

Table S1: Primers used in this study

Primer name ^a	Sequence (5'-3') ^b		Functions
	Forward	Reverse	
EF0408_EF0409U	AAAGGATCCAATTGAAAGAAGAGTTTAAGCG	AATGTCGACATTTCAAATTGAATTGATTTTTTCAG	Cloning in pLT06
EF0408_EF0409D	TAAGTCGACTTGTGACAAAGTCGTGCAT	AATGAATTCACACCACGTGCCATT	Cloning in pLT06
EF0408_EF0409V	AGCTACTTTGTTATTTGTCGTTGCT	TATGCTATACTCAAATTGGCGACTT	Cloning verification
EF0408_EF0409P	AAA <u>ACTAGT</u> GTGTATATCGGTA <u>ACTTCG</u>	GTACTGCAGTTGACCCCATCAGGC	Cloning in pVEPhoZ
EF0407	AACCGTTCAACAAGCTCTCG	AATAGGCGCTTGCTCGTAAC	RTqPCR
EF0408	ATTACCTCATGCGGAAGGAC	CGATCTGCTTCCGTACCAA	RTqPCR
EF0409	AGGTGCATCACATGTACGAGA	TCGTTCTGTTTTTCCAACCA	RTqPCR
EF0411	GGTGCACAGGTAGTTTGGT	CCATTGGTGTCATCGCTAAA	RTqPCR
EF0605_EF0606U	ACCCCGGGAGTTAGCACTGTTAATATTAC	TTGGTCGACTTAGTAGATTTTTCTTGTTAATA	Cloning in pLT06
EF0605_EF0606D	ATAGTCGACGACTGAAATCGGTCACTTA	CGAGGATCCATTGGAGCAAAGAATG	Cloning in pLT06
EF0605_EF0606V	TTCTCTCCTTTCAACTGTATAACTT	AGTAGAGTTAGGTA <u>ACTCACCTGA</u>	Cloning verification
EF0605_EF0606P	AAA <u>ACTAGT</u> ACTAAGTCAAACAAAATGAACG	GTGCTGCAGAGAGTGATATTGGGATAC	Cloning in pVEPhoZ
EF0604 (<i>gls24</i>)	GATGGTCTTCTAACGATTGATGG	TCCTACTTCAACATCCACTCCA	RTqPCR
EF0605	TGCTGCAAAAGAAGAACCTTT	AGCTTTGCGTATTTTTCTTGT	RTqPCR
EF0606	TGCGTGAGGAAGATTTCTAA	AGCGTAATCAGTCGTTCTGAAA	RTqPCR
EF0820_EF0821U	AATGGATCCACTAGGTAAGCTAGAAACAA	TTTGTGACAAGAACA <u>ACTGAAAAAAGAGT</u>	Cloning in pLT06
EF0820_EF0821D	CTTGTGACCGTAACACTTATATTTTTATACGTC	ACACCATGGTCAAATAAGGCATGTAGCG	Cloning in pLT06
EF0820_EF0821V	TGCTTTGCACATTAATGTGTTGATGTT	ACAGTGACCTGCTTGCCTTTGATTAAT	Cloning verification
EF0820_EF0821P	GGT <u>ACTAGT</u> ATAGTGAATCCGTTAAAG	GTTCTGCAGAAACCTTTATTTACTTTAC	Cloning in pVEPhoZ
EF0819	AGAAATGGCCATCGACTTACC	GCAGGTAATAAAATCGTTTTACG	RTqPCR
EF0820 (<i>rplY</i>)	CCTGCCATTGTTTACGGTTAC	AACGGTGTTAGCACCATGTTTC	RTqPCR
EF0821	ACTGTTCTTGCAGCGACTGA	TTCCCCACGGATAAAAACA	RTqPCR
EF0822	ATTGGCGATTCTTTGCATTC	AATGGTTGGTGTTGCTGGAG	RTqPCR
EF1368_EF1369U	TGACCCGGGAATTTACGATCTAGTAATTTG	TATGTCGACACCATTAACAGTCCTTTATTTAGA	Cloning in pLT06

EF1368_EF1369D	ATTG <u>TTCGAC</u> GTGTAATAAGAAGGTGAACATCT	GTCGGATCCGCAATGGCAATACAAGCAAAT	Cloning in pLT06
EF1368_EF1369Cgene	GTCCCCGGGCTCATGAGATGTTACCTTC	CGGGGATCCCTATCAATTGACTAGGAGAAG	Cloning in p3535
EF1368_EF1369CsRNA	GTCCCCGGGATCTAAATAAAGGACTGTAA	CGGGGATCCAACAGTTTACTTACTAATAAT	Cloning in p3535
EF1368_EF1369V	ACGGTCCATGAACTTCTTCAGA	TGAAGGTAAACATAGCCACAGA	Cloning verification
EF1368_EF1369P	TCT <u>ACTAGT</u> AAGTGTAGCACAGGAAATCG	AGGCTGCAGTATGAAAAACCAATTCGGG	Cloning in pVEPhoZ
EF1368	CTAGCTGATGCTTCCTTCTGG	CGTCAACGGGCACATCTAAT	RTqPCR
EF1369	ATGGACAAATTCGTCGTTGG	CGGCCCATTAATAGTCCAAG	RTqPCR
EF1370 (<i>emrB</i>)	TGGCGAAAAGTTCCTACCAA	GCCGAAGAACGTCATAATCG	RTqPCR
EF3314_EF3315U	TTCGGATCCGTCAAATCAATATCAACACC	CAGGTCGACCGTTATTTAATTATCGATTTATCAA	Cloning in pLT06
EF3314_EF3315D	TCT <u>GTCGAC</u> CTTTCATAGGCATATAAGGTCA	GATGAATTCGATGCAGGCGCCCATCA	Cloning in pLT06
EF3314_EF3315V	TCCTCCCCGATCATTAAAGATAAATAAATT	TTATTCAAAGAAAAAATTGGAGTATTGGT	Cloning verification
EF3314_EF3315P	AAA <u>ACTAGT</u> TACAACGCTGATTTGGTCA	CAACTGCAGATTCGCTTCAACTGTTTATC	Cloning in pVEPhoZ
EF3311 (<i>gidA</i>)	CCGTAGTCAAGCAGTGGTGA	AGGTTGCGAATTGTTTGGTC	RTqPCR
EF3312 (<i>trmE</i>)	ACTTAATCCGTGCCAAAACG	TGTTGGAATCTGCGCTTTCAC	RTqPCR
EF3313	TTTCAGAAAATCGAAGGAACAA	AAAAAGCGCCCACTCCTC	RTqPCR
EF3314	CAGCACCAACTGTGACGACT	CTTCCCAGCAGCATCTTTC	RTqPCR
EF3315 (<i>citG</i>)	AAGCAGAACGAGCGATGTTT	GCGAGGTTTTCAAAGTCAGC	RTqPCR
pLT06 KSO5SeqR/OR1F	CCTATTATACCATATTTTGGA	CAATAATCGCATCCGATTGCAG	Cloning verification
p3535For/Rev	GATACAATGATTTTCGTTCTGAAGG	GCTTATCGAAATTAATACGACTCAC	Cloning verification

