# Structure-based analyses of *Salmonella* RcsB variants unravel new features of the Rcs regulon

Juanjo Huesa[1,2†], Joaquín Giner-Lamia[3,4†] M. Graciela Pucciarelli[3,5], Francisco Paredes-Martínez[1,2], Francisco García-del Portillo[3*], Alberto Marina[6,7*] and Patricia Casino[1,2,7]*.

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**Supplementary Table S1. Primers used for cloning and mutagenesis as well as for EMSA experiments.**

| Product | Primer sequences (5’ to 3’) |
|---|---|
| Cloning REC-RcsB | Fw: CAGGGACCCGGTATGAACAATATGAACGTAATTATTGCC<br>Rw: CGAGGAGAAGCCCGGTTATGCGCTGATTTTCTCCAGCAGAC |
| L108A | Fw: AGGGATCGTAgccAAACAGGGTG<br>Rw: TCAATATCAAGATCCAACAC |
| L108F | Fw: AGGGATCGTAggcAAACAGGGTG<br>Rw: TCAATATCAAGATCCAACAC |
| N90Y | Fw: GACCATGAACtacAACCCGGCGA<br>Rw: AGAACGATAATAGACAGGCTCG |
| N90A | Fw: GACCATGAACgccAACCCGGCGATC<br>Rw: AGAACGATAATAGACAGGC |
| Q110A | Fw: CGTACTCAAAgccGGTGCGCCAAC<br>Rw: ATCCCTTCAATATCAAGATC |
| Q110G | Fw: CGTACTCAAAggtGGTGCGCCAAC<br>Rw: ATCCCTTCAATATCAAGATC |
| **Commercial hybridized sequences** | |
| $P1_{flhDC}$ | 5′-CGAATTAGGAAAAATCTTAGGCG |
| $P_{rprA}$ | 5′-CCTATTGAGACGAATCTGATCGG |
| *fepE* | 5′-TTGTTTCGGATAATTCTGACTTG |
| *ytfK* | 5′-GATGTTTAGATAATTCTGAATAA |
| *osmB* | 5′-CTCTCTAAGACTTTTCTGACATC |
| *nlpD* | 5′-ACCTTTCGGAATATTCCCATACT |
| *flgA* | 5′-GTTAATAAGAATATTCCCATCAG |
| *fepE** | 5′-TTGTTTCGTATAATTATGACTTG |
| *ytfK** | 5′-GATGTTTATATAATTATGAATAA |
| *osmB** | 5′-CTCTCTAATACTTTTATGACATC |
| *flgA** | 5′-GTTAATAATAATATTACCATCAG |
| *nlpD** | 5′-ACCTTTCGTAATATTACCATACT |
| **Primers for qPCR** | |
| ***flgA*** | FW: AACTGACGGCATCCTGAATC<br>RW: GCGACCGGCAATTATGTC |
| ***nlpD*** | FW: TGCGTTACAGGACGCTGA<br>RW: TGTGGACAGTGGTTCGTCAT |
| ***ytfK*** | FW: AGGTGGCGAAGTACGTGAAG<br>RW: GACATCACAGACAAGTGCTGCT |
| ***fepE*** | FW: GTGGACAGTAATGTCGGCAAG<br>RW: TTCCAGCGTCTCTTTCACG |
| ***fepC*** | FW: AATATCCAGCCACGTTGTCG<br>RW: CCATGCGTGCAACAGGTAT |
| ***fes*** | FW: ATATTGACGACCGGAGACGA<br>RW: GAAGCAGGCGTTGATGAGTC |
| ***entF*** | FW: CACGCTTAGCGATTTGGTG<br>RW: ACAACCTGTTCGCGCATT |
| **qPCR Housekeeping gene** | |
| ***aroC*** | FW: CAGGCCGTATTTCTGCTCAT<br>RW: CCAGCATTGGCCTACTGATT |

