.0
Z2479	<i>pspC</i>	Phage shock protein: activates the <i>psp</i> operon in response to phage infection, exposure to ethanol or	COG1983KT	2.1

		osmotic shock		
Z2868	<i>cspC</i>	Cold shock protein	COG1278K	2.7
Z3804	<i>csiE</i>	Stationary phase inducible protein CsiE	COG3711K	2.0
<b>Z4198</b>	<i>Z4198</i>	Putative regulatory protein for type III secretion apparatus	COG2207K	2.5
Z4208	<i>ygeV</i>	Putative transcriptional regulator	COG3829KT	3.6
Z5524	<i>yijC</i>	DNA-binding transcriptional repressor FabR	COG1309K	2.4
<b>Z5684<sup>c</sup></b>	<i>Z5684</i>	Putative transcriptional regulator	COG0745TK	3.1
<b>Z1871</b>	<i>Z1871</i>	Unknown protein encoded by prophage CP-933X	COG1961L	3.1
Z2253	<i>Z2253</i>	H repeat-associated protein of Rhs element	COG5433L	2.0
<b>Z0608<sup>c</sup></b>	<i>Z0608</i>	Putative outer membrane export protein	COG1538MU	2.6
Z1670	<i>csgG</i>	Curli production assembly/transport component, 2nd curli operon	COG1462M	7.9
Z1931	<i>Z1931</i>	Outer membrane protein 3b (a), protease VII	COG4571M	2.6
Z1953	<i>dadX</i>	Alanine racemase 2, catabolic	COG0787M	2.2
Z2222	<i>Z2222</i>	D-alanyl-D-alanine dipeptidase	COG2173M	2.3
Z2446	<i>Z2446</i>	Unknown function	COG0451MG	2.2
<b>Z3195</b>	<i>manC</i>	Mannose-1-P guanosyltransferase	COG0836M	2.6
<b>Z3197</b>	<i>fcI</i>	Fucose synthetase	COG0451MG	2.3
<b>Z3198</b>	<i>Z3198</i>	GDP-mannose dehydratase	COG1089M	2.2
<b>Z3199</b>	<i>wbdP</i>	Glycosyl transferase	COG0438M	2.3
<b>Z3200</b>	<i>per</i>	Perosamine synthetase	COG0399M	2.7
Z3205	<i>galF</i>	Homolog of Salmonella UTP--glucose-1-P uridyltransferase, probably a UDP-gal transferase	COG1210M	3.0
Z5227	<i>glmS</i>	D-fructose-6-phosphate amidotransferase	COG0449M	3.5
Z0291	<i>mbhA</i>	Putative motility protein	COG1360N	2.1
Z4280	<i>yggG</i>	Hypothetical protein	COG0501O	2.0
L7017	<i>katP</i>	EHEC-catalase/peroxidase	COG0376P	2.1
Z0724	<i>fepA</i>	outer membrane receptor for ferric enterobactin (enterochelin) and colicins	COG4771P	2.6
Z2477	<i>pspE</i>	Phage shock protein	COG0607P	2.2
<b>Z3392<sup>c</sup></b>	<i>Z3392</i>	Putative isomerase-decarboxylase	COG0179Q	2.2
<b>Z3393<sup>c</sup></b>	<i>Z3393</i>	Putative 1,2-dioxygenase	COG3435Q	2.4
Z2010	<i>yckK</i>	Hypothetical protein	COG1752R	2.1
<b>Z3192</b>	<i>wbdR</i>	Acetyl transferase; O-antigen biosynthesis	COG0110R	3.1
<b>Z3201</b>	<i>wzx</i>	O antigen flippase Wzx	COG2244R	3.1
Z3693	<i>murQ</i>	N-acetylmuramic acid-6-phosphate etherase	COG2103R	2.1
Z4052	<i>surE</i>	Stationary phase survival protein SurE	COG0496R	2.0
Z4216	<i>ygfJ</i>	Hypothetical protein	COG2068R	3.0
<b>Z5153<sup>c</sup></b>	<i>Z5153</i>	Hypothetical protein	COG2252R	2.3
Z5666	<i>yjcG</i>	Acetate permease	COG4147R	5.2
Z5743	<i>dcuA</i>	Anaerobic C4-dicarboxylate transporter	COG2704R	2.7
Z5827	<i>ytfJ</i>	Hypothetical protein	COG3054R	2.6
Z0503	<i>yajB</i>	Putative glycoprotein, converts holo-ACP to apo-ACP by hydrolytic cleavage of the phosphopantetheine prosthetic group from ACP	COG3124S	2.4
Z1315	<i>Z1315</i>	Hypothetical protein	COG3110S	2.6

Z2187	Z2187	Autoinducer-2 (AI-2) modifying protein LsrG	COG1359S	2.2
Z2292	<i>ycdH</i>	Unknown function	COG2841S	3.9
Z4053	<i>ygbO</i>	tRNA pseudouridine synthase D	COG0585S	2.1
Z5667	<i>yjcH</i>	Hypothetical protein	COG3162S	6.0
Z0156	<i>dksA</i>	Suppressor protein of the <i>dnaK</i>	COG1734T	2.1
Z0481	<i>yaiC</i>	Diguanylate cyclase AdrA, catalyzes the conversion of 2 GTP into c-di-GMP	COG2199T	3.2
Z0539	<i>bolA</i>	Transcriptional regulator BolA, positive transcriptional regulator of morphogenetic pathway; controlling several genes involved in stress	COG0271T	2.1
Z0740	<i>cstA</i>	Carbon starvation protein	COG1966T	3.0
Z1522	<i>phoH</i>	PhoB-dependent, ATP-binding pho regulon component; may be helicase; induced by P starvation	COG1702T	3.7
<b>Z1528<sup>c</sup></b>	Z1528	Unknown function	COG2200T	3.4
Z2219	Z2219	Hypothetical protein	COG2199T	2.1
Z2421	Z2421	Hypothetical protein	COG2199T	4.7
Z0065	Z0065	Unknown function	-	2.3
Z0301	<i>crl</i>	Transcriptional regulator of cryptic <i>csgA</i> gene for curli surface fibers	-	2.1
Z0425	<i>yahO</i>	Hypothetical protein	-	2.3
Z0573	<i>hha</i>	Haemolysin expression modulating protein, with Hns involved in transcriptional regulation of hemolysin	-	2.2
Z0574	<i>ybaJ</i>	Hypothetical protein	-	3.0
<b>Z0609<sup>c</sup></b>	Z0609	Unknown function	-	2.1
Z1010	<i>ybhQ</i>	Hypothetical protein	-	3.2
Z1062	Z1062	Biofilm formation regulatory protein BssR.	-	2.8
Z1421	<i>agp</i>	Periplasmic glucose-1-phosphatase	-	2.1
Z1671	<i>csgF</i>	Curli production assembly/transport component, 2nd curli operon	-	15.8
Z1672	<i>csgE</i>	Curli production assembly/transport component, 2nd curli operon	-	11.2
Z1675	<i>csgB</i>	Minor curlin subunit precursor, similar ro CsgA	-	97.5
Z1676	<i>csgA</i>	Curlin major subunit, coiled surface structures; cryptic	-	93.4
Z1677	<i>csgC</i>	Putative curli production protein	-	8.1
Z1678	Z1678	Hypothetical protein	-	2.5
Z1697	<i>yceP</i>	BssS; a regulator of biofilm through signal secretion;	-	2.7
Z1939	<i>ycgJ</i>	Hypothetical protein	-	2.2
Z1976	<i>ychH</i>	YchH; transcription activated by CRP (cyclic AMP receptor protein), a global transcription factor involved in regulation of metabolism in enteric bacteria	-	5.5
Z2480	<i>pspB</i>	Phage shock protein, putative inner membrane protein (acts together with PspC to induce <i>psp</i> operon during infection with phage, exposure to ethanol or osmotic shock	-	2.2
<b>Z2565</b>	Z2565	Putative chaperone protein, T3SS secreted effector EspM-like protein	-	2.8
Z2591	<i>asr</i>	Required for growth and survival under moderately acid conditions	-	2.8
Z2703	Z2703	Hypothetical protein	-	2.1
Z2755	Z2755	Hypothetical protein	-	2.8

Z2853	Z2853	Hypothetical protein	-	2.2
Z2869	Z2869	Hypothetical protein	-	3.4
Z2945	<i>flhC</i>	Regulator of flagellar biosynthesis acting on class 2 operons	-	2.8
Z2946	<i>flhD</i>	Regulator of flagellar biosynthesis, acting on class 2 operons	-	3.8
<b>Z3203</b>	<i>wzy</i>	O antigen polymerase	-	2.4
Z3642	Z3642	Hypothetical protein	-	2.4
Z3970	Z3970	Hypothetical protein	-	2.1
Z4041	<i>ygbA</i>	Hypothetical protein	-	3.8
<b>Z4326</b>	Z4326	Putative enterotoxin	-	2.1
Z4443	<i>ygjV</i>	Hypothetical protein	-	2.0
Z5525	<i>yijD</i>	Hypothetical protein	-	2.9
Z5795	<i>yjfN</i>	Hypothetical protein	-	5.9
Z5828	<i>ytfK</i>	Hypothetical protein	-	2.7
<b>Z6020</b>	<i>nleF</i>	Hypothetical protein	-	2.0
<b>Z6025</b>	<i>nleG</i>	Unknown protein encoded by cryptic prophage CP-933P	-	2.2

<sup>a</sup>The COGs was assigned based on the annotation of *E. coli* O157:H7 strain EDL933. -: not available; <sup>b</sup>The ratio of normalized hybridization intensities of the gene in C<sup>+</sup> variant RM6607R to that of in the C<sup>-</sup> variant RM6607W. All genes listed here passed the significance test as detailed in the materials and method section. Genes in bold are *E. coli* O157:H7 specific genes. <sup>c</sup>The common up-regulated genes in both C<sup>+</sup> variants.