^a From the annotated sequence available at <http://www.tigr.org>. U and D primers are used to clone upstream (U) and downstream (D) sequences of the corresponded sRNAs in order to construct the deletion mutant by a double-crossover. V primers are used to prove the right size of the deletion. P primers are used to clone the promoter regions of the corresponded sRNAs.

^b The underlined sequences are restriction enzyme recognition sites.

Table S2. List of putative targets up-and down-regulated in the sRNA mutant strains identified by proteomic analysis.

Category and locus	Genes product function	Fold change in expression
<i>ef0408-0409</i>		
Amino acid biosynthesis		
<i>aspartate family</i>		
EF_1314	aspartate aminotransferase, putative	+2.61
EF_2372 (AspB)	aspartate aminotransferase	+2.16
<i>Serine family</i>		
EF_2550 (GlyA)	serine hydroxymethyltransferase	+2.20
Biosynthesis of cofactors, prosthetic groups, and carriers		
<i>Pantothenate and coenzyme A</i>		
EF_1860 (PanB)	3-methyl-2-oxobutanoate hydroxymethyltransferase	+5.81
Cell envelope		
<i>Biosynthesis and degradation of murein sacculus and peptidoglycan</i>		
EF_0849 (Alr)	alanine racemase	+3.64
EF_1908 (MurC)	UDP-N-acetylmuramate--alanine ligase	+2.37
<i>Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides</i>		
EF_2191	dTDP-4-dehydrorhamnose reductase	+3.69
EF_2487 (Glf)	UDP-galactopyranose mutase	-4.44
EF_2491	glycosyl transferase, group 2 family protein	-5.13 to -2.1
EF_2917	UDP-N-acetylglucosamine 2-epimerase	-2.16
Cellular processes		
<i>Adaptations to atypical conditions</i>		
EF_1646 (HslU)	heat shock protein HslIVU, ATPase subunit HslU	-5.24
<i>Pathogenesis</i>		
EF_0982 (TlyA)	hemolysin A	+2.60
<i>toxin production and resistance</i>		
EF_A0061	6-aminoglycoside N-acetyltransferase	-2.37
EF_2150	FemAB family protein	+4.20
EF_2698	tellurite resistance protein, putative	+2.73
Central intermediary metabolism		
<i>Phosphorus compound</i>		
EF_1611 (PpaC)	inorganic pyrophosphatase, manganese-dependent	+2.11
DNA metabolism		
<i>DNA replication, recombination, and repair</i>		
EF_0721 (PcrA)	ATP-dependent DNA helicase PcrA	-3.04
EF_0722 (LigA)	DNA ligase, NAD-dependent	-5.81 to -2.08
EF_3171 (RecA)	recA protein	-2.17
Energy metabolism		
<i>Amino acids and amines</i>		
EF_0104 (ArcA)	arginine deiminase	+2.06
EF_0105 (ArgF-1)	ornithine carbamoyltransferase	+2.09
EF_0106 (ArcC-1)	carbamate kinase	+2.57
<i>ATP-proton motive force interconversion</i>		
EF_1498	V-type ATPase, subunit	+3.58
EF_2610 (AtpA)	ATP synthase F1, alpha subunit	-2.53
<i>Biosynthesis and degradation of polysaccharides</i>		
EF_0957	glycosyl hydrolase, family 65	-2.03
<i>Electron transport</i>		
EF_1211 (Npr)	NADH peroxidase	+2.37
<i>Glycolysis/gluconeogenesis</i>		
EF_1046 (Pyk)	pyruvate kinase	-3.17
EF_1961 (Eno)	enolase	+4.27 to 58.6
<i>Sugars</i>		
EF_2425	phosphoglucomutase/phosphomannomutase family protein	+2.56 to 3.2
Fatty acid and phospholipid metabolism		
<i>Biosynthesis</i>		
EF_2881 (FabG)	3-oxoacyl-(acyl-carrier-protein) reductase	+2.849
Hypothetical proteins		
EF_1753/ EF_1918/ EF_2866/ EF_3303	conserved hypothetical proteins	+2.24 to 3.55
Mobile and extrachromosomal element functions		
<i>Plasmid functions</i>		
EF_A0001 (RepA-1)	replication-associated protein RepA	+2.21
Protein fate		
<i>Degradation of proteins, peptides, and glycopeptides</i>		
EF_0973 (PepQ-1)	proline dipeptidase	+4.68
<i>Protein and peptide secretion and trafficking</i>		
EF_1763 (SecA)	preprotein translocase, SecA subunit	-6.71 to -2.34