## Supplementary Table S2. Terminology used to describe the structures presented in the manuscript.

| Name | Protein | Organism | P-mimetic | DNA | PDB |
|---|---|---|---|---|---|
| RcsB-P | full-length | *S.* Typhimurium | BeF$_3^-$ | No | 5O8Z (Casino et al, Nucleic Acids Res. 2018) |
| *rprA*-RcsB-P | full-length | *S.* Typhimurium | BeF$_3^-$ | P$_{rprA}$ | 6ZJ2 this work |
| *flhDC*-RcsB-P | full-length | *S.* Typhimurium | BeF$_3^-$ | P1$_{flhDC}$ | 6ZIX this work |
| *flhDC*-RcsB$_{EC}$ | full-length | *E. coli* | None | P1$_{flhDC}$ | 5W43 (Filippova et al, mBio 2018) |
| RcsB$_{REC}$ | REC domain | *S.* Typhimurium | None | None | 6ZIL This work |
| RcsB$_{REC}$-P | REC domain | *S.* Typhimurium | BeF$_3^-$ | None | 6ZII This work |

## Supplementary Table S3. Root mean square deviations (r.m.s.d.), in Å, for superposition of REC dimer between RcsB structures.

| | **RcsB$_{ST}$~P (PDB: 5O8Z)** | ***rprA*-RcsB$_{ST}$** | **P1$_{flhDC}$-RcsB$_{ST}$** | **P1$_{flhDC}$-RcsB$^{unP}_{EC}$ (PDB: 5W43)** |
|---|---|---|---|---|
| **Rmsd *rprA*-RcsB$_{ST}$** | 1.1 (247 residues) | | | |
| **Rmsd P1$_{flhDC}$-RcsB$_{ST}$** | 1.1 (246 residues) | 0.5 (248 residues) | | |
| **Rmsd P1$_{flhDC}$-RcsB$^{unP}_{EC}$ (PDB: 5W43)** | 1.0 (247 residues) | 0.9 (248 residues) | 0.9 (248 residues) | |
| **Rmsd REC- RcsB$_{ST}$~P** | 0.6 (248 residues) | 1.3 (247 residues) | 1.2 (246 residues) | 1.1 (248 residues) |
| **Rmsd REC- RcsB$_{ST}$** | 3.5 (168 residues) | | | |

The number of Cα atoms superimposed is indicated between parentheses.

## Supplementary Table S4. DBD interactions and interface area at the RcsB structures.

| **P*rprA*-RcsB$_{ST}$; interface area 230.4 Å$^2$** | **RcsB$_{ST}$-P (PDB: 5O8Z); interface area 381 Å$^2$** |
|---|---|
| /1/A/ **165(GLY)**. / CA [ C]: /1/B/ **199(ILE)**. / CD1[ C]: 3.85<br>/1/A/ **165(GLY)**. / O [ O]: /1/B/ **197(ASN)**. / ND2[ N]: 3.33<br>/1/A/ **197(ASN)**. / OD1[ O]: /1/B/ **165(GLY)**. / O [ O]: 3.22<br>/1/A/ **199(ILE)**. / CD1 [ C]: /1/B/ **165(GLY)**. / CA [ C]: 2.89<br>/1/A/ **202(LEU)**. / CD1[ C]: /1/B/ **202(LEU)**. / CD1[ C]: 3.63 | /1/A/ **165(GLY)**. / CA [ C]: /1/B/ **199(ILE)**. / CD1[ C]: 3.49<br>/1/A/ **197(ASN)**. / CB [ C]: /1/B/ **167(LEU)**. / CD1[ C]: 3.76<br>/1/A/ **199(ILE)**. / CG1[ C]: /1/B/ **198(ASP)**. / CB [ C]: 3.81<br>/1/A/ **199(ILE)**. / CD1[ C]: /1/B/ **162(PHE)**. / CE2[ C]: 3.40<br>/1/A/ **202(LEU)**. / CB [ C]: /1/B/ **202(LEU)**. / CD2[ C]: 3.82<br>/1/A/ **203(ASN)**. / ND2[ N]: /1/B/ **165(GLY)**. / O [ O]: 2.90 |
| **P1$_{flhDC}$-RcsB$_{ST}$; interface area 271 Å$^2$** | |
| /1/A/ **165(GLY)**. / CA [ C]: /1/B/ **199(ILE)**. / CG2[ C]: 3.65<br>/1/A/ **165(GLY)**. / O [ O]: /1/B/ **197(ASN)**. / ND2[ N]: 2.99<br>/1/A/ **197(ASN)**. / OD1[ O]: /1/B/ **165(GLY)**. / O [ O]: 3.81<br>/1/A/ **199(ILE)**. / CD1 [ C]: /1/B/ **165(GLY)**. / CA [ C]: 2.92 | |
| **P1$_{flhDC}$-RcsB$^{unP}_{EC}$ (PDB: 5W43) ; interface area 313.5 Å$^2$** | |
| /1/A/ **165(GLY)**. / CA [ C]: /1/B/ **199(ILE)**. / CD1[ C]: 3.50<br>/1/A/ **199(ILE)**. / CD1[ C]: /1/B/ **165(GLY)**. / C [ C]: 3.51<br>/1/A/ **202(LEU)**. / CD1[ C]: /1/B/ **199(ILE)**. / CG1[ C]: 3.87<br>/1/A/ **202(LEU)**. / CD1[ C]: /1/B/ **202(LEU)**. / CD1[ C]: 3.92 | |

