

Supplementary Table 1. Comparative analysis of 'Keio' deletion mutants displaying increased sensitivities to the antibiotic rifampicin from the current study (with a log₂ score ≤ -2) to that of Tamae et al. (2008) study.

bnum ^a	Gene Name	Log ₂ ^b score	Tamae et al. (2008) ^c	MIC ^d tested for rifampicin		Description
				This study	Tamae et al. (2008)	
b3612	gpmI	-10.3	Y	20 µM	> 10	phosphoglycerate mutase III, cofactor-independent
b2512	yfgL	-6.4	Y	20 µM	> 10	protein assembly complex, lipoprotein component
b0462	acrB	-2.5	Y	20 µM	10	multidrug efflux system protein
b3613	envC	-4.4	Y	20 µM	10	protease with a role in cell division
b4172	hfq	-10.2	Y	20 µM	10	HF-I, host factor for RNA phage Q beta replication
b3619	rfaD	-10.4	Y	20 µM	10	ADP-L-glycero-D-mannoheptose-6-epimerase
b3838	tatB	-2.1	Y	20 µM	10	TatABCE protein translocation system subunit
b3839	tatC	-6.0	Y	20 µM	10	TatABCE protein translocation system subunit
b0659	ybeY	-5.3	Y	20 µM	10	hypothetical protein
b1237	hns	-10.3	Y	20 µM	7.5	DNA-binding transcriptional dual regulator H-NS
b1855	lpxM	-3.0	Y	20 µM	7.5	myristoyl-acyl carrier protein (ACP)-dependent acyltransferase
b2822	recC	-10.1	Y	20 µM	7.5	exonuclease V (RecBCD complex), gamma chain
b3052	rfaE	-10.6	Y	20 µM	7.5	fused heptose 7-phosphate kinase
b3984	rplA	-2.8	Y	20 µM	7.5	50S ribosomal subunit protein L1
b3299	rpmJ	-2.7	Y	20 µM	7.5	50S ribosomal subunit protein L36
b2572	rseA	-7.4	Y	20 µM	7.5	anti-sigma factor
b1280	yciM	-2.6	Y	20 µM	7.5	hypothetical protein
b0178	hlpA	-10.6	Y	20 µM	5	periplasmic chaperone
b1677	lpp	-10.7	Y ^e	20 µM	5	murein lipoprotein
b0677	nagA	-3.4	Y	20 µM	5	N-acetylglucosamine-6-phosphate deacetylase
b0741	pal	-6.4	Y	20 µM	5	peptidoglycan-associated outer membrane lipoprotein
b0738	tolR	-5.8	Y	20 µM	3.5	membrane spanning protein in TolA-TolQ-TolR complex
b3631	rfaG	-7.1	Y	20 µM	2	glucosyltransferase I
b0053	surA	-10.4	Y	20 µM	2	peptidyl-prolyl cis-trans isomerase
b3240	aaeB	-2.8		20 µM		p-hydroxybenzoic acid efflux system component
b3243	aaeR	-2.0		20 µM		predicted DNA-binding transcriptional regulator, efflux system
b0263	afuB	-3.2		20 µM		predicted ferric transporter subunit
b0506	allR	-6.3		20 µM		DNA-binding transcriptional regulator
b2817	amiC	-10.6		20 µM		N-acetylmuramoyl-L-alanine amidase
b2714	ascG	-6.0		20 µM		DNA-binding transcriptional regulator
b3731	atpC	-2.7		20 µM		F1 sector of membrane-bound ATP synthase, epsilon subunit
b2786	barA	-5.4		20 µM		hybrid sensory histidine kinase