Category and locus	Genes product function	Fold change in expression
<u>ef0408-0409</u>		
Protein fate		
<i>Protein folding and stabilization</i>		
EF_0266	chaperonin, 33 kDa	+2.09
EF_0715 (Tig)	trigger factor	-3.15
EF_2633 (GroEL)	chaperonin, 60 kDa	+2.27
Protein synthesis		
<i>Ribosomal proteins: synthesis and modification</i>		
EF_1548	ribosomal protein S1	+2.06
<i>Translation factors</i>		
EF_0200 (FusA)	translation elongation factor G	-3.1 to -2.7
EF_0701 (PrfC)	peptide chain release factor 3	-2.29
EF_1764 (YfiA)	ribosomal subunit interface protein	+2.92
<i>tRNA aminoacylation</i>		
EF_1379 (AlaS)	alanyl-tRNA synthetase	-3.6 to -2.36
EF_1970 (AspS)	aspartyl-tRNA synthetase	-2.7
EF_2379 (ProS)	prolyl-tRNA synthetase	+3.56
Purines, pyrimidines, nucleosides, and nucleotides		
<i>2'-Deoxyribonucleotide metabolism</i>		
EF_0470 (NrdF)	ribonucleoside-diphosphate reductase 2, beta subunit	+2.11
EF_0471 (NrdE)	ribonucleoside-diphosphate reductase 2, alpha subunit	-5.52 to -2
<i>Nucleotide and nucleoside interconversions</i>		
EF_2429 (GuaC)	GMP reductase	+2.61
<i>Other</i>		
EF_0185 (DeoB)	phosphopentomutase	+2.06
EF_2902	2,3-cyclic-nucleotide 2-phosphodiesterase, putative	-2.28
<i>Purine ribonucleotide biosynthesis</i>		
EF_0014 (PurA)	Adenylosuccinate synthetase	-2.7 to -2.22
EF_0167 (GuaA)	GMP synthase	-2.37
EF_2361 (PurB)	pur operon repressor PurR	+2.37
Regulatory functions		
<i>DNA interactions</i>		
EF_0074 (Ers)	transcriptional regulator, Crp/Fnr family	+4.14
EF_0578	helix-turn-helix protein, iron-dependent repressor family	+2.37
EF_1613	transcriptional regulator, Cro/CI family	-2.46 to -2.15
EF_2203	transcriptional regulator, TetR family	+2.01
<i>Small molecule interactions</i>		
EF_2410 (Era)	GTP-binding protein Era	-2.17
Transcription		
<i>DNA-dependent RNA polymerase</i>		
EF_0233 (RpoA)	DNA-directed RNA polymerase, alpha subunit	+3.06
EF_3237 (RpoC)	DNA-directed RNA polymerase, beta-prime subunit	-5.18 to -2.55
<i>Transcription factors</i>		
EF_2914 (GreA)	transcription elongation factor GreA	+2.73
Transport and binding proteins		
<i>Carbohydrates, organic alcohols, and acids</i>		
EF_0710 (PtsI)	phosphoenolpyruvate-protein phosphotransferase enzyme I	-3.1
Unknown function		
EF_0684	cmp-binding protein, putative	+3.45
EF_0691	methyltransferase, putative	+4.27
EF_1008	oxidoreductase, Gfo/Idh/MocA family	+3.06
EF_1549	GTPase, putative	-4.1
EF_1644	lacX protein, putative	+2.09
EF_1671	oxidoreductase, zinc-binding	+2.01
EF_2352 (LepA)	GTP-binding protein LepA	-2.65
EF_2353	acetyltransferase, GNAT family	+2.06
EF_2460	GTP-binding protein TypA	-2.41
EF_2870	HD domain protein	+2.1
EF_2901	D-isomer specific 2-hydroxyacid dehydrogenase family protein	+2.11
<u>ef0605-0606</u>		
Amino acid biosynthesis		
<i>Aspartate family</i>		
EF_1314	aspartate aminotransferase, putative	+2.1
EF_2372 (AspB)	aspartate aminotransferase	+2.17
Biosynthesis of cofactors, prosthetic groups, and carriers		
<i>Pantothenate and coenzyme A</i>		
EF_1860 (PanB)	3-methyl-2-oxobutanoate hydroxymethyltransferase	+4.25

Category and locus	Genes product function	Fold change in expression
Cell envelope		
<i>Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides</i>		
EF_2191	dTDP-4-dehydrorhamnose reductase	+43.75
EF_2487 (Glf)	UDP-galactopyranose mutase	-2.46
Cellular processes		
<i>Adaptations to atypical conditions</i>		
EF_1646 (HslU)	heat shock protein HslVU, ATPase subunit HslU	-3.29
<i>Pathogenesis</i>		
EF_0982 (TlyA)	hemolysin A	+2.8
<i>Toxin production and resistance</i>		
EF_A0061	6-aminoglycoside N-acetyltransferase	-2.79
EF_2150	FemAB family protein	+4.97
Energy metabolism		
<i>Amino acids and amines</i>		
EF_0104 (ArcA)	arginine deiminase	+3.48
EF_0105 (ArgF-1)	ornithine carbamoyltransferase	+3.16
EF_0106 (ArcC-1)	carbamate kinase	+6.84
<i>Glycolysis/gluconeogenesis</i>		
EF_1961 (Eno)	enolase	+2.27
Fatty acid and phospholipid metabolism		
<i>Biosynthesis</i>		
EF_2881 (FabG)	3-oxoacyl-(acyl-carrier-protein) reductase	+2.04
EF_2883 (FabK)	enoyl-(acyl-carrier-protein) reductase II	+2.1
Hypothetical proteins		
EF_2260/EF_2866/EF_3228	Conserved hypothetical proteins	+2.06 to +3.05
Mobile and extrachromosomal element functions		
<i>Plasmid functions</i>		
EF_A0001 (RepA-1)	replication-associated protein RepA	+3.95
Protein fate		
<i>Degradation of proteins, peptides, and glycopeptides</i>		
EF_0973 (PepQ-1)	proline dipeptidase	-2.69
<i>Protein folding and stabilization</i>		
EF_0715 (Tig)	trigger factor	+2.23
EF_1307 (GrpE)	heat shock protein GrpE	+2.15
Protein synthesis		
<i>Ribosomal proteins: synthesis and modification</i>		
EF_2398 (RpsB)	ribosomal protein S2	-2.07
<i>Translation factors</i>		
EF_0287 (Efp)	translation elongation factor P	+2.58
EF_1764 (YfiA)	ribosomal subunit interface protein	+2.32
<i>tRNA aminoacylation</i>		
EF_1379 (AlaS)	alanyl-tRNA synthetase	-2.03
EF_1970 (AspS)	aspartyl-tRNA synthetase	-2.16
EF_2931 (ValS)	valyl-tRNA synthetase	-2.43
Purines, pyrimidines, nucleosides, nucleotides		
<i>2'-Deoxyribonucleotide metabolism</i>		
EF_0471 (NrdE)	ribonucleoside-diphosphate reductase 2, alpha subunit	-3.91
<i>Nucleotide and nucleoside interconversions</i>		
EF_2429 (GuaC)	GMP reductase	+2.65
<i>Other</i>		
EF_0185 (DeoB)	phosphopentomutase	+3.48
<i>Purine ribonucleotide biosynthesis</i>		
EF_0014 (PurA)	adenylosuccinate synthetase	-3.65 to -2.71
EF_0167 (GuaA)	GMP synthase	-2.79
EF_2361 (PurB)	adenylosuccinate lyase	+2.11
EF_3163 (PrsA-2)	ribose-phosphate pyrophosphokinase	-2.28
<i>Pyrimidine ribonucleotide biosynthesis</i>		
EF_0285 (PyrD-1)	dihydroorotate dehydrogenase	-2.07
EF_1147 (PyrG)	CTP synthase	-2.55
<i>Salvage of nucleosides and nucleotides</i>		
EF_2549 (Upp)	uracil phosphoribosyltransferase	+2.06
Regulatory functions		
<i>DNA interactions</i>		
EF_0074 (Ers)	transcriptional regulator, Crp/Fnr family	+3.4
EF_0578	helix-turn-helix protein, iron-dependent repressor family	+2.89
EF_2962	sugar-binding transcriptional regulator, LacI family	+2.04
Transcription		
<i>DNA-dependant RNA polymerase</i>		
EF_3238 (RpoB)	DNA-directed RNA polymerase, beta subunit	-2.55
<i>Transcription factors</i>		
EF_2914 (GreA)	transcription elongation factor GreA	+2.51