Table S3. Up-regulated genes in C<sup>-</sup> variant of *E. coli* O157:H7 strain RM6607

ID	Gene	Product	COG <sup>a</sup>	Fold Change <sup>b</sup>
Z0044	<i>caiB</i>	l-carnitine dehydratase	COG1804C	2.2
Z1241	<i>dmsB</i>	Anaerobic dimethyl sulfoxide reductase subunit B	COG0437C	2.2
Z3067	<i>yodB</i>	Putative cytochrome	COG3038C	14.0
Z3747	<i>hyfG</i>	Hydrogenase 4 subunit	COG3261C	2.5
Z4370	<i>Z4370</i>	Hypothetical protein	COG1032C	2.1
Z0099	<i>ftsW</i>	Cell division; membrane protein involved in shape determination	COG0772D	2.5
Z0037	<i>carA</i>	Carbamoyl-phosphate synthetase, glutamine (small) subunit	COG0505EF	3.3
Z0038	<i>carB</i>	Carbamoyl-phosphate synthase large subunit	COG0458EF	3.6
Z0715	<i>pheP</i>	Phenylalanine-specific transport system	COG1113E	2.4
Z0752	<i>ybdR</i>	Putative oxidoreductase	COG1063ER	5.9
Z1090	<i>artJ</i>	Arginine 3rd transport system periplasmic binding protein	COG0834ET	4.3
Z2216	<i>gadC</i>	Acid sensitivity protein, putative transporter	COG0531E	99.2
Z2793	<i>gdhA</i>	NADP-specific glutamate dehydrogenase	COG0334E	2.5
Z3176	<i>yeeF</i>	Putative amino acid/amine transport protein	COG0531E	3.1
Z3182	<i>hisD</i>	L-histidinol:NAD <sup>+</sup> oxidoreductase; L-histidinol:NAD <sup>+</sup> oxidoreductase	COG0141E	2.2
Z3401	<i>Z3401</i>	Putative oxidoreductase	COG0493ER	3.2
Z4156	<i>lysA</i>	Diaminopimelate decarboxylase	COG0019E	3.9
Z4442	<i>ygjU</i>	Serine/threonine transporter SstT	COG3633E	2.9
Z4930	<i>gadA</i>	Glutamate decarboxylase isozyme	COG0076E	100.6
Z5516	<i>argC</i>	N-acetyl-gamma-glutamyl-phosphate reductase	COG0002E	5.2
Z5517	<i>argB</i>	Acetylglutamate kinase	COG0548E	2.4
Z3761	<i>upp</i>	Uracil phosphoribosyltransferase	COG0035F	6.4
Z3772	<i>guaB</i>	Inositol-5-monophosphate dehydrogenase	COG0516F	2.9
Z4299	<i>yggV</i>	Putative deoxyribonucleotide triphosphate pyrophosphatase	COG0127F	2.1
Z3982	<i>Z3982</i>	Putative transport protein	COG2814G	2.5
Z4932	<i>treF</i>	Trehalase	COG1626G	2.6
Z0075	<i>yabJ</i>	Putative ATP-binding component of a transport system	COG3840H	2.2
Z0526	<i>yajK</i>	Putative oxidoreductase	COG0301H	2.2
Z3472	<i>yojL</i>	Thiamine biosynthesis lipoprotein ApbE	COG1477H	2.2
Z4300	<i>yggW</i>	Coproporphyrinogen III oxidase	COG0635H	2.3
Z3586	<i>fabB</i>	3-oxoacyl-(acyl carrier protein) synthase I	COG0304IQ	2.9
Z5794	<i>aidB</i>	Isovaleryl CoA dehydrogenase	COG1960I	3.1
Z1017	<i>rhlE</i>	Putative ATP-dependent RNA helicase	COG0513LKJ	4.5
Z1061	<i>yliG</i>	Orf, hypothetical protein	COG0621J	2.4
Z4754	<i>yrfH</i>	Ribosome-associated heat shock protein Hsp15	COG1188J	2.3
Z5809	<i>rpsF</i>	30S ribosomal protein S6	COG0360J	2.4
Z0067	<i>Z0067</i>	Putative enzyme; Unknown function	COG0553KL	2.9
Z0376	<i>ykgA</i>	Putative AraC-like transcriptional regulator	COG4977K	3.3
<b>Z1503</b>	<i>Z1503</i>	Unknown protein encoded by bacteriophage BP-933W	COG3561K	3.5
Z3692	<i>yfeT</i>	Hypothetical protein	COG1737K	65.9
Z4377	<i>ygiX</i>	DNA-binding transcriptional regulator QseB	COG0745TK	2.6

Z4762	<i>yhgF</i>	Hypothetical protein	COG2183K	2.6
<b>Z0307</b>	<i>intH</i>	Putative integrase for prophage CP-933H	COG4974L	2.9
Z2536	<i>topA</i>	DNA topoisomerase type I, omega protein	COG0550L	2.4
Z4043	<i>mutS</i>	DNA mismatch repair protein	COG0249L	2.1
Z4115	<i>exo</i>	Exonuclease IX	COG0258L	2.6
Z5059	<i>mutM</i>	Formamidopyrimidine-DNA glycosylase	COG0266L	3.6
Z5191	<i>recF</i>	Recombination protein F	COG1195L	3.1
Z3213	<i>cpsB</i>	Mannose-1-phosphate guanyltransferase	COG0836M	2.2
Z3217	<i>gmd</i>	GDP-D-mannose dehydratase	COG1089M	3.1
Z3397	<i>yohK</i>	Putative serotonin transporter	COG1346M	2.1
Z3643	<i>ddg</i>	Lipid A biosynthesis palmitoleoyl acyltransferase	COG1560M	3.5
Z4261	<i>yggB</i>	Mechanosensitive channel MscS	COG0668M	2.8
Z3030	<i>fliH</i>	Flagellar biosynthesis; export of flagellar proteins?	COG1317NU	2.1
Z3033	<i>fliK</i>	Flagellar hook-length control protein	COG3144N	2.4
Z0014	<i>dnaK</i>	Chaperone Hsp70; DNA biosynthesis; heat shock proteins	COG0443O	3.0
Z0015	<i>dnaJ</i>	Chaperone with DnaK; heat shock protein	COG0484O	3.0
Z0545	<i>lon</i>	DNA-binding, ATP-dependent protease La; heat shock K-protein	COG0466O	2.2
Z0590	<i>htpG</i>	Chaperone Hsp90, heat shock protein C 62.5	COG0326O	2.7
Z0645	<i>ybbN</i>	Putative thioredoxin-like protein	COG3118O	2.4
Z1418	<i>cbpA</i>	Curved DNA-binding protein; functions closely related to DnaJ	COG0484O	2.8
Z3886	<i>clpB</i>	Protein disaggregation chaperone	COG0542O	3.5
Z3907	<i>grpE</i>	Heat shock protein GrpE	COG0576O	2.0
Z4344	<i>hybG</i>	Hydrogenase 2 accessory protein HypG	COG0298O	2.8
Z4844	<i>yhhP</i>	Cell developmental protein SirA	COG0425O	2.2
Z5478	<i>hslU</i>	ATP-dependent protease ATP-binding subunit	COG1220O	2.2
Z5479	<i>hslV</i>	ATP-dependent protease peptidase subunit	COG5405O	2.6
Z5747	<i>groES</i>	Co-chaperonin GroES	COG0234O	3.7
Z5748	<i>groEL</i>	Chaperonin GroEL	COG0459O	3.5
Z5990	<i>sms</i>	DNA repair protein RadA	COG1066O	2.5
Z0843	<i>kdpC</i>	High-affinity potassium transport system	COG2156P	2.4
<b>Z1921<sup>c</sup></b>	<i>Z1921</i>	Unknown protein encoded by prophage CP-933X	COG3546P	8.2
Z2761	<i>katE</i>	Catalase; hydroperoxidase HPII(III)	COG0753P	2.3
Z3657	<i>Z3657</i>	Putative transport system permease	COG1914P	2.3
Z4150	<i>Z4150</i>	Putative transport protein	COG0861P	2.5
Z4931	<i>yhjA</i>	Putative cytochrome C peroxidase	COG1858P	3.2
Z5217	<i>pstA</i>	Phosphate transporter permease subunit	COG0581P	4.2
Z5219	<i>pstS</i>	Phosphate transporter subunit	COG0226P	3.4
Z0447	<i>mhpC</i>	2-hydroxy-6-ketono-2,4-dienedioic acid hydrolase	COG0596R	2.9
Z1044	<i>Z1044</i>	Hypothetical protein	COG0561R	2.2
Z1416	<i>torD</i>	Part of trimethylamine-N-oxide oxidoreductase	COG3381R	3.7
<b>Z1773<sup>c</sup></b>	<i>Z1773</i>	Unknown protein encoded by prophage CP-933N	COG5529R	2.5
<b>Z2093</b>	<i>Z2093</i>	Unknown protein encoded within prophage CP-933O	COG5529R	2.1
Z2458	<i>ycjX</i>	Putative EC 2.1 enzymes	COG3106R	3.7
Z2653	<i>ydhA</i>	Unknown function	COG3895R	3.3