b3723	bglG	-2.0		20 µM		transcriptional antiterminator of the bgl operon
b1737	chbC	-10.2		20 µM		N,N'-diacetylchitobiose-specific enzyme IIC component of PTS
b2155	cirA	-3.3		20 µM		ferric iron-catecholate outer membrane transporter
b0624	crcB	-8.5		20 µM		predicted inner membrane protein
b1040	csgD	-2.1		20 µM		DNA-binding transcriptional activator
b0623	cspE	-3.8		20 µM		DNA-binding transcriptional repressor
b3809	dapF	-10.9		20 µM		diaminopimelate epimerase
b3472	dcrB	-4.8		20 µM		periplasmic protein
b1485	ddpC	-2.0		20 µM		D-Ala-D-Ala transporter subunit
b2314	dedD	-6.5		20 µM		hypothetical protein
b1061	dinI	-3.4		20 µM		DNA damage-inducible protein I
b0646	djlB	-2.7		20 µM		predicted chaperone
b2455	eutE	-7.1		20 µM		predicted aldehyde dehydrogenase, ethanolamine utilization protein
b2461	eutP	-4.3		20 µM		conserved hypothetical protein
b1091	fabH	-2.4		20 µM		3-oxoacyl-[acyl-carrier-protein] synthase III
b2525	fdx	-3.8		20 µM		[2Fe-2S] ferredoxin
b0589	fepG	-6.9		20 µM		iron-enterobactin transporter subunit
b4315	fimI	-2.3		20 µM		fimbrial protein involved in type 1 pilus biosynthesis
b0028	fkpB	-5.8		20 µM		FKBP-type peptidyl-prolyl cis-trans isomerase
b1878	flhE	-2.4		20 µM		flagellar protein
b2321	flk	-2.5		20 µM		predicted flagella assembly protein
b0200	gmhB	-10.4		20 µM		D,D-heptose 1,7-bisphosphate phosphatase
b3509	hdeB	-2.6		20 µM		acid-resistance protein
b3511	hdeD	-5.6		20 µM		acid-resistance membrane protein
b4350	hsdR	-6.0		20 µM		endonuclease R
b3754	hsrA	-3.3		20 µM		predicted multidrug or homocysteine efflux system
b2995	hybB	-5.2		20 µM		predicted hydrogenase 2 cytochrome b type component
b0697	kdpB	-2.3		20 µM		potassium translocating ATPase, subunit B
b2569	lepA	-10.6		20 µM		GTP binding membrane protein
b0439	lon	-5.5		20 µM		DNA-binding ATP-dependent protease La
b0222	lpcA	-10.4		20 µM		D-sedoheptulose 7-phosphate isomerase
b1054	lpxL	-3.2		20 µM		lauryl-acyl carrier protein (ACP)-dependent acyltransferase
b3514	mdtF	-5.7		20 µM		multidrug transporter, RpoS-dependent
b0198	metI	-2.1		20 µM		DL-methionine transporter subunit
b3940	metL	-8.4		20 µM		fused aspartokinase II and homoserine dehydrogenase II
b0197	metQ	-2.7		20 µM		DL-methionine transporter subunit
b0149	mrcB	-6.1		20 µM		fused glycosyl transferase and transpeptidase
b2205	napG	-2.3		20 µM		ferredoxin-type protein essential for electron transfer
b1467	narY	-2.2		20 µM		nitrate reductase 2 (NRZ), beta subunit