Category and locus	Genes product function	Fold change in expression
<u>ef0605-0606</u>		
Unknown function		
EF_0371	aminotransferase, class V	+2.08
EF_0684	cmp-binding protein, putative	+2.35
EF_0691	methyltransferase, putative	+3.74
EF_1008	oxidoreductase, Gfo/Idh/MocA family	+2.18
EF_1142	hydrolase, haloacid dehalogenase-like family	+2.08
EF_1549	GTPase, putative	-2.67
EF_2353	acetyltransferase, GNAT family	+3.48
EF_3310	oxidoreductase, short chain dehydrogenase/reductase family	-2.04
<u>ef1368-1369</u>		
Cell envelope		
<i>Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides</i>		
EF_2191	dTDP-4-dehydrorhamnose reductase	+4.77
Cellular processes		
<i>Detoxification</i>		
EF_2739 (AhpC)	alkyl hydroperoxide reductase, C subunit	-2.99
Central intermediary metabolism		
<i>Phosphorus compounds</i>		
EF_1611 (PpaC)	inorganic pyrophosphatase, manganese-dependent	-2.26
Energy metabolism		
<i>Amino acids and amines</i>		
EF_0105 (ArgF-1)	ornithine carbamoyltransferase	+2.55
EF_0106 (ArcC-1)	carbamate kinase	+4.24
<i>ATP-proton motive force interconversion</i>		
EF_2610 (AtpA)	ATP synthase F1, alpha subunit	-2.14
<i>Glycolysis/gluconeogenesis</i>		
EF_1961 (Eno)	enolase	+3.58
EF_1964 (Gap-2)	glyceraldehyde 3-phosphate dehydrogenase	+2.07
Fatty acid and phospholipid metabolism		
<i>Biosynthesis</i>		
EF_0282 (FabI)	enoyl-(acyl-carrier-protein) reductase	+4.24
EF_2882 (FabD)	malonyl CoA-acyl carrier protein transacylase	+2.35
Mobile and extrachromosomal element functions		
<i>Plasmid functions</i>		
EF_A0001 (RepA-1)	replication-associated protein RepA	+2.57
EF_2005	phage major tail protein, phi13 family	+2.05
Protein fate		
<i>Protein folding and stabilization</i>		
EF_2633 (GroEL)	chaperonin, 60 kDa	+2.21
Protein synthesis		
<i>Translation factors</i>		
EF_0200 (FusA)	translation elongation factor G	-2.21
<i>tRNA and rRNA base modification</i>		
EF_0728	RNA methyltransferase, TrmA family	+2.22
Purines, pyrimidines, nucleosides, and nucleotides		
<i>Other</i>		
EF_0185 (DeoB)	phosphopentomutase	+2.66
<i>Purine ribonucleotide biosynthesis</i>		
EF_0014	adenylosuccinate synthetase	-2.05
Transcription		
<i>DNA-dependent RNA polymerase</i>		
EF_3238 (RpoB)	DNA-directed RNA polymerase, beta subunit	+2.55
Unknown function		
EF_1138	oxidoreductase, aldo/keto reductase family	+2.09
EF_2353	acetyltransferase, GNAT family	+2.66
<u>ef3314-3315</u>		
Amino acid biosynthesis		
<i>Glutamate family</i>		
EF_0105 (ArgF-1)	ornithine carbamoyltransferase	+2.28 to 2.3
EF_1415 (GdhA)	glutamate dehydrogenase	-2.09
Cell envelope		
<i>Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides</i>		
EF_2191	dTDP-4-dehydrorhamnose reductase	+9.5
EF_2491	glycosyl transferase, group 2 family protein	-2.01