Z2893	Z2893	Unknown function	COG0388R	5.4
<b>Z3092</b>	Z3092	Unknown protein encoded within prophage CP-933U	COG4397R	2.4
<b>Z3124</b>	Z3124	Unknown protein encoded within prophage CP-933U	COG5529R	2.3
Z3239	Z3239	Putative chaperonin	COG4248R	2.5
Z3396	<i>yohJ</i>	Hypothetical protein	COG1380R	3.3
Z4438	<i>ygiP</i>	Hypothetical protein	COG1451R	3.5
Z4753	<i>yrfG</i>	Putative phosphatase	COG1011R	2.2
Z4768	<i>yhgH</i>	Gluconate periplasmic binding protein	COG1040R	2.8
<b>Z1457</b>	Z1457	Putative DNA-binding protein Roi of bacteriophage BP-933W	COG3645S	2.1
Z1752	<i>yefS</i>	Hypothetical protein	COG1376S	3.5
<b>Z1771<sup>c</sup></b>	Z1771	Unknown protein encoded by prophage CP-933N	COG4197S	5.3
<b>Z1922<sup>c</sup></b>	Z1922	Unknown protein encoded by prophage CP-933X	COG3685S	9.6
<b>Z1923<sup>c</sup></b>	Z1923	Unknown protein encoded by prophage CP-933X	COG3685S	6.8
Z2456	<i>ycjF</i>	Hypothetical protein	COG3768S	2.5
Z2554	<i>yciF</i>	Putative structural proteins	COG3685S	3.0
Z2555	<i>yciE</i>	Hypothetical protein	COG3685S	2.7
Z2921	<i>yecE</i>	Hypothetical protein	COG1801S	2.2
Z3965	Z3965	Hypothetical protein	COG0401S	2.0
Z4766	<i>yhgA</i>	Hypothetical protein	COG5464S	2.1
Z4920	<i>yhiD</i>	Putative Mg(2+) transport ATPase	COG1285S	5.3
Z4923	<i>hdeD</i>	Acid-resistance membrane protein	COG3247S	70.6
Z5628	<i>yjbA</i>	Phosphate-starvation-inducible protein PsiE	COG3223S	2.8
Z2775	<i>spy</i>	Periplasmic protein related to spheroblast formation	COG3678UNTP	2.8
Z2948	<i>yecG</i>	Universal stress protein UspC	COG0589T	2.4
Z4425	<i>aer</i>	Aerotaxis sensor receptor, flavoprotein	COG0840NT	2.4
Z5458	<i>yiiO</i>	Periplasmic repressor CpxP	COG3678UNTP	2.1
Z0108	<i>secA</i>	Preprotein translocase; secretion protein	COG0653U	2.5
Z0005	Z0005	Hypothetical protein	-	2.1
Z0277	<i>ykfE</i>	Hypothetical protein	-	3.2
<b>Z0312</b>	Z0312	Partial O replication protein for prophage CP-933H	-	2.1
Z0475	Z0475	Hypothetical protein	-	6.3
<b>Z0753<sup>c</sup></b>	Z0753	Unknown function	-	2.9
<b>Z0951<sup>c</sup></b>	Z0951	Putative exonuclease encoded by prophage CP-933K	-	5.4
<b>Z0952<sup>c</sup></b>	Z0952	Putative Bet recombination protein of prophage CP-933K	-	5.4
Z1023	<i>ybiJ</i>	Hypothetical protein	-	2.5
Z1046m	Z1045	Putative pyruvate formate-lyase 2	-	2.7
<b>Z1201</b>	Z1201	Unknown function	-	3.8
<b>Z1335</b>	Z1335	Unknown protein encoded by cryptic prophage CP-933M	-	2.3
<b>Z1428<sup>c</sup></b>	Z1428	Unknown protein encoded by bacteriophage BP-933W	-	3.3
<b>Z1429<sup>c</sup></b>	Z1429	Unknown protein encoded by bacteriophage BP-933W	-	5.2
<b>Z1432</b>	Z1432	Unknown protein encoded by bacteriophage BP-933W	-	4.4
Z1435	<i>exoW</i>	Putative exonuclease of bacteriophage BP-933W	-	4.7
<b>Z1437<sup>c</sup></b>	<i>betW</i>	Putative Bet recombination protein of bacteriophage BP-933W	-	5.2
<b>Z1440<sup>c</sup></b>	<i>ssbW</i>	Putative single-stranded DNA binding protein	-	6.8

<b>Z1464</b>	<i>stx2A</i>	Shiga-like toxin II A subunit encoded by bacteriophage BP-933W	-	2.2
<b>Z1471</b>	<i>Z1471</i>	Putative antirepressor protein Ant of bacteriophage BP-933W	-	2.0
<b>Z1501<sup>c</sup></b>	<i>Z1501</i>	Unknown protein encoded by bacteriophage BP-933W	-	4.1
Z1751	<i>ycfR</i>	Hypothetical protein	-	3.3
<b>Z1772</b>	<i>Z1772</i>	Unknown protein encoded by prophage CP-933N	-	2.3
<b>Z1776</b>	<i>Z1776</i>	Unknown protein encoded by prophage CP-933N	-	2.5
<b>Z1777<sup>c</sup></b>	<i>Z1777</i>	Unknown protein encoded by prophage CP-933N	-	2.8
Z1868	<i>Z1868</i>	Putative replication protein O of prophage CP-933X	-	2.1
<b>Z1869<sup>c</sup></b>	<i>Z1869</i>	Putative replication protein P of prophage CP-933X	-	2.4
<b>Z2049</b>	<i>Z2049</i>	Unknown protein encoded by prophage CP-933O	-	2.1
<b>Z2092</b>	<i>Z2092</i>	Unknown protein encoded within prophage CP-933O	-	2.4
Z2229	<i>Z2229</i>	Biofilm-dependent modulation protein	-	12.2
Z2631	<i>Z2631</i>	<i>oriC</i> -binding nucleoid-associated protein	-	5.0
Z2632	<i>Z2632</i>	Hypothetical protein	-	2.1
Z2958	<i>Z2958</i>	Hypothetical protein	-	2.6
<b>Z3088</b>	<i>Z3088</i>	Putative tail fiber component U of prophage CP-933U	-	2.4
<b>Z3125</b>	<i>Z3125</i>	Unknown protein encoded within prophage CP-933U	-	2.2
<b>Z3349</b>	<i>Z3349</i>	Putative DNA methyltransferase encoded within prophage CP-933V	-	2.1
<b>Z3355<sup>c</sup></b>	<i>Z3355</i>	Putative DNA replication protein P of prophage CP-933V	-	2.1
<b>Z3363<sup>c</sup></b>	<i>Z3363</i>	Putative single-stranded DNA binding protein of prophage CP-933V	-	5.4
<b>Z3366<sup>c</sup></b>	<i>Z3366</i>	Putative recombination protein Bet of prophage CP-933V	-	4.5
<b>Z3367<sup>c</sup></b>	<i>Z3367</i>	Putative exonuclease of prophage CP-933V	-	4.6
<b>Z3370<sup>c</sup></b>	<i>Z3370</i>	Unknown protein encoded within prophage CP-933V	-	3.2
<b>Z3371<sup>c</sup></b>	<i>Z3371</i>	Unknown protein encoded within prophage CP-933V	-	2.9
<b>Z3372<sup>c</sup></b>	<i>Z3372</i>	Unknown protein encoded within prophage CP-933V	-	2.5
Z3516	<i>Z3516</i>	Hypothetical protein	-	2.0
Z3585	<i>Z3585</i>	Transport	-	2.3
Z3656	<i>Z3656</i>	Hypothetical protein	-	2.9
Z3722	<i>Z3722</i>	Hypothetical protein	-	7.1
Z4126	<i>Z4126</i>	Hypothetical protein	-	4.3
Z4286	<i>yqgD</i>	Hypothetical protein	-	2.8
Z4890	<i>yhiM</i>	Inner membrane protein, acid resistance protein	-	101.1
Z4921	<i>hdeB</i>	Acid-resistance protein	-	100.8
Z4922	<i>hdeA</i>	Acid-resistance protein	-	83.2
Z5694	<i>Z5694</i>	Hypothetical protein	-	4.0
<b>Z6071</b>	<i>Z6071</i>	Unknown protein encoded by cryptic prophage CP-933P	-	2.3

<sup>a</sup>The COGs was assigned based on the annotation of *E. coli* O157:H7 strain EDL933. “-” stands for COG group is not available. <sup>b</sup>The ratio of normalized hybridization intensities of the gene in C<sup>-</sup> variant RM6607W to that of in the C<sup>+</sup> variant RM6607R. All genes listed here passed the significance test as detailed in the materials and method section. Genes in bold are *E. coli* O157:H7 specific genes. <sup>c</sup>The common up-regulated genes in both C<sup>+</sup> variants.