b0548	ninE	-5.2	20 µM	hypothetical protein
b2051	nudD	-2.0	20 µM	GDP-mannose mannosyl hydrolase
b0957	ompA	-10.3	20 µM	outer membrane protein A (3a;II*;G;d)
b1638	pdxH	-2.4	20 µM	pyridoxine 5'-phosphate oxidase
b3164	pnp	-3.4	20 µM	polynucleotide phosphorylase/polyadenylase
b1494	pqqL	-2.3	20 µM	predicted peptidase
b1062	pyrC	-2.3	20 µM	dihydro-orotase
b3167	rbfA	-5.7	20 µM	30s ribosome binding factor
b3886	rbn	-4.6	20 µM	tRNA processing exoribonuclease BN
b2216	rdsD	-2.1	20 µM	phosphotransfer intermediate protein
b2820	recB	-7.0	20 µM	exonuclease V (RecBCD complex), beta subunit
b2784	relA	-2.2	20 µM	(p)ppGpp synthetase I/GTP pyrophosphokinase
b3621	rfaC	-7.6	20 µM	ADP-heptose:LPS heptosyl transferase I
b3620	rfaF	-10.5	20 µM	ADP-heptose:LPS heptosyltransferase II
b3630	rfaP	-10.5	20 µM	kinase that phosphorylates core heptose of lipopolysaccharide
b2608	rimM	-9.3	20 µM	16S rRNA processing protein
b1286	rnb	-6.2	20 µM	ribonuclease II
b3179	rrmJ	-11.2	20 µM	23S rRNA methyltransferase
b2183	rsuA	-2.2	20 µM	16S rRNA pseudouridylylate 516 synthase
b0550	rusA	-6.1	20 µM	endonuclease RUS
b1861	ruvA	-2.0	20 µM	component of RuvABC resolvosome, regulatory subunit
b1294	sapA	-2.7	20 µM	predicted antimicrobial peptide transporter subunit
b4301	sgcE	-3.2	20 µM	predicted epimerase
b1656	sodB	-5.4	20 µM	superoxide dismutase, Fe
b2965	speC	-6.5	20 µM	ornithine decarboxylase, constitutive
b0120	speD	-6.9	20 µM	S-adenosylmethionine decarboxylase
b1743	spy	-2.2	20 µM	envelope stress induced periplasmic protein
b3035	tolC	-2.4	20 µM	transport channel
b0737	tolQ	-3.0	20 µM	membrane spanning protein in TolA-TolQ-TolR complex
b3641	ttk	-2.6	20 µM	division inhibitor
b2907	ubiH	-5.4	20 µM	2-octaprenyl-6-methoxyphenol hydroxylase, FAD/NAD(P)-binding
b0949	uup	-4.2	20 µM	fused predicted transporter subunits
b0779	uvrB	-8.9	20 µM	exonuclease of nucleotide excision repair
b2050	wcaI	-2.7	20 µM	predicted glycosyl transferase
b2045	wcaK	-8.8	20 µM	predicted pyruvyl transferase
b3811	xerC	-6.4	20 µM	site-specific tyrosine recombinase
b0006	yaaA	-2.4	20 µM	hypothetical protein
b0010	yaaH	-2.9	20 µM	conserved inner membrane protein associated with acetate transport
b0227	yafL	-2.1	20 µM	predicted lipoprotein and C40 family peptidase
b0232	yafN	-2.1	20 µM	predicted antitoxin of the YafO-YafN toxin-antitoxin system
b0279	yagM	-2.2	20 µM	hypothetical protein
b0359	yaiX	-7.4	20 µM	predicted acyl transferase
b0454	ybaZ	-2.6	20 µM	predicted methyltransferase
b0709	ybgH	-3.4	20 µM	predicted transporter
b0710	ybgI	-2.3	20 µM	conserved metal-binding protein
b0795	ybhG	-2.4	20 µM	predicted membrane fusion protein (MFP)
b0801	ybiC	-2.5	20 µM	predicted dehydrogenase
b0844	ybjI	-2.1	20 µM	hypothetical protein
b0865	ybjP	-4.4	20 µM	predicted lipoprotein
b1105	ycfM	-7.2	20 µM	predicted outer membrane lipoprotein
b1178	ycgK	-2.1	20 µM	hypothetical protein
b1284	yciT	-7.1	20 µM	predicted DNA-binding transcriptional regulator
b1360	ydaV	-2.7	20 µM	predicted DNA replication protein
b1471	yddK	-6.1	20 µM	hypothetical protein
b1510	ydeK	-2.4	20 µM	predicted lipoprotein
b1515.1	ydeZ	-4.2	20 µM	AI2 transporter
b1565	ydfV	-5.9	20 µM	hypothetical protein
b1724	ydiZ	-2.3	20 µM	hypothetical protein
b1769	ydjE	-3.3	20 µM	predicted transporter
b1776	ydjL	-2.1	20 µM	predicted oxidoreductase, Zn-dependent and NAD(P)-binding
b1932	yedL	-2.3	20 µM	predicted acyltransferase
b2112	yehE	-4.2	20 µM	hypothetical protein
b2172	yeiQ	-2.4	20 µM	predicted dehydrogenase, NAD-dependent
b2290	yfbQ	-2.2	20 µM	predicted aminotransferase
b2379	yfdZ	-2.5	20 µM	predicted aminotransferase, PLP-dependent
b2833	ygdR	-2.0	20 µM	hypothetical protein
b2865	ygeR	-3.1	20 µM	Tettrapeptide repeat transcriptional regulator
b2912	ygfA	-7.3	20 µM	predicted ligase
b2878	ygfK	-5.4	20 µM	predicted oxidoreductase, Fe-S subunit
b2887	ygfT	-3.0	20 µM	fused predicted oxidoreductase Fe-S subunit
b2888	ygfU	-4.9	20 µM	predicted transporter
b2952	yggT	-11.2	20 µM	predicted inner membrane protein
b2969	yghE	-7.6	20 µM	predicted secretion pathway protein
b2970	yghF	-5.1	20 µM	predicted secretion pathway protein, C-type protein
b4466	yghJ	-2.3	20 µM	predicted inner membrane lipoprotein
b2984	yghR	-6.3	20 µM	hypothetical protein with nucleoside triphosphate hydrolase domain
b3000	yghY	-3.2	20 µM	predicted dienlactone hydrolase
b3073	ygiG	-2.5	20 µM	putrescine:2-oxoglutaric acid aminotransferase