Category and locus	Genes product function	Fold change in expression
<i>ef3314-3315</i>		
Cellular processes		
<i>Adaptations to atypical conditions</i>		
EF_1646 (HslU)	heat shock protein HslVU, ATPase subunit HslU	-2.33
<i>Cell division</i>		
EF_0996 (FfsA)	cell division protein FtsA	-2.17
<i>Detoxification</i>		
EF_0463 (SodA)	superoxide dismutase, Mn	+2.03
Central intermediary metabolism		
<i>Phosphorus compounds</i>		
EF_1611 (PpaC)	inorganic pyrophosphatase, manganese-dependent	-2.66
DNA metabolism		
<i>DNA replication, recombination, and repair</i>		
EF_0005 (GyrA)	DNA gyrase, B subunit	+2.47
EF_0006	DNA gyrase, A subunit	+12.77
Energy metabolism		
<i>Amino acids and amines</i>		
EF_0106 (ArcC-1)	carbamate kinase	+3.56
<i>ATP-proton motive force interconversion</i>		
EF_2608 (AtpD)	ATP synthase F1, beta subunit	-2.06
<i>Fermentation</i>		
EF_0900	aldehyde-alcohol dehydrogenase	-2.18 to -2.04
<i>Glycolysis/gluconeogenesis</i>		
EF_1167	fructose-bisphosphate aldolase class-II	+2.54
EF_1961 (Eno)	enolase	+2.07 to 10.42
Fatty acid and phospholipid metabolism		
<i>Biosynthesis</i>		
EF_0282 (FabI)	enoyl-(acyl-carrier-protein) reductase	+3.56
Mobile and extrachromosomal element functions		
<i>Plasmid functions</i>		
EF_A0001 (RepA-1)	replication-associated protein RepA	+2.43 to 2.76
Protein fate		
<i>Degradation of proteins, peptides, and glycopeptides</i>		
EF_0973 (PepQ-1)	proline dipeptidase	+2.22
<i>Protein folding and stabilization</i>		
EF_2633 (GroEL)	chaperonin, 60 kDa	-2.56
Protein synthesis		
<i>Ribosomal proteins: synthesis and modification</i>		
EF_1548	ribosomal protein S1	-4.15
<i>Translation factors</i>		
EF_1764 (YfiA)	ribosomal subunit interface protein	+3.44
<i>tRNA aminoacylation</i>		
EF_0043 (GltX)	glutamyl-tRNA synthetase	+2.66
EF_2471 (ArgS)	arginyl-tRNA synthetase	-2
Purines, pyrimidines, nucleosides, and nucleotides		
<i>Purine ribonucleotide biosynthesis</i>		
EF_0014 (PurA)	adenylosuccinate synthetase	-2.05 to -3.69
Regulatory functions		
<i>DNA interactions</i>		
EF_1613	transcriptional regulator, Cro/CI family	-2.24
Transcription		
<i>DNA-dependent RNA polymerase</i>		
EF_3238 (RpoB)	DNA-directed RNA polymerase, beta subunit	+2.44 to 3.98
<i>Transcription factors</i>		
EF_2914 (GreA)	transcription elongation factor GreA	+2.185
Unknown function		
EF_0684	cmp-binding protein, putative	+2.49
EF_1549	GTPase, putative	-2.32
EF_2901	D-isomer specific 2-hydroxyacid dehydrogenase family protein	+2.69

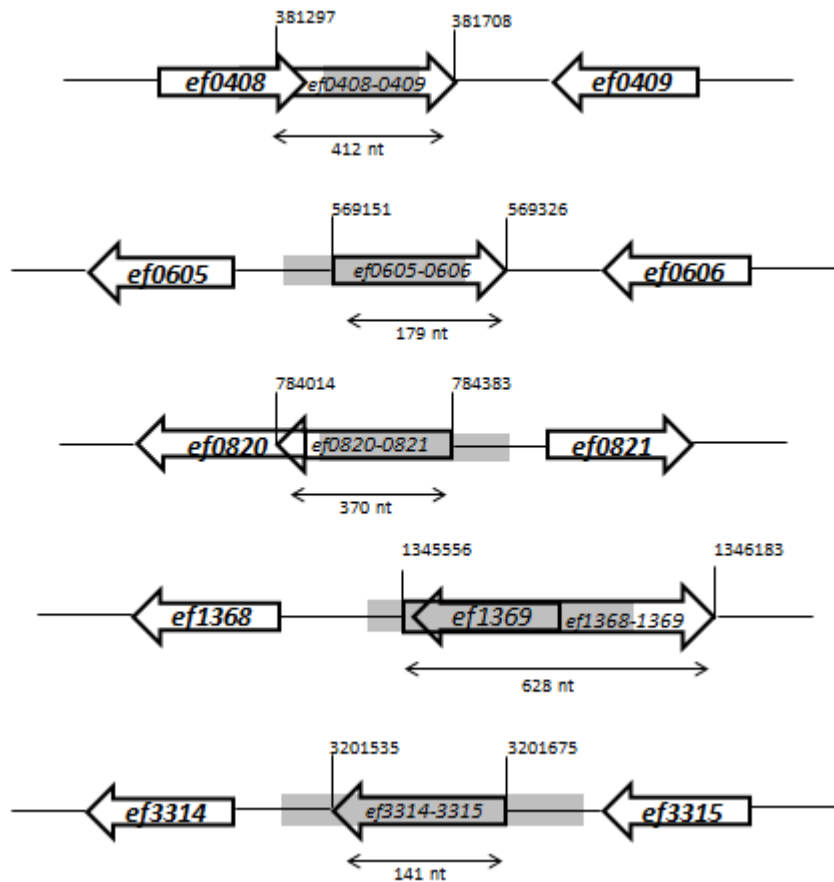


Figure S1. Schematic view of the studied sRNAs. For each sRNA, upstream and downstream genes are written in bold and represented by arrows. Their orientations show the transcriptional direction. The two numbers flanking each sRNA arrow correspond to sRNAs coordinates. Grey areas represent the part removed to obtain the different sRNA mutant strains.