Table S4. Up-regulated genes in C<sup>+</sup> variant of *E. coli* O157:H7 strain RM6608

ID	Gene	Product	COG <sup>a</sup>	Fold Change <sup>b</sup>
Z0072	<i>araB</i>	L-ribulokinase	COG1069C	4.1
Z0672	<i>ylbC</i>	putative malate dehydrogenase (EC 1.1.1.37)	COG2055C	2.0
Z1106	Z1106	putative enzyme	COG1018C	3.3
Z2235	<i>fdnH</i>	formate dehydrogenase-N, nitrate-inducible, iron-sulfur beta subunit	COG0437C	2.1
Z2275	Z2275	putative aldehyde dehydrogenase	COG1012C	3.1
Z2577	Z2577	putative oxidoreductase, Fe-S subunit	COG0437C	2.3
Z2702	Z2702	putative oxidoreductase, Fe-S subunit	COG0437C	2.2
Z2726	<i>ydiQ</i>	putative transport protein	COG2086C	3.3
Z3633	<i>yfdE</i>	orf; Unknown function	COG1804C	2.7
Z3828	<i>hmpA</i>	nitric oxide dioxygenase	COG1018C	3.0
Z4354	Z4354	aldo-keto reductase	COG0667C	2.0
Z4434	<i>yglL</i>	putative NADPH dehydrogenase	COG1902C	7.6
Z5435	<i>fdoH</i>	formate dehydrogenase-O, iron-sulfur subunit	COG0437C	2.3
Z0562	<i>glnK</i>	nitrogen regulatory protein P-II 2	COG0347E	2.0
Z1056	Z1056	putative transport system permease protein	COG1173EP	2.7
Z1832	<i>pepT</i>	putative peptidase T	COG2195E	2.5
Z2276	Z2276	putative transport system permease protein	COG1177E	3.0
Z2277	Z2277	putative transport system permease protein	COG1176E	2.2
Z2278	Z2278	putative ATP-binding component of a transport system	COG3842E	3.0
Z2279	Z2279	putative transport protein	COG0687E	5.3
Z2592	Z2592	orf, hypothetical protein	COG3591E	2.2
Z3637	Z3637	putative oxalyl-CoA decarboxylase	COG0028EH	2.8
Z4211	<i>ygeY</i>	peptidase	COG0624E	5.4
Z4217	Z4217	putative selenate reductase subunit YgfK	COG0493ER	2.1
Z4463	<i>yhaO</i>	putative transport system permease protein	COG0814E	3.8
Z4826	<i>livM</i>	leucine/isoleucine/valine transporter permease subunit	COG4177E	2.5
Z5744	<i>aspA</i>	aspartate ammonia-lyase	COG1027E	3.1
Z0805	<i>ybeJ</i>	putative periplasmic binding transport protein	COG0834ET	2.8
Z3010	<i>fliY</i>	putative periplasmic binding transport protein	COG0834ET	5.6
Z3571	<i>hisJ</i>	histidine-binding periplasmic protein of high-affinity histidine transport system	COG0834ET	2.5
Z3572	<i>argT</i>	lysine-, arginine-, ornithine-binding periplasmic protein	COG0834ET	3.6
Z0427	<i>prpB</i>	putative phosphonmutase 2	COG2513G	2.1
Z0826	<i>nagE</i>	PTS system, N-acetylglucosamine-specific enzyme IIABC	COG1263G	2.6
Z1109	<i>aqpZ</i>	transmembrane water channel; aquaporin Z	COG0580G	2.6
Z1314	<i>mgsA</i>	methylglyoxal synthase	COG1803G	2.5
Z1968	<i>treA</i>	trehalase, periplasmic	COG1626G	2.0
Z2191	<i>ydeY</i>	putative transport system permease protein	COG1172G	2.3
Z2590	<i>ynfM</i>	putative transport protein	COG2814G	6.3
<b>Z3394</b>	Z3394	putative transporter	COG2271G	2.1
Z3427	<i>fruB</i>	bifunctional fructose-specific PTS IIA/HPr protein	COG4668G	2.7
Z3431	<i>yeiQ</i>	putative oxidoreductase	COG0246G	4.9

Z3683	<i>crr</i>	glucose-specific PTS system component	COG2190G	2.1
Z3807	<i>hcaT</i>	putative 3-phenylpropionic acid transporter	COG2814G	2.7
Z4023	<i>ascF</i>	cellobiose/arbutin/salicin-specific PTS system components IIBC	COG1263G	2.1
Z4444	<i>uxaA</i>	altronate hydrolase	COG2721G	2.3
Z4822	<i>ugpB</i>	glycerol-3-phosphate transporter periplasmic binding protein	COG1653G	2.5
Z5417	<i>yihS</i>	hypothetical protein	COG2942G	2.1
Z5447	<i>rhaA</i>	L-rhamnose isomerase	COG4806G	3.5
Z5633	<i>malK</i>	maltose/maltodextrin transporter ATP-binding protein	COG3839G	3.6
Z5839	Z5839	putative ATP-binding component of ABC transporter	COG1129G	2.1
Z5920	<i>uxuA</i>	mannonate dehydratase	COG1312G	2.1
Z0993	<i>bioA</i>	7,8-diaminopelargonic acid synthetase	COG0161H	2.0
Z1000	<i>moaA</i>	molybdopterin biosynthesis, protein A	COG2896H	2.1
Z0278	<i>yafH</i>	putative acyl-CoA dehydrogenase (EC 1.3.99.-)	COG1960I	7.9
<b>Z1549</b>	Z1549	putative beta-ketoacyl-[acyl carrier protein] synthase	COG0304IQ	2.7
Z2848	<i>fadD</i>	acyl-CoA synthetase, long-chain-fatty-acid--CoA ligase	COG0318IQ	7.9
Z3604	Z3604	multifunctional fatty acid oxidation complex subunit alpha	COG1250I	3.4
Z3605	Z3605	3-ketoacyl-CoA thiolase	COG0183I	4.2
Z3608	<i>fadL</i>	long-chain fatty acid outer membrane transporter	COG2067I	4.3
Z3691	<i>ucpA</i>	short chain dehydrogenase	COG1028IQR	3.4
Z3813	<i>hcaB</i>	2,3-dihydroxy-2,3-dihydrophenylpropionate dehydrogenase	COG1028IQR	2.2
Z5366	<i>fadA</i>	3-ketoacyl-CoA thiolase	COG0183I	5.2
Z5367	<i>fadB</i>	multifunctional fatty acid oxidation complex subunit alpha	COG1250I	5.7
Z5668	<i>acs</i>	acetyl-CoA synthetase	COG0365I	3.6
Z1509	Z1509	orf, hypothetical protein	COG0251J	2.1
Z3890	<i>yfiA</i>	translation inhibitor protein RaiA	COG1544J	2.7
Z4657	<i>def</i>	peptide deformylase	COG0242J	2.2
Z0201	<i>yaeO</i>	orf, hypothetical protein	COG4568K	2.6
Z0426	<i>prpR</i>	regulator for prp operon	COG3829KT	2.4
<b>Z0463</b>	Z0463	putative response regulator; hexosephosphate transport	COG2197TK	3.2
Z1117	<i>cspD</i>	cold shock protein	COG1278K	2.5
<b>Z1531</b>	Z1531	putative regulator; Not classified	COG3710K	2.4
Z2479	<i>pspC</i>	phage shock protein: activates phage shock-protein expression	COG1983KT	2.7
Z2589	<i>ynfL</i>	putative transcriptional regulator LYSR-type	COG0583K	2.4
Z2874	Z2874	putative regulator	COG1414K	2.6
Z3804	<i>csiE</i>	stationary phase inducible protein CsiE	COG3711K	3.3
Z4208	<i>ygeV</i>	putative transcriptional regulator	COG3829KT	4.6
Z4435	<i>ygjM</i>	hypothetical protein	COG5499K	2.6
Z4470	<i>tdcA</i>	DNA-binding transcriptional activator TdcA	COG0583K	3.5
Z5524	<i>yijC</i>	DNA-binding transcriptional repressor FabR	COG1309K	2.3
Z5661	<i>soxS</i>	DNA-binding transcriptional regulator SoxS	COG2207K	2.9