b3085	ygjP	-2.3	20 µM	predicted metal dependent hydrolase
b3205	yhbJ	-3.6	20 µM	hypothetical protein
b3233	yhcB	-5.5	20 µM	hypothetical protein
b3248	yhdE	-2.7	20 µM	hypothetical protein
b4472	yhdP	-4.9	20 µM	conserved membrane protein, predicted transporter
b3344	yheM	-2.3	20 µM	predicted intracellular sulfur oxidation protein
b3356	yhfA	-2.3	20 µM	hypothetical protein
b3378	yhfU	-2.4	20 µM	hypothetical protein
b3381	yhfX	-9.2	20 µM	predicted amino acid racemase
b3411	yhgA	-2.1	20 µM	predicted transposase
b3434	yhgN	-2.2	20 µM	predicted antibiotic transporter
b3470	yhhP	-10.3	20 µM	conserved hypothetical protein required for cell growth
b3474	yhhT	-2.1	20 µM	predicted inner membrane protein
b3439	yhhW	-2.9	20 µM	hypothetical protein
b3441	yhhY	-3.5	20 µM	predicted acetyltransferase
b3442	yhhZ	-4.5	20 µM	hypothetical protein
b3508	yhiD	-5.3	20 µM	predicted Mg(2) transport ATPase inner membrane protein
b3489	yhiK	-2.1	20 µM	predicted protein
b3534	yhjQ	-4.0	20 µM	cell division protein
b3539	yhjV	-3.3	20 µM	predicted transporter
b3563	yiaB	-3.7	20 µM	conserved inner membrane protein
b3554	yiaF	-2.5	20 µM	hypothetical protein
b3575	yiaK	-2.9	20 µM	2,3-diketo-L-gulonate dehydrogenase, NADH-dependent
b3578	yiaN	-4.0	20 µM	predicted transporter
b3663	yicN	-3.5	20 µM	hypothetical protein
b3697	yidA	-2.3	20 µM	predicted hydrolase
b3866	yihI	-5.2	20 µM	hypothetical protein
b3878	yihQ	-3.2	20 µM	alpha-glucosidase
b3896	yiiG	-4.0	20 µM	hypothetical protein
b3920	yiiQ	-4.8	20 µM	hypothetical protein
b3921	yiiR	-3.1	20 µM	conserved inner membrane protein
b3999	yjaG	-4.7	20 µM	hypothetical protein
b4048	yjbM	-3.6	20 µM	hypothetical protein
b4255	yjgD	-3.0	20 µM	hypothetical protein
b4279	yjhB	-6.6	20 µM	predicted transporter
b4326	yjiD	-2.2	20 µM	DNA replication/recombination/repair protein
b4330	yjiH	-2.2	20 µM	conserved inner membrane protein
b4354	yjiY	-4.2	20 µM	predicted inner membrane protein
b4374	yjjG	-2.5	20 µM	predicted hydrolase
b4391	yjjK	-2.1	20 µM	fused predicted transporter subunits
b4358	yjjN	-3.9	20 µM	predicted oxidoreductase
b4377	yjjU	-2.6	20 µM	predicted esterase
b0457	ylaB	-2.8	20 µM	conserved inner membrane protein
b0563	ylcE	-6.0	20 µM	hypothetical protein
b0838	yliJ	-2.4	20 µM	predicted glutathione S-transferase
b1046	ymdC	-2.7	20 µM	predicted hydrolase
b1148	ymfM	-4.8	20 µM	hypothetical protein
b1753	ynjA	-7.9	20 µM	hypothetical protein
b2790	yqcA	-3.1	20 µM	predicted flavoprotein
b2875	yqeB	-3.7	20 µM	conserved hypothetical protein
b2844	yqeF	-2.3	20 µM	predicted acyltransferase
b3002	yqhA	-3.0	20 µM	conserved inner membrane protein
b3152	yraR	-2.4	20 µM	predicted nucleoside-diphosphate-sugar epimerase
b3393	yrfB	-6.5	20 µM	hypothetical protein
b3394	yrfC	-3.0	20 µM	predicted fimbrial assembly protein

^a b-number represent "Blattner" number.

^b Sensitivity of each single gene deletion mutant was measured using the log₂ (C/T) ratio, where C represents normalized colony sizes of the single mutant pinned onto the LB (Luria-Bertani) media in the absence of antibiotic rifampicin, and T represents normalized colony sizes of the single mutant pinned onto the LB media in the presence of the rifampicin.

^c 63 mutants shown to be sensitive to the antibiotic rifampicin from Tamae et al (2008) [data taken from table S3] was used for the comparative study.

^d MIC, minimum inhibitory concentration tested.

^e 'Y' represent if a deletion mutant strain is identified to be sensitive to antibiotic rifampicin in both studies.