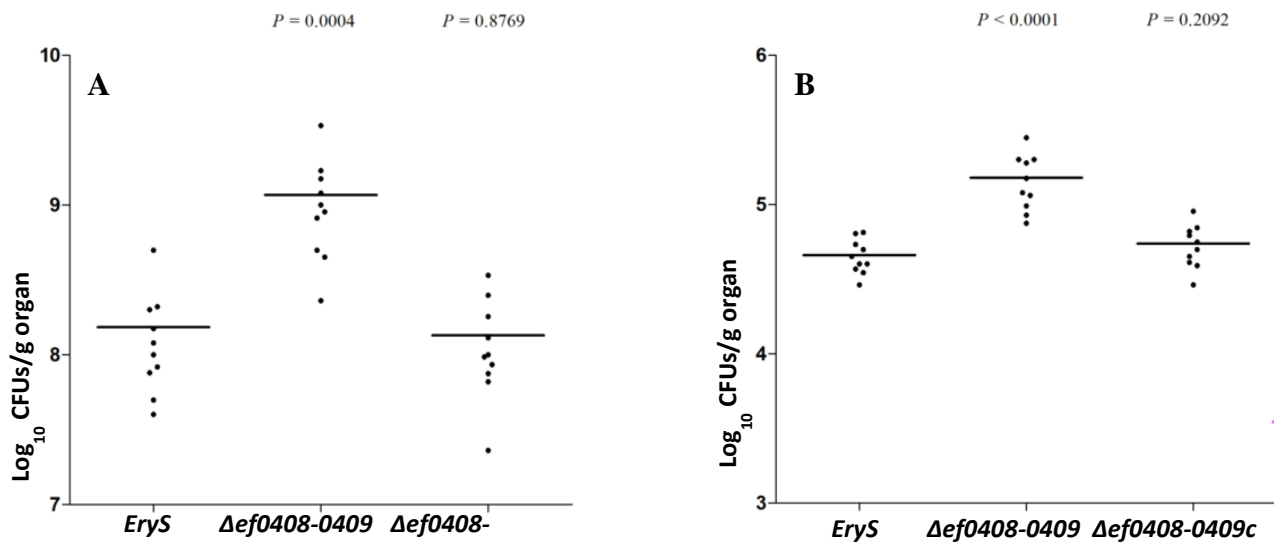


Figure S2. Bacterial persistence within mouse organs in systemic infection. Enterococcal tissue burdens in kidneys and in livers from BALB/c mice infected intravenously with 1×10^9 bacteria/ml of the EryS wild-type, the $\Delta ef0408-0409$ mutant and the complemented strains are shown. Kidney pair (A) and liver (B) homogenates were obtained from groups of 10 mice sacrificed and necropsied at day 7 post-infection. The results, expressed as \log_{10} CFU per gram of tissue, represent values recorded separately for each of the 10 mice. Horizontal bars represent the geometric means. *P* values of less than 0.05 were considered to be significant.

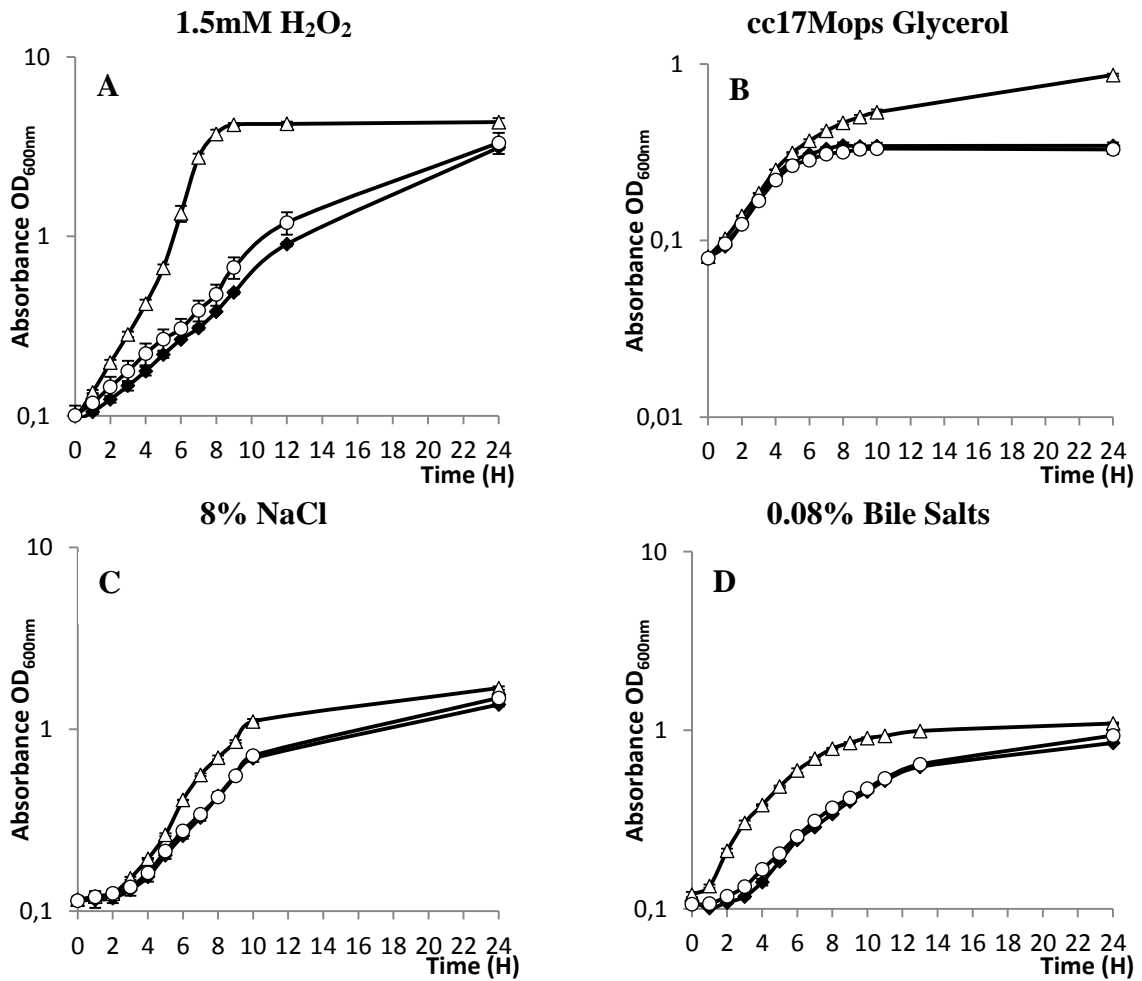


Figure S3. The *E. faecalis* wild-type (black diamonds), the $\Delta ef0408-0409$ sRNAs mutant (white triangles) and the complemented (white circle) strains were grown in GM17 medium supplemented by 1.5mM of H₂O₂ with shaking (A), in cc17MOPS medium supplemented by glycerol with shaking (B), in GM17 medium supplemented by 8% of NaCl (C) or by 0.08% of Bile salts (D) and optical density at 600 nm (OD₆₀₀) was determined. The curves shown represent the average of, at least, three independent experiments and the results represent the means \pm standard deviations.