<b>Z5684</b>	Z5684	putative transcriptional regulator	COG0745TK	4.0
Z5957	<i>yjjM</i>	hypothetical protein	COG1802K	3.5
Z0285	<i>dinJ</i>	damage-inducible protein J	COG3077L	2.9
Z1871	Z1871	unknown protein encoded by prophage CP-933X	COG1961L	3.0
Z2741	<i>himA</i>	integration host factor (IHF), alpha subunit; site specific recombination	COG0776L	2.6
Z4656	<i>smf</i>	hypothetical protein	COG0758LU	2.4
Z0272	Z0272	orf; Unknown function (Rhs Element Associated)	COG3209M	2.1
<b>Z0608</b>	Z0608	putative outer membrane export protein	COG1538MU	2.2
Z1524	<i>ycdQ</i>	orf, hypothetical protein	COG1215M	2.0
Z2222	Z2222	orf, hypothetical protein	COG2173M	2.0
Z2437	Z2437	orf, hypothetical protein	COG0668M	2.3
Z4908	<i>slp</i>	outer membrane protein induced after carbon starvation	COG3065M	2.4
Z0291	<i>mbhA</i>	putative motility protein	COG1360N	2.3
Z1292	Z1292	putative fimbrial-like protein	COG3539NU	4.2
Z3599	<i>yfcS</i>	putative fimbrial chaperone	COG3121NU	3.3
Z5913	<i>fimI</i>	fimbrial protein	COG3539NU	3.9
Z0642	<i>ybbK</i>	putative protease	COG0330O	3.0
Z4280	<i>yggG</i>	hypothetical protein	COG0501O	2.0
Z2477	<i>pspE</i>	phage shock protein	COG0607P	2.4
Z3553	<i>yfbS</i>	putative transport protein	COG0471P	2.1
Z4441	<i>ygiT</i>	putative transport protein	COG0861P	2.0
Z5825	<i>cysQ</i>	PAPS (adenosine 3'-phosphate 5'-phosphosulfate) 3'(2'),5'-bisphosphate nucleotidase	COG1218P	2.6
<b>Z3392</b>	Z3392	putative isomerase-decarboxylase	COG0179Q	2.1
<b>Z3393</b>	Z3393	putative 1,2-dioxygenase	COG3435Q	2.1
Z0157	<i>sfsA</i>	sugar fermentation stimulation protein A	COG1489R	2.7
Z0670	<i>ylbA</i>	orf, hypothetical protein	COG3257R	3.4
Z2251	Z2251	orf; Unknown function	COG1853R	2.3
Z2665	Z2665	orf, hypothetical protein	COG3313R	2.8
Z3239	Z3239	putative chaperonin	COG4248R	2.2
Z4216	<i>ygfJ</i>	hypothetical protein	COG2068R	3.3
<b>Z5153</b>	Z5153	hypothetical protein	COG2252R	2.0
Z5666	<i>yjcG</i>	acetate permease	COG4147R	2.5
Z5743	<i>dcuA</i>	anaerobic C4-dicarboxylate transporter	COG2704R	2.3
Z5827	<i>ytfJ</i>	hypothetical protein	COG3054R	2.6
<b>Z0414</b>	Z0414	orf; Unknown function	COG4405S	2.4
Z1315	Z1315	orf, hypothetical protein	COG3110S	4.3
Z2292	<i>ydcH</i>	orf; Unknown function	COG2841S	5.1
Z4462	Z4462	hypothetical protein	COG3681S	3.3
Z4655	<i>smg</i>	hypothetical protein	COG2922S	2.6
Z5667	<i>yjcH</i>	hypothetical protein	COG3162S	3.3
Z5867	<i>yjgD</i>	hypothetical protein	COG3076S	2.4
Z0156	<i>dksA</i>	dnaK suppressor protein	COG1734T	3.5
Z0481	<i>adrA</i>	diguanylate cyclase AdrA	COG2199T	5.1
Z0740	<i>cstA</i>	carbon starvation protein	COG1966T	2.8

Z0751	<i>ybdQ</i>	orf, hypothetical protein	COG0589T	3.4
Z1024	<i>ybiI</i>	orf, hypothetical protein	COG1734T	2.9
Z1058	Z1058	orf, hypothetical protein	COG2199T	2.6
Z1522	<i>phoH</i>	PhoB-dependent, ATP-binding pho regulon component	COG1702T	3.2
<b>Z1528</b>	Z1528	orf; Unknown function	COG2200T	3.2
Z2421	Z2421	orf, hypothetical protein	COG2199T	3.9
Z5158	<i>uhpB</i>	sensory histidine kinase UhpB	COG3851T	2.4
Z5953	<i>yjiY</i>	putative carbon starvation protein	COG1966T	2.6
<b>L7032</b>	<i>etpC</i>		COG3031U	2.1
Z3695	Z3695	hypothetical protein	COG1680V	2.1
Z0065	Z0065	orf; Unknown function	-	2.9
Z0425	<i>yahO</i>	orf, hypothetical protein	-	3.3
Z0480	<i>psiF</i>	induced by phosphate starvation	-	2.4
Z0574	<i>ybaJ</i>	orf, hypothetical protein	-	2.9
<b>Z0609</b>	Z0609	orf; Unknown function	-	3.2
Z0846	<i>ybfA</i>	orf, hypothetical protein	-	2.4
Z1010	<i>ybhQ</i>	orf, hypothetical protein	-	2.9
Z1062	Z1062	biofilm formation regulatory protein BssR	-	2.8
<b>Z1530</b>	Z1530	orf; Unknown function	-	2.3
Z1672	<i>csgE</i>	curli production assembly/transport component, 2nd curli operon	-	2.4
Z1675	<i>csgB</i>	minor curlin subunit precursor, similar to CsgA	-	108.2
Z1676	<i>csgA</i>	curlin major subunit, coiled surface structures	-	60.2
Z1677	<i>csgC</i>	putative curli production protein	-	5.0
Z1678	Z1678	orf, hypothetical protein	-	2.4
Z1697	<i>yceP</i>	biofilm formation regulatory protein BssS	-	3.0
<b>Z1919</b>	Z1919	unknown protein encoded by prophage CP-933X	-	2.4
Z2301	Z2301	orf, hypothetical protein	-	2.2
<b>Z2360</b>	Z2360	putative capsid protein of prophage CP-933R	-	2.4
Z2478	<i>pspD</i>	peripheral inner membrane phage-shock protein	-	2.4
Z2755	Z2755	orf, hypothetical protein	-	2.5
Z2869	Z2869	orf, hypothetical protein	-	2.1
Z3050	<i>yedA</i>	putative transmembrane subunit	-	7.4
Z3440	<i>yejG</i>	hypothetical protein	-	2.7
Z3642	Z3642	hypothetical protein	-	4.7
Z3970	Z3970	hypothetical protein	-	2.1
Z4041	<i>ygbA</i>	hypothetical protein	-	2.4
Z4215	Z4215	hypothetical protein	-	2.0
Z4894	<i>yhiO</i>	universal stress protein UspB	-	2.6
<b>Z5094</b>	Z5094	hypothetical protein	-	2.0
Z5525	<i>yijD</i>	hypothetical protein	-	2.9
Z5648	<i>yjbO</i>	phage shock protein G	-	2.0
Z5795	<i>yjfN</i>	hypothetical protein	-	7.0
Z5828	<i>ytfK</i>	hypothetical protein	-	3.4

<sup>a</sup>The COGs was assigned based on the annotation of *E. coli* O157:H7 strain EDL933. -: COG group is not available; <sup>b</sup>The ratio of normalized hybridization intensities of the gene in C<sup>+</sup> variant RM6608R to that of in the C<sup>-</sup> variant RM6608W. All genes listed here passed the significance test as detailed in the materials and method section. Genes in bold are *E. coli* O157:H7 specific genes.