## Supplementary Table S5. Interactions between RcsB and P*rprA* promoter

| **Chain A with DNA (chain I and G)** | **Chain B with DNA (chain I and G)** |
|---|---|
| A 192(LYS)NZ [ N]: I 19( DG) OP1[ O] 3.48<br>A 152(SER)OG [ O]: I 20( DA) OP2[ O] 2.39<br>A 181(THR)CG2[ C]: I 21( DT) C6 [ C] 3.88<br>A 184(SER)CB [ C]: I 21( DT) C7 [ C] 3.80<br>A 185(GLN)NE2[ N]: I 21( DT) OP2[ O] 2.39<br>A 178(SER)N [ N]: I 22( DC) OP2[ O] 3.73<br>A 180(LYS)NZ [ N]: I 23( DA) OP2[ O] 3.54<br>A 180(LYS)CE [ C]: I 23( DA) C5 [ C] 3.51<br>A 180(LYS)NZ [ N]: I 23( DA) N7 [ N] 2.82<br>A 180(LYS)CE [ C]: I 23( DA) C8 [ C] 3.56 | B 192(LYS) NZ [ N]: G 4( DA) OP2[ O] 3.11<br>B 154(LYS) NZ [ N]: G 5( DT) OP1[ O] 3.47<br>B 152(SER) OG [ O]: G 5( DT) OP2[ O] 2.66<br>B 155(GLU) OE2[ O]: G 5( DT) OP2[ O] 3.25<br>B 181(THR) OG1[ O]: G 6( DT) O5'[ O] 3.46<br>B 185(GLN) NE2[ N]: G 6( DT) OP2[ O] 2.68<br>B 178(SER) CB [ C]: G 7( DG) C5'[ C] 3.89<br>B 178(SER) N [ N]: G 7( DG) OP2[ O] 3.44<br>B 181(THR) OG1[ O]: G 7( DG) OP2[ O] 3.14<br>B 180(LYS) NZ [ N]: G 8( DA) N7 [ N] 3.02<br>B 180(LYS) NZ [ N]: G 9( DG) N7 [ N] 2.70<br>B 180(LYS) CE [ C]: G 9( DG) C6 [ C] 3.78<br>B 180(LYS) NZ [ N]: G 9( DG) O6 [ O] 2.65 |
| A 169(THR)N [ N]: G 14( DA) OP2[ O] 3.08<br>A 169(THR)OG1[ O]: G 14( DA) OP2[ O] 2.54<br>A 168(VAL)CG2[ C]: G 14( DA) C5'[ C] 3.88<br>A 183(SER)OG [ O]: G 15( DT) OP2[ O] 2.76 | B 169(THR) CG2[ C]: I 28( DC) C2'[ C] 3.56<br>B 168(VAL) N [ N]: I 29( DG) OP2[ O] 3.55<br>B 169(THR) N [ N]: I 29( DG) OP2[ O] 2.78<br>B 179(ILE) CG2[ C]: I 30( DT) C7 [ C] 3.79<br>B 183(SER) CB [ C]: I 30( DT) C7 [ C] 3.62<br>B 183(SER) OG [ O]: I 30( DT) OP2[ O] 3.02 |