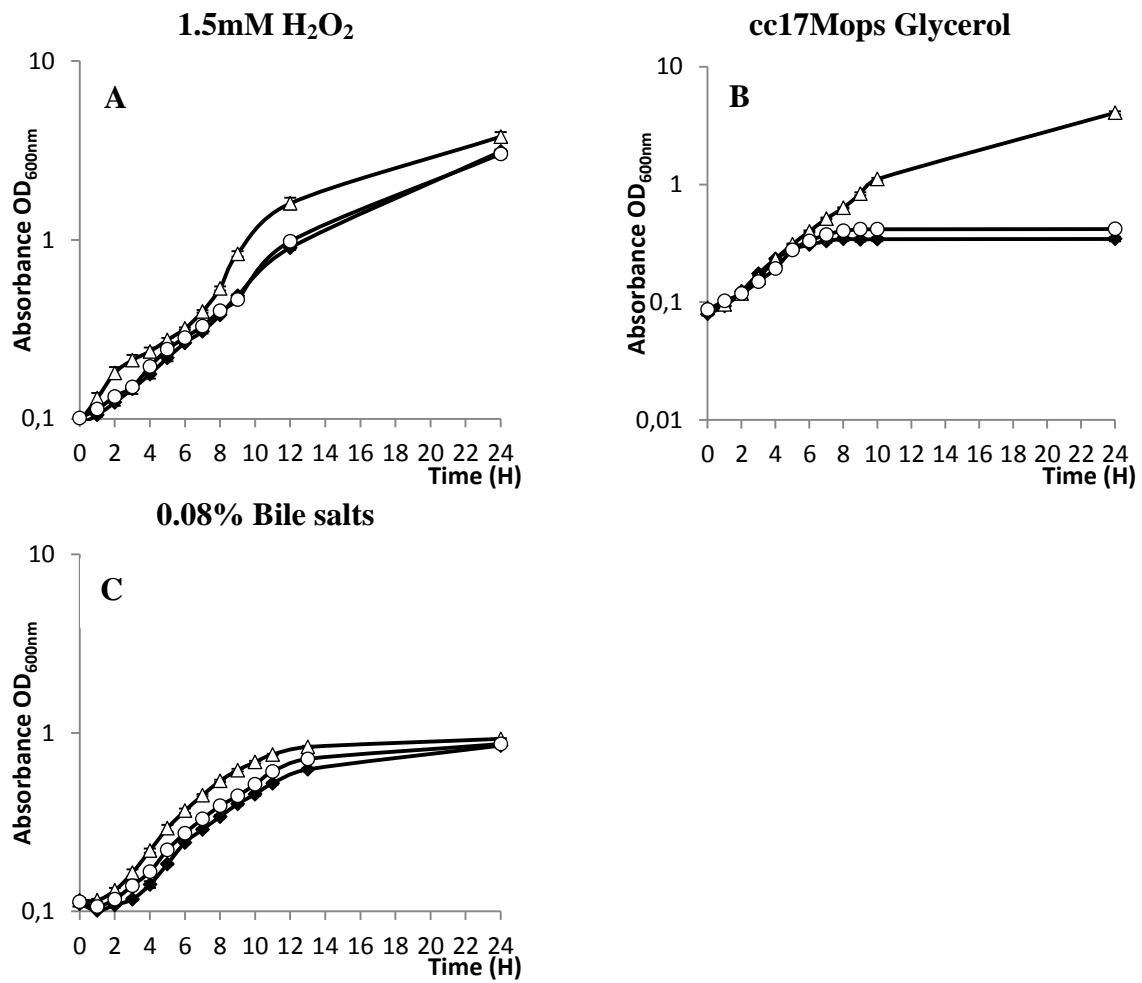


Figure S4. The *E. faecalis* wild-type (black diamonds), the $\Delta ef0605-0606$ sRNAs mutant (white triangles) and the complemented (white circle) strains were grown in GM17 medium supplemented by 1.5mM of H₂O₂ with shaking (A), in cc17MOPS medium supplemented by glycerol with shaking (B) and in GM17 medium supplemented by 0.08% of Bile salts (C) and optical density at 600 nm (OD₆₀₀) was determined. The curves shown represent the average of, at least, three independent experiments and the results represent the means \pm standard deviations.

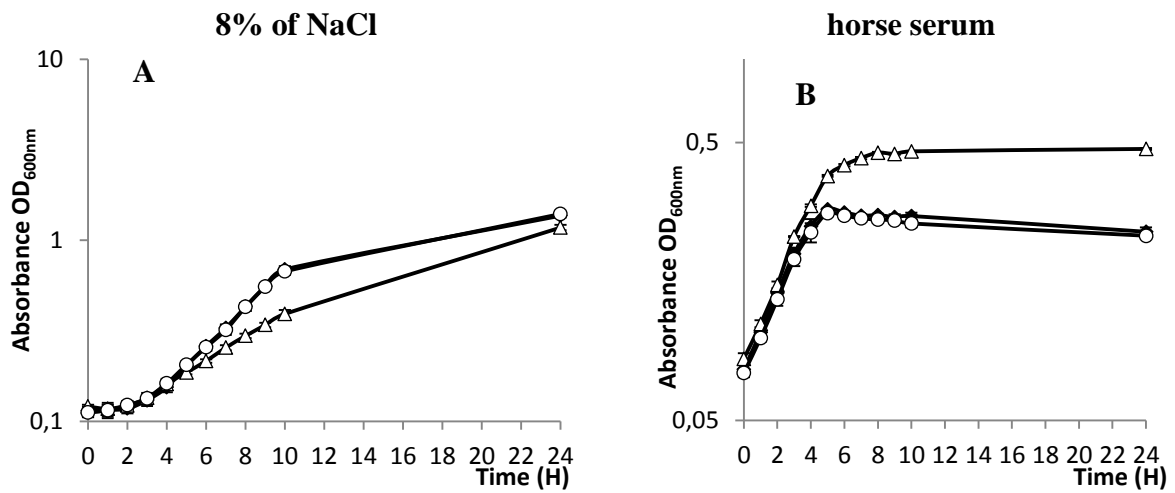


Figure S5. The *E. faecalis* wild-type (black diamonds), the $\Delta ef1368-1369$ sRNAs mutant (white triangles) and the complemented (white circle) strains were grown in GM17 medium supplemented by 8% of NaCl (A), in horse serum (B) and optical density at 600 nm (OD₆₀₀) was determined. The curves shown represent the average of, at least, three independent experiments and the results represent the means \pm standard deviations.

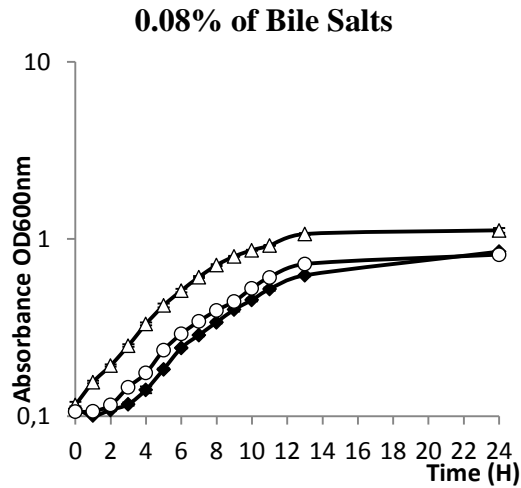


Figure S6. The *E. faecalis* wild-type (black diamonds), the $\Delta ef3314-3315$ sRNAs mutant (white triangles) and the complemented (white circle) strains were grown in GM17 medium supplemented by 0.08% of Bile salts and optical density at 600 nm (OD_{600}) was determined. The curves shown represent the average of, at least, three independent experiments and the results represent the means \pm standard deviations.