Table S5. Up-regulated genes in C<sup>-</sup> variant of *E. coli* O157:H7 strain RM6608

ID	Gene	Product	COG <sup>a</sup>	Fold Change <sup>b</sup>
Z0880	<i>sucA</i>	2-oxoglutarate dehydrogenase (decarboxylase component)	COG0567C	2.2
Z0881	<i>sucB</i>	2-oxoglutarate dehydrogenase (dihydrolipoyltranssuccinase E2 component)	COG0508C	2.8
Z0882	<i>sucC</i>	succinyl-CoA synthetase, beta subunit	COG0045C	2.9
Z0883	<i>sucD</i>	succinyl-CoA synthetase, alpha subunit	COG0074C	3.3
Z2633	Z2633	orf, hypothetical protein	COG4657C	2.3
Z2715	<i>ydiJ</i>	putative oxidase	COG0277C	2.1
Z3067	<i>yodB</i>	putative cytochrome	COG3038C	6.6
Z4370	Z4370	hypothetical protein	COG1032C	2.1
Z4612	<i>yhdH</i>	putative dehydrogenase	COG0604CR	4.0
Z5230	<i>atpD</i>	F0F1 ATP synthase subunit beta	COG0055C	3.3
Z5233	<i>atpH</i>	F0F1 ATP synthase subunit delta	COG0712C	5.3
Z5234	<i>atpF</i>	F0F1 ATP synthase subunit B	COG0711C	3.1
Z5236	<i>atpB</i>	F0F1 ATP synthase subunit A	COG0356C	2.8
Z5238	<i>atpI</i>	F0F1 ATP synthase subunit I	COG3312C	2.6
Z0099	<i>ftsW</i>	cell division; membrane protein involved in shape determination	COG0772D	2.0
Z4610	<i>mreB</i>	regulator of ftsI, penicillin binding protein 3, septation function	COG1077D	3.2
Z5241	<i>gidA</i>	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA	COG0445D	2.4
Z0002	<i>thrA</i>	aspartokinase I, homoserine dehydrogenase I	COG0527E	2.2
Z0037	<i>carA</i>	carbamoyl-phosphate synthetase, glutamine (small) subunit	COG0505EF	7.3
Z0038	<i>carB</i>	carbamoyl-phosphate synthase large subunit	COG0458EF	4.9
Z0752	<i>ybdR</i>	putative oxidoreductase	COG1063ER	6.8
Z1253	<i>serC</i>	3-phosphoserine aminotransferase	COG1932HE	2.0
Z1275	<i>aspC</i>	aspartate aminotransferase	COG1448E	3.2
Z1763	<i>potC</i>	spermidine/putrescine transport system permease	COG1177E	2.6
Z1978	<i>prsA</i>	phosphoribosylpyrophosphate synthetase	COG0462FE	3.6
Z2216	<i>gadC</i>	acid sensitivity protein, putative transporter	COG0531E	92.9
Z3176	<i>yeeF</i>	putative amino acid/amine transport protein	COG0531E	7.3
Z3185	<i>hisH</i>	glutamine amidotransferase subunit of heterodimer with HisF = imidazole glycerol phosphate synthase holoenzyme	COG0118E	2.3
Z3827	<i>glyA</i>	serine hydroxymethyltransferase	COG0112E	2.8
Z4930	<i>gadA</i>	glutamate decarboxylase isozyme	COG0076E	106.0
Z5164	<i>ilvN</i>	acetolactate synthase I regulatory subunit	COG0440E	3.7
Z5165	<i>ilvB</i>	acetolactate synthase catalytic subunit	COG0028EH	2.4
Z0299	<i>gpt</i>	guanine-hypoxanthine phosphoribosyltransferase	COG0503F	2.2
Z0586	<i>apt</i>	adenine phosphoribosyltransferase	COG0503F	2.1
Z0591	<i>adk</i>	adenylate kinase activity; pleiotropic effects on glycerol-3-phosphate acyltransferase activity	COG0563F	5.7
Z3234	<i>udk</i>	uridine/cytidine kinase	COG0572F	2.8

Z3489	<i>nrdA</i>	ribonucleotide-diphosphate reductase subunit alpha	COG0209F	2.2
Z3491	<i>nrdB</i>	ribonucleotide-diphosphate reductase subunit beta	COG0208F	2.0
Z3574	<i>purF</i>	amidophosphoribosyltransferase	COG0034F	2.1
Z3761	<i>upp</i>	uracil phosphoribosyltransferase	COG0035F	4.8
Z3771	<i>guaA</i>	bifunctional GMP synthase/glutamine amidotransferase protein	COG0519F	3.4
Z3772	<i>guaB</i>	inositol-5-monophosphate dehydrogenase	COG0516F	3.6
Z3781	<i>ndk</i>	nucleoside diphosphate kinase	COG0105F	2.7
Z4144	<i>thyA</i>	thymidylate synthase	COG0207F	2.8
Z4299	<i>yggV</i>	putative deoxyribonucleotide triphosphate pyrophosphatase	COG0127F	2.2
Z5064	<i>dut</i>	deoxyuridine 5'-triphosphate nucleotidohydrolase	COG0756F	2.1
Z0837	<i>pgm</i>	phosphoglucomutase	COG0033G	2.2
Z2304	<i>gapC</i>	glyceraldehyde-3-phosphate dehydrogenase	COG0057G	2.7
Z2949	<i>otsA</i>	trehalose-6-phosphate synthase	COG0380G	2.3
Z3260	Z3260	orf, hypothetical protein	COG1830G	2.5
Z4790	<i>glgP</i>	glycogen phosphorylase	COG0058G	2.1
Z4932	<i>treF</i>	trehalase	COG1626G	2.1
Z0524	<i>ispA</i>	geranyltranstransferase (farnesyl diphosphate synthase)	COG0142H	2.6
Z0526	<i>yajK</i>	putative oxidoreductase	COG0301H	2.2
Z0775	<i>lipB</i>	lipoate biosynthesis protein B	COG0321H	2.3
Z3409	<i>folE</i>	GTP cyclohydrolase I	COG0302H	2.2
Z4287	<i>metK</i>	S-adenosylmethionine synthetase	COG0192H	2.1
Z5063	<i>dfp</i>	bifunctional phosphopantothenoylecysteine decarboxylase/phosphopantothenate synthase	COG0452H	2.5
Z1734	<i>fabF</i>	3-oxoacyl-[acyl-carrier-protein] synthase II	COG0304IQ	2.2
Z1979	<i>yehB</i>	orf, hypothetical protein	COG1947I	2.7
Z3586	<i>fabB</i>	3-oxoacyl-(acyl carrier protein) synthase I	COG0304IQ	2.1
Z4615	<i>accB</i>	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	COG0511I	2.6
Z0154	<i>pcnB</i>	poly(A) polymerase I	COG0617J	2.1
Z0180	<i>rpsB</i>	30S ribosomal subunit protein S2	COG0052J	3.8
Z0181	<i>tsf</i>	protein chain elongation factor EF-Ts	COG0264J	3.8
Z0206	<i>proS</i>	proline tRNA synthetase	COG0442J	2.0
Z0505	<i>tgt</i>	tRNA-guanine transglycosylase	COG0343J	2.1
Z1017	<i>rhIE</i>	putative ATP-dependent RNA helicase	COG0513LKJ	2.4
Z1228	<i>infA</i>	protein chain initiation factor IF-1	COG0361J	3.5
Z1257	<i>rpsA</i>	30S ribosomal subunit protein S1	COG0539J	2.2
Z1974	<i>yehF</i>	putative GTP-binding protein	COG0012J	2.5
Z1982	<i>prfA</i>	peptide chain release factor RF-1	COG0216J	3.1
Z2417	<i>dbpA</i>	ATP-dependent RNA helicase	COG0513LKJ	2.2
Z2745	<i>rplT</i>	50S ribosomal subunit protein L20, and regulator	COG0292J	2.7
Z2919	<i>aspS</i>	aspartate tRNA synthetase	COG0173J	2.3
Z3593	<i>yfcB</i>	N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase	COG2890J	2.3
Z3900	<i>rplS</i>	50S ribosomal protein L19	COG0335J	3.2
Z3901	<i>trmD</i>	tRNA (guanine-N(1)-)-methyltransferase	COG0336J	2.9