## Supplementary Table S6

**Genes denoted by RNASeq as differentially expressed by S. Typhimurium producing distinct RcsB variants after exponential growth**

| RcsB variant Strain | Gene | Log 2 fold change | Adj. p-*val* | Symbol | Gene product |
|---|---|---|---|---|---|
| WT | *SL1344_0008* | -0.43 | 4.6E-02 | *mog* | molybdopterin biosynthesis Mog protein |
| WT | *SL1344_0009* | -0.74 | 9.4E-03 | *yaaH* | conserved hypothetical protein |
| WT | *SL1344_0023* | 0.60 | 4.6E-02 | *bcfC* | fimbrial usher protein |
| WT | *SL1344_0036* | 1.14 | 4.4E-06 | *NA* | hypothetical secreted sulfatase |
| WT | *SL1344_0081* | 4.50 | 3.9E-24 | *NA* | hypothetical lipoprotein |
| WT | *SL1344_0082* | 0.70 | 2.0E-02 | *NA* | probable secreted protein |
| WT | *SL1344_0105* | 0.69 | 1.2E-02 | *yabI* | DedA family integral membrane protein |
| WT | *SL1344_0137* | 0.99 | 8.8E-04 | *mutT* | 7,8-dihydro-8-oxoguanine-triphosphatase |
| WT | *SL1344_0160* | -0.85 | 3.4E-02 | *NA* | HNH endonuclease |
| WT | *SL1344_0169* | 0.66 | 6.3E-03 | *cueO* | possible multicopper oxidase precursor |
| WT | *SL1344_0170* | 1.61 | 4.2E-15 | *gcd* | glucose dehydrogenase |
| WT | *SL1344_0191* | 0.62 | 9.6E-05 | *mrcB* | penicillin-binding protein 1b; peptidoglycan synthetase |
| WT | *SL1344_0228* | -0.43 | 4.6E-03 | *fabZ* | (3R)-hydroxymyristol acyl carrier protein dehydrase |
| WT | *SL1344_0236* | 0.67 | 7.9E-05 | *yaeR* | conserved hypothetical protein |
| WT | *SL1344_0242* | 0.63 | 2.1E-03 | *cutF* | copper homeostasis protein CutF precursor (lipoprotein nlpE) |
| WT | *SL1344_0329* | 0.81 | 4.7E-02 | | |
| WT | *SL1344_0338* | 0.73 | 4.7E-03 | *NA* | hypothetical rtn protein |
| WT | *SL1344_0354* | 4.13 | 4.6E-15 | | |
| WT | *SL1344_0355* | 2.80 | 4.8E-26 | *NA* | probable terminal oxidase subunit I |
| WT | *SL1344_0356* | 2.30 | 2.1E-09 | *NA* | probable terminal oxidase subunit II |
| WT | *SL1344_0361* | 3.18 | 8.4E-29 | *yahO* | probable secreted protein |
| WT | *SL1344_0370* | 0.61 | 3.7E-02 | *ampH* | penicillin-binding protein AmpH |
| WT | *SL1344_0373* | 2.30 | 1.9E-12 | *yaiY* | hypothetical membrane protein |
| WT | *SL1344_0376* | 1.97 | 6.0E-05 | *NA* | annotation |
| WT | *SL1344_0379* | 1.46 | 9.0E-03 | *psiF* | phosphate starvation-inducible protein PsiF |
| WT | *SL1344_0384* | 1.05 | 2.7E-10 | *yaiA* | conserved hypothetical protein |
| WT | *SL1344_0385* | 0.79 | 2.0E-03 | *aroM* | AroM protein |
| WT | *SL1344_0408* | 1.79 | 8.9E-16 | *yajI* | hypothetical lipoprotein |
| WT | *SL1344_0441* | -0.35 | 2.4E-02 | *tig* | trigger factor |
| WT | *SL1344_0457* | -1.15 | 2.5E-02 | *amtB* | probable ammonium transporter |
| WT | *SL1344_0459* | 2.95 | 9.4E-36 | *ybaY* | conserved hypothetical lipoprotein |
| WT | *SL1344_0465* | 0.76 | 3.2E-06 | *maa* | maltose O-acetyltransferase |
| WT | *SL1344_0466* | 0.70 | 2.8E-04 | *hha* | haemolysin expression modulating protein |
| WT | *SL1344_0467* | 1.13 | 8.6E-07 | *ybaJ* | conserved hypothetical protein |