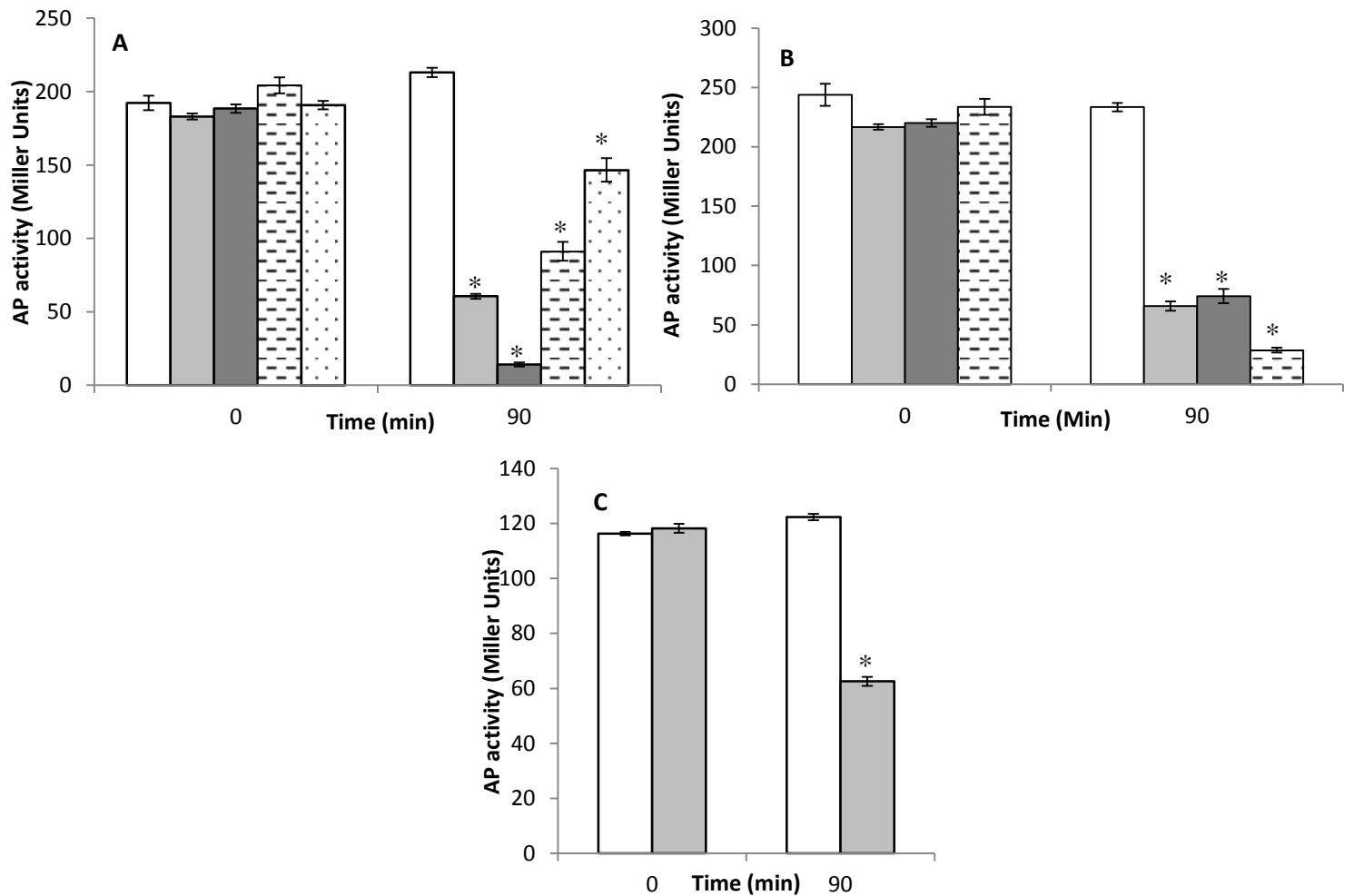


Figure S7. Quantitative assays of AP activity under osmotic, oxidative, detergent and acid stresses conditions of transcriptional fusion constructions.

Cells of pVEPhoZPef0408-0409 strain (A), (where *phoZ* transcription is under the control of *ef0408-0409* promoter), pVEPhoZPef0605-0606 strain (B), and pVEPhoZPef3314-3315 strain (C) grown at mid log phase were subjected to the following conditions (control, white bars), 0.08% of bile salt (grey bars), 1.5mM of H₂O₂ (dark grey bars), Glycerol (dashed bars) and 8% of NaCl (dotted bars). Error bars represent standard errors of at least three independent experiments. *P*-values of less than 0.001 (*) for the comparison of the same condition at T0 and T90 were considered to be significant.

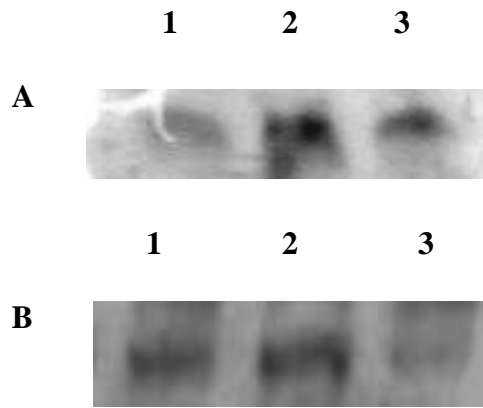


Figure S8. Western blot analysis with polyclonal antibody against Ers (A) and GroEL (B) of *E. faecalis* wild type (lines A1 and B1), $\Delta ef0408-409$ mutant (lines A2 and B2), $\Delta ef0605-0606$ mutant (line A3) and $\Delta ef3314-3315$ mutant (line B3). Protein extracts (40 μ g) were obtained from cells harvested at OD_{600nm} of 0.5.