Z3902	<i>yfiA</i>	16S rRNA-processing protein	COG0806J	3.1
Z3903	<i>rpsP</i>	30S ribosomal protein S16	COG0228J	3.0
Z4418	<i>rpsU</i>	30S ribosomal protein S21	COG0828J	2.2
Z4523	<i>deaD</i>	ATP-dependent RNA helicase DeaD	COG0513LKJ	3.8
Z4529	<i>infB</i>	translation initiation factor IF-2	COG0532J	2.0
Z4547	<i>rpmA</i>	50S ribosomal protein L27	COG0211J	2.2
Z4588	<i>rpsI</i>	30S ribosomal protein S9	COG0103J	2.4
Z4589	<i>rplM</i>	50S ribosomal protein L13	COG0102J	3.0
Z4664	<i>rplQ</i>	50S ribosomal protein L17	COG0203J	4.0
Z4666	<i>rpsD</i>	30S ribosomal protein S4	COG0522J	3.9
Z4667	<i>rpsK</i>	30S ribosomal protein S11	COG0100J	3.2
Z4668	<i>rpsM</i>	30S ribosomal protein S13	COG0099J	3.2
Z4671	<i>rplO</i>	50S ribosomal protein L15	COG0200J	2.5
Z4672	<i>rpmD</i>	50S ribosomal protein L30	COG1841J	3.4
Z4673	<i>rpsE</i>	30S ribosomal protein S5	COG0098J	4.4
Z4674	<i>rplR</i>	50S ribosomal protein L18	COG0256J	3.8
Z4675	<i>rplF</i>	50S ribosomal protein L6	COG0097J	3.7
Z4676	<i>rpsH</i>	30S ribosomal protein S8	COG0096J	4.0
Z4677	<i>rpsN</i>	30S ribosomal protein S14	COG0199J	3.9
Z4678	<i>rplE</i>	50S ribosomal protein L5	COG0094J	3.9
Z4680	<i>rplN</i>	50S ribosomal protein L14	COG0093J	2.5
Z4681	<i>rpsQ</i>	30S ribosomal protein S17	COG0186J	3.1
Z4683	<i>rpmC</i>	50S ribosomal protein L29	COG0255J	2.9
Z4684	<i>rplP</i>	50S ribosomal protein L16	COG0197J	3.6
Z4685	<i>rpsC</i>	30S ribosomal protein S3	COG0092J	4.2
Z4686	<i>rplV</i>	50S ribosomal protein L22	COG0091J	4.2
Z4687	<i>rpsS</i>	30S ribosomal protein S19	COG0185J	4.0
Z4688	<i>rplB</i>	50S ribosomal protein L2	COG0090J	4.6
Z4689	<i>rplW</i>	50S ribosomal protein L23	COG0089J	4.2
Z4690	<i>rplD</i>	50S ribosomal protein L4	COG0088J	4.7
Z4691	<i>rplC</i>	50S ribosomal protein L3	COG0087J	3.3
Z4692	<i>rpsJ</i>	30S ribosomal protein S10	COG0051J	3.9
Z4697	<i>tufA</i>	elongation factor Tu	COG0050J	2.4
Z4754	<i>yrfH</i>	ribosome-associated heat shock protein Hsp15	COG1188J	3.8
Z5194	<i>rpmH</i>	50S ribosomal protein L34	COG0230J	2.3
Z5195	<i>rnpA</i>	ribonuclease P	COG0594J	5.6
Z5556	<i>rplK</i>	50S ribosomal protein L11	COG0080J	3.1
Z5557	<i>rplA</i>	50S ribosomal protein L1	COG0081J	2.9
Z5558	<i>rplJ</i>	50S ribosomal protein L10	COG0244J	2.7
Z5559	<i>rplL</i>	50S ribosomal protein L7/L12	COG0222J	2.2
Z5809	<i>rpsF</i>	30S ribosomal protein S6	COG0360J	3.7
Z5811	<i>rpsR</i>	30S ribosomal protein S18	COG0238J	3.7
Z5812	<i>rplI</i>	50S ribosomal protein L9	COG0359J	2.9
Z0067	Z0067	ATP-dependent helicase HepA	COG0553KL	2.9
<b>Z0321</b>	Z0321	putative AraC-type regulatory protein encoded in	COG2207K	2.4

		prophage CP-933H		
Z0376	<i>ykgA</i>	putative AraC-like transcriptional regulator	COG4977K	2.8
Z1754	<i>mfd</i>	transcription-repair coupling factor; mutation frequency decline	COG1197LK	2.0
Z2514	<i>rnb</i>	RNase II, mRNA degradation	COG4776K	2.1
Z3476	<i>rcsB</i>	transcriptional regulator RcsB	COG2197TK	2.1
Z4258	Z4258	partial putative transcriptional regulator LYSR-type	COG0583K	2.2
Z4553	<i>yrbA</i>	hypothetical protein	COG5007K	2.7
Z4665	<i>rpoA</i>	DNA-directed RNA polymerase subunit alpha	COG0202K	3.5
Z4762	<i>yhgF</i>	hypothetical protein	COG2183K	2.6
Z5293	<i>rho</i>	transcription termination factor Rho	COG1158K	3.8
Z5560	<i>rpoB</i>	DNA-directed RNA polymerase subunit beta	COG0085K	3.1
Z5561	<i>rpoC</i>	DNA-directed RNA polymerase subunit beta'	COG0086K	2.5
Z2536	<i>topA</i>	DNA topoisomerase type I, omega protein	COG0550L	2.9
Z2917	Z2917	dATP pyrophosphohydrolase	COG0494LR	2.4
Z5191	<i>recF</i>	recombination protein F	COG1195L	2.2
Z5192	<i>dnaN</i>	DNA polymerase III subunit beta	COG0592L	2.6
Z5193	<i>dnaA</i>	chromosomal replication initiation protein	COG0593L	2.7
Z5343	<i>recQ</i>	ATP-dependent DNA helicase RecQ	COG0514L	2.1
<b>Z5902</b>	Z5902	putative helicase	COG0210L	2.5
Z5973	<i>hold</i>	DNA polymerase III subunit psi	COG3050L	2.1
Z0031	<i>lspA</i>	prolipoprotein signal peptidase (SPase II)	COG0597MU	2.0
Z0034	<i>lytB</i>	control of stringent response; involved in penicillin tolerance	COG0761IM	2.4
Z0101	<i>murC</i>	L-alanine adding enzyme, UDP-N-acetyl-muramate:alanine ligase	COG0773M	2.4
Z0194	<i>lpxB</i>	tetraacyldisaccharide-1-P; lipid A biosynthesis, penultimate step	COG0763M	2.2
Z0204	<i>cutF</i>	copper homeostasis protein (lipoprotein)	COG3015MP	2.8
Z0777	<i>dacA</i>	D-alanyl-D-alanine carboxypeptidase, fraction A; penicillin-binding protein 5	COG1686M	2.4
Z1980	<i>hemM</i>	an enzyme in main pathway of synthesis of 5-aminolevulinate, possibly glutamyl-tRNA dehydrogenase	COG3017M	2.1
Z2822	<i>yeaF</i>	orf, hypothetical protein	COG3713M	2.0
Z3189	<i>wzzB</i>	regulator of length of O-antigen component of lipopolysaccharide chains	COG3765M	2.4
Z3473	<i>ompC</i>	outer membrane porin protein C	COG3203M	3.2
Z4261	<i>yggB</i>	mechanosensitive channel MscS	COG0668M	2.4
Z4392	<i>tolC</i>	outer membrane channel protein	COG1538MU	2.1
Z4552	<i>murA</i>	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	COG0766M	2.3
Z4926	<i>yhiU</i>	multidrug resistance efflux protein MdtE	COG0845M	2.2
Z5299	<i>rffG</i>	dTDP-glucose 4,6-dehydratase	COG1088M	2.3
Z0014	<i>dnaK</i>	chaperone Hsp70; DNA biosynthesis; autoregulated heat shock proteins	COG0443O	4.6
Z0015	<i>dnaJ</i>	chaperone with DnaK; heat shock protein	COG0484O	3.6
Z0033	<i>slpA</i>	probable FKBPX-type 16KD peptidyl-prolyl cis-trans isomerase (a rotamase)	COG1047O	2.5

Z0541	<i>tig</i>	trigger factor; a molecular chaperone involved in cell division	COG0544O	3.9
Z0545	<i>lon</i>	DNA-binding, ATP-dependent protease La; heat shock K-protein	COG0466O	3.4
Z0590	<i>htpG</i>	chaperone Hsp90, heat shock protein C 62.5	COG0326O	5.1
Z0645	<i>ybbN</i>	putative thioredoxin-like protein	COG3118O	2.6
Z2330	<i>hslJ</i>	heat shock protein hslJ	COG3187O	2.3
Z3886	<i>clpB</i>	protein disaggregation chaperone	COG0542O	3.3
Z3907	<i>grpE</i>	heat shock protein GrpE	COG0576O	2.7
Z5183	<i>ibpA</i>	heat shock protein		3.8
Z5478	<i>hslU</i>	ATP-dependent protease ATP-binding subunit	COG1220O	3.2
Z5479	<i>hslV</i>	ATP-dependent protease peptidase subunit	COG5405O	3.2
Z5747	<i>groES</i>	co-chaperonin GroES	COG0234O	7.6
Z5748	<i>groEL</i>	chaperonin GroEL	COG0459O	6.4
Z1034	<i>dps</i>	global regulator, starvation conditions	COG0783P	3.0
<b>Z1921</b>	Z1921	unknown protein encoded by prophage CP-933X	COG3546P	21.4
Z2761	<i>katE</i>	catalase; hydroperoxidase HP(III)	COG0753P	6.0
Z4931	<i>yhjA</i>	putative cytochrome C peroxidase	COG1858P	2.6
Z5219	<i>pstS</i>	phosphate transporter subunit	COG0226P	2.4
Z1044	Z1044	orf, hypothetical protein	COG0561R	2.4
<b>Z1773</b>	Z1773	unknown protein encoded by prophage CP-933N	COG5529R	2.0
Z2214	<i>pqqL</i>	putative peptidase	COG0612R	2.1
Z2458	<i>ycjX</i>	putative EC 2.1 enzymes	COG3106R	3.3
Z2653	<i>ydhA</i>	orf; Unknown function	COG3895R	5.8
Z3059	<i>yedU</i>	chaperone protein HchA	COG0693R	2.9
Z3396	<i>yohJ</i>	orf, hypothetical protein	COG1380R	2.3
Z3445	<i>yejK</i>	nucleoid-associated protein NdpA	COG3081R	2.7
Z3575	<i>cvpA</i>	colicin V production protein	COG1286R	2.3
Z4753	<i>yrfG</i>	putative phosphatase	COG1011R	2.3
Z5198	<i>thdF</i>	tRNA modification GTPase TrmE	COG0486R	2.9
Z0010	<i>yaaH</i>	orf, hypothetical protein	COG1584S	2.0
Z0202	Z0202	orf; Unknown function	COG4681S	2.1
Z1273	<i>ycbK</i>	orf, hypothetical protein	COG3108S	2.1
<b>Z1498</b>	Z1498	unknown protein encoded by bacteriophage BP-933W	COG3111S	3.3
<b>Z1771</b>	Z1771	unknown protein encoded by prophage CP-933N	COG4197S	2.6
<b>Z1922</b>	Z1922	unknown protein encoded by prophage CP-933X	COG3685S	20.4
<b>Z1923</b>	Z1923	unknown protein encoded by prophage CP-933X	COG3685S	40.5
<b>Z2099</b>	Z2099	unknown protein encoded within prophage CP-933O	COG3111S	2.9
Z2554	<i>yciF</i>	putative structural proteins	COG3685S	4.4
Z2555	<i>yciE</i>	orf, hypothetical protein	COG3685S	4.0
Z2916	<i>yebC</i>	orf, hypothetical protein	COG0217S	2.2
Z3579	<i>dedA</i>	hypothetical protein	COG0586S	3.0
Z4298	<i>yggU</i>	hypothetical protein	COG1872S	2.9
Z4920	<i>yhiD</i>	putative Mg(2+) transport ATPase	COG1285S	4.3
Z4923	<i>hdeD</i>	acid-resistance membrane protein	COG3247S	65.5