| | | | | | |
|---|---|---|---|---|---|
| WT | *SL1344_0471* | 0.57 | 1.9E-03 | *aefA* | integral membrane protein AefA |
| WT | *SL1344_0502* | -0.85 | 2.6E-04 | *NA* | outer membrane protein |
| WT | *SL1344_0536* | 1.42 | 1.5E-02 | *fimA* | type-1 fimbrial protein, a chain precursor |
| WT | *SL1344_0537* | 2.48 | 9.5E-03 | *fimI* | major pilin protein |
| WT | *SL1344_0555* | -1.17 | 2.7E-04 | *NA* | conserved hypothetical protein |
| WT | *SL1344_0571* | 1.78 | 2.2E-08 | *ybdK* | conserved hypothetical protein |
| WT | *SL1344_0577* | -1.05 | 2.4E-08 | *fepE* | responsible for production of very long modal length LPS Oag |
| WT | *SL1344_0595* | 0.45 | 2.7E-02 | *dsbG* | thiol:disulfide interchange protein DsbG precursor |
| WT | *SL1344_0603* | 1.96 | 4.9E-09 | *ybdR* | hypothetical zinc-dependant alcohol dehydrogenase |
| WT | *SL1344_0613* | 1.06 | 1.6E-05 | *citA* | sensor kinase DpiB |
| WT | *SL1344_0622* | 1.16 | 2.6E-04 | *ybeF* | lysR-family transcriptional regulator |
| WT | *SL1344_0641* | 0.83 | 2.1E-03 | *ybeL* | conserved hypothetical protein |
| WT | *SL1344_0690* | 1.70 | 2.9E-13 | *phrB* | deoxyribodipyrimidine photolyase |
| WT | *SL1344_0723* | -0.67 | 1.7E-03 | *cydB* | cytochrome d ubiquinol oxidase subunit II |
| WT | *SL1344_0724* | -0.70 | 3.4E-02 | *ybgT* | hypothetical membrane protein |
| WT | *SL1344_0730* | -0.44 | 6.3E-03 | *tolB* | tolB protein precursor |
| WT | *SL1344_0733* | 0.87 | 4.7E-03 | *nadA* | quinolinate synthetase A protein |
| WT | *SL1344_0735* | 1.24 | 1.0E-02 | *ybgR* | probable cation transport protein |
| WT | *SL1344_0736* | 4.73 | 3.0E-24 | *ybgS* | hypothetical exported protein |
| WT | *SL1344_0740* | -0.67 | 4.7E-02 | *NA* | LysR-family transcriptional regulator |
| WT | *SL1344_0752* | 0.77 | 2.5E-03 | *galT* | galactose-1-phosphate uridylyltransferase |
| WT | *SL1344_0758* | -2.22 | 7.3E-13 | *modA* | molybdate-binding periplasmic protein precursor |
| WT | *SL1344_0759* | -2.35 | 4.1E-11 | *modB* | molybdenum transport system permease protein ModB |
| WT | *SL1344_0760* | -2.39 | 3.8E-19 | *modC* | molybdenum transport ATP-binding protein ModC |
| WT | *SL1344_0762* | 0.48 | 9.3E-03 | *ybhE* | conserved hypothetical protein |
| WT | *SL1344_0769* | 0.94 | 1.9E-02 | *ybhB* | conserved hypothetical protein |
| WT | *SL1344_0776* | 0.45 | 5.3E-03 | *slrP* | Type III secretion system effector protein |
| WT | *SL1344_0787* | 2.52 | 4.9E-16 | *ybhN* | hypothetical membrane protein |
| WT | *SL1344_0788* | 2.95 | 1.4E-12 | *ybhO* | hypothetical phospholipase |
| WT | *SL1344_0789* | 3.12 | 6.1E-15 | *ybhP* | conserved hypothetical protein |
| WT | *SL1344_0791* | 0.58 | 4.5E-02 | *ybhR* | hypothetical inner membrane protein |
| WT | *SL1344_0792* | 0.65 | 1.5E-02 | *ybhS* | hypothetical inner membrane protein |
| WT | *SL1344_0803* | -1.71 | 2.6E-08 | *glnQ* | glutamine transport ATP-binding protein GlnQ |
| WT | *SL1344_0804* | -1.74 | 2.6E-08 | *glnP* | glutamine transport system permease protein GlnP |
| WT | *SL1344_0805* | -1.57 | 2.5E-05 | *glnH* | glutamine-binding periplasmic protein precursor |
| WT | *SL1344_0806* | 1.65 | 5.6E-06 | *dps* | DNA protection during starvation protein |
| WT | *SL1344_0808* | 0.89 | 1.1E-03 | *ompX* | outer membrane protein x precursor |
| WT | *SL1344_0823* | 0.57 | 1.0E-03 | *ybiK* | hypothetical L-asparaginase |