Z5628	<i>yjbA</i>	phosphate-starvation-inducible protein PsiE	COG3223S	2.2
Z2858	Z2858	orf, hypothetical protein	COG2200T	2.4
Z2948	<i>yecG</i>	putative regulator	COG0589T	3.0
Z4408	<i>ygiM</i>	putative signal transduction protein	COG3103T	2.1
Z5407	<i>yihK</i>	GTP-binding protein	COG1217T	2.3
Z0108	<i>secA</i>	preprotein translocase; secretion protein	COG0653U	2.8
<b>Z3097</b>	Z3097	putative peptidase encoded within prophage CP-933U	COG0740OU	2.9
Z5197	<i>yidC</i>	putative inner membrane protein translocase component YidC	COG0706U	2.4
Z4927	<i>yhiV</i>	putative transport system permease protein	COG0841V	2.3
<b>Z5900</b>	Z5900	hypothetical protein	COG1002V	2.4
Z0028	Z0028	orf, hypothetical protein	-	5.6
Z0208	<i>rscF</i>	regulator in colanic acid synthesis; interacts with RcsB	-	2.3
Z0277	<i>ykfE</i>	C-lysozyme inhibitor	-	2.7
<b>Z0311</b>	Z0311	partial O replication protein for prophage CP-933H	-	3.1
<b>Z0340</b>	Z0340	unknown protein encoded in prophage CP-933I	-	2.3
<b>Z0753</b>	Z0753			3.4
Z0879	Z0879	orf, hypothetical protein	-	2.6
<b>Z0948</b>	Z0948	unknown protein encoded by prophage CP-933K	-	2.2
<b>Z0951</b>	Z0951	putative exonuclease encoded by prophage CP-933K	-	3.4
<b>Z0952</b>	Z0952	putative Bet recombination protein of prophage CP-933K	-	3.8
Z1023	<i>ybiJ</i>	orf, hypothetical protein	-	3.2
<b>Z1428</b>	Z1428	unknown protein encoded by bacteriophage BP-933W	-	2.8
<b>Z1429</b>	Z1429	unknown protein encoded by bacteriophage BP-933W	-	2.5
<b>Z1435</b>	<i>exoW</i>	putative exonuclease of bacteriophage BP-933W	-	2.8
<b>Z1437</b>	<i>betW</i>	putative Bet recombination protein of bacteriophage BP-933W	-	3.8
<b>Z1440</b>	<i>ssbW</i>	putative single-stranded DNA binding protein	-	4.1
<b>Z1451</b>	Z1451	putative replication protein P of bacteriophage BP-933W	-	2.9
<b>Z1501</b>	Z1501	unknown protein encoded by bacteriophage BP-933W	-	3.4
<b>Z1764</b>	<i>intN</i>	partial integrase for prophage CP-933N	-	2.4
<b>Z1777</b>	Z1777	unknown protein encoded by prophage CP-933N	-	2.5
<b>Z1780</b>	Z1780	unknown protein encoded by prophage CP-933N	-	2.1
<b>Z1824</b>	Z1824	unknown protein encoded by prophage CP-933N	-	3.1
<b>Z1869</b>	Z1869	putative replication protein P of prophage CP-933X	-	3.1
<b>Z1930</b>	Z1930	putative protease encoded within prophage CP-933X	-	3.5
Z2229	Z2229	biofilm-dependent modulation protein	-	5.0
Z2493	<i>ymjA</i>	orf, hypothetical protein	-	2.2
<b>Z2560</b>	Z2560	orf; Unknown function	-	2.4
Z2632	Z2632	orf, hypothetical protein	-	3.1
Z2713	Z2713	orf, hypothetical protein	-	2.3
Z2883	Z2883	orf, hypothetical protein	-	2.7
<b>Z3071</b>	<i>espJ</i>	unknown protein encoded within prophage CP-933U	-	2.8
<b>Z3352</b>	Z3352	unknown protein encoded within prophage CP-933V	-	2.3

<b>Z3355</b>	Z3355	putative DNA replication protein P of prophage CP-933V	-	2.5
<b>Z3363</b>	Z3363	putative single-stranded DNA binding protein of prophage CP-933V	-	4.5
<b>Z3366</b>	Z3366	putative recombination protein Bet of prophage CP-933V	-	3.5
<b>Z3367</b>	Z3367	putative exonuclease of prophage CP-933V	-	3.2
<b>Z3370</b>	Z3370	unknown protein encoded within prophage CP-933V	-	3.0
<b>Z3371</b>	Z3371	unknown protein encoded within prophage CP-933V	-	3.7
<b>Z3372</b>	Z3372	unknown protein encoded within prophage CP-933V	-	3.0
Z3722	Z3722	hypothetical protein	-	3.5
<b>Z4000</b>	Z4000	hypothetical protein	-	2.3
Z4126	Z4126	hypothetical protein	-	5.8
Z4285	<i>yqgC</i>	hypothetical protein	-	3.1
Z4663	<i>yhdN</i>	hypothetical protein	-	2.1
Z4890	<i>yhiM</i>	acid resistance protein	-	44.3
Z4921	<i>hdeB</i>	acid-resistance protein	-	101.4
Z4922	<i>hdeA</i>	acid-resistance protein	-	96.5
Z5808	<i>yjfY</i>	hypothetical protein	-	2.1
Z5858	<i>yjgG_1</i>	hypothetical protein	-	2.5

<sup>a</sup>The COGs was assigned based on the annotation of *E. coli* O157:H7 strain EDL933. -: COG group is not available; <sup>b</sup>The ratio of normalized hybridization intensities of the gene in C<sup>-</sup> variant RM6608W to that of in the C<sup>+</sup> variant RM6608R. All genes listed here passed the significance test as detailed in the materials and method section. Genes in bold are *E. coli* O157:H7 specific genes.

Table S6. Other direct repeats with perfect match identified in the *rcsB* gene<sup>a</sup>

Number	First position of DR	Second position of DR	Sequence of DR
1	1-8	262-269	ATGAACAA
2	19-25	247-254	ATTATTG
3	30-36	257-264	TGACCAT
4	51-57	290-296	CGGTATT
5	126-133	267-274	CAACAACC
6	133-141	347-355	CTGCCGAAA
7	163-170	340-348	ACCGATCT
8	186-192	213-220	TAAGTAC
<b>9</b>	<b>192-198</b>	<b>275-281</b>	<b>CGGCGAT</b>
10	304-310	592-599	GATATCG
11	320-326	602-609	TGCTGAA
12	379-385	556-563	AAGAAAT
<b>13</b>	<b>403-408</b>	<b>452-458</b>	<b>TCTCGCC</b>
14	406-413	478-485	CGCCTGTT

<sup>a</sup>Repeats in bold are the ones bordering the fragment that was eliminated in C<sup>+</sup> variant RM6607R (#13) and RM6608R (#9).

1. **Carter, M. Q., J. W. Louie, C. K. Fagerquist, O. Sultan, W. G. Miller, and R. E. Mandrell.** 2012. Evolutionary silence of the acid chaperone protein HdeB in enterohemorrhagic *Escherichia coli* O157:H7. *Appl Environ Microbiol* **78**:1004-14.