| | | | | | |
|---|---|---|---|---|---|
| WT | *SL1344_0824* | 0.68 | 2.3E-04 | *yliA* | hypothetical ABC transporter ATP-binding protein |
| WT | *SL1344_0826* | 0.80 | 4.4E-02 | *yliC* | hypothetical ABC transporter permease protein |
| WT | *SL1344_0827* | 0.81 | 5.1E-03 | *yliD* | hypothetical ABC transporter permease protein |
| WT | *SL1344_0839* | 0.70 | 1.4E-03 | *dacC* | D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 6 precursor) |
| WT | *SL1344_0842* | -0.48 | 3.1E-02 | *mdfA* | multidrug translocase MdfA |
| WT | *SL1344_0874* | 2.50 | 1.2E-27 | *poxB* | pyruvate dehydrogenase |
| WT | *SL1344_0913* | 2.99 | 2.2E-33 | *ycaP* | hypothetical membrane protein |
| WT | *SL1344_0927* | 0.70 | 5.0E-02 | *ycbC* | hypothetical membrane protein |
| WT | *SL1344_1010* | 1.02 | 4.6E-05 | *ompA* | outer membrane protein A |
| WT | *SL1344_1029* | -2.20 | 2.4E-20 | *pipC* | cell invasion protein |
| WT | *SL1344_1030* | -2.93 | 4.6E-34 | *sopB* | Type III secretion system effector protein. |
| WT | *SL1344_1057* | 1.97 | 2.4E-11 | *yccJ* | conserved hypothetical protein |
| WT | *SL1344_1058* | 2.26 | 6.6E-19 | *wrbA* | trp repressor binding protein |
| WT | *SL1344_1059* | 1.72 | 6.9E-12 | *ymdF* | conserved hypothetical protein |
| WT | *SL1344_1064* | 0.95 | 4.1E-04 | *phoH* | PhoH protein (phosphate starvation-inducible protein PsiH) |
| WT | *SL1344_1082* | -1.41 | 6.9E-03 | *csgC* | curli prooduction protein |
| WT | *SL1344_1083* | -2.00 | 3.1E-08 | *ymdA* | conserved hypothetical protein |
| WT | *SL1344_1084* | -1.16 | 2.8E-07 | *NA* | Hypothetical UPF0189 protein ORFName>. |
| WT | *SL1344_1090* | 2.24 | 6.2E-36 | *msyB* | acidic protein MsyB; multicopy suppressor of SecY |
| WT | *SL1344_1102* | 0.75 | 4.6E-02 | *grxB* | glutaredoxin 2 |
| WT | *SL1344_1108* | -2.94 | 2.1E-29 | *flgN* | flagella synthesis protein FlgN |
| WT | *SL1344_1109* | -2.93 | 3.5E-16 | *flgM* | negative regulator of flagellin synthesis (anti-sigma factor) |
| WT | *SL1344_1110* | -2.28 | 3.8E-12 | *flgA* | flagellar basal body P-ring protein FlgA precursor |
| WT | *SL1344_1111* | -2.35 | 1.4E-07 | *flgB* | hypothetical flagellar basal-body rod protein FlgB (proximal rod protein) |
| WT | *SL1344_1112* | -2.30 | 1.1E-09 | *flgC* | hypothetical flagellar basal-body rod protein FlgC (proximal rod protein) |
| WT | *SL1344_1113* | -2.30 | 4.7E-07 | *flgD* | flagellar hook formation protein FlgD |
| WT | *SL1344_1114* | -2.38 | 3.2E-07 | *flgE* | flagellar hook protein FlgE |
| WT | *SL1344_1115* | -2.44 | 2.9E-08 | *flgF* | hypothetical flagellar basal-body rod protein FlgF (proximal rod protein) |
| WT | *SL1344_1116* | -2.37 | 1.1E-06 | *flgG* | flagellar basal-body rod protein FlgG (distal rod protein) |
| WT | *SL1344_1117* | -2.45 | 5.0E-07 | *flgH* | Flagellar L-ring protein precursor |
| WT | *SL1344_1118* | -2.34 | 7.0E-07 | *flgI* | Flagellar P-ring protein precursor |
| WT | *SL1344_1119* | -2.30 | 7.0E-07 | *flgJ* | flagellar protein FlgJ |
| WT | *SL1344_1120* | -3.11 | 4.1E-16 | *flgK* | flagellar hook-associated protein 1 |
| WT | *SL1344_1121* | -3.07 | 7.0E-19 | *flgL* | flagellar hook-associated protein 3 |
| WT | *SL1344_1149* | 3.35 | 1.5E-35 | *ycfJ* | hypothetical secreted protein |
| WT | *SL1344_1152* | 0.84 | 4.3E-02 | *ycfS* | hypothetical exported protein |
| WT | *SL1344_1181* | 1.78 | 2.0E-15 | *envE* | hypothetical lipoprotein |
| WT | *SL1344_1185* | 3.71 | 1.2E-28 | *pliC* | hypothetical secreted protein |

| | | | | | |
|---|---|---|---|---|---|
| WT | *SL1344_1186* | 1.05 | 1.6E-02 | | |
| WT | *SL1344_1196* | 2.12 | 2.2E-07 | *NA* | hypothetical membrane protein |
| WT | *SL1344_1197* | 1.79 | 2.9E-07 | *NA* | conserved hypothetical protein |
| WT | *SL1344_1198* | 1.10 | 4.0E-05 | *NA* | conserved hypothetical protein |
| WT | *SL1344_1200* | 2.67 | 1.4E-07 | *NA* | hypothetical regulatory protein |
| WT | *SL1344_1202* | 4.27 | 2.4E-30 | *NA* | annotation |
| WT | *SL1344_1210* | 2.77 | 2.9E-40 | *yeaQ* | hypothetical inner membrane protein |
| WT | *SL1344_1219* | 1.15 | 5.2E-10 | *yeaH* | conserved hypothetical protein |
| WT | *SL1344_1220* | 2.52 | 2.1E-44 | *yeaG* | conserved hypothetical protein |
| WT | *SL1344_1235* | -3.35 | 1.5E-16 | *NA* | hypothetical exported protein |
| WT | *SL1344_1243* | 2.89 | 1.4E-32 | *NA* | exported protein |
| WT | *SL1344_1246* | 2.88 | 1.7E-20 | *osmE* | osmotically inducible lipoprotein E precursor |
| WT | *SL1344_1253* | 3.34 | 3.4E-61 | *katE* | catalase HPII |
| WT | *SL1344_1255* | 0.84 | 4.7E-02 | *ydjN* | hypothetical sodium:dicarboxylate symporter |
| WT | *SL1344_1260* | 1.06 | 5.5E-08 | *ydiZ* | conserved hypothetical protein |
| WT | *SL1344_1261* | 1.27 | 7.1E-06 | *pfkB* | 6-phosphofructokinase isozyme |
| WT | *SL1344_1263* | -1.42 | 3.1E-07 | *NA* | hypothetical outer membrane protein |
| WT | *SL1344_1277* | 0.74 | 7.4E-03 | *nlpC* | hypothetical lipoprotein |
| WT | *SL1344_1278* | 1.68 | 2.3E-09 | *ydiV* | conserved hypothetical protein |
| WT | *SL1344_1297* | 2.14 | 4.6E-05 | *ydiL* | Conserved hypothetical protein |
| WT | *SL1344_1303* | 1.11 | 6.1E-03 | *sufA* | conserved hypothetical protein |
| WT | *SL1344_1306* | 0.88 | 1.4E-02 | *sufD* | conserved hypothetical protein |
| WT | *SL1344_1307* | 0.68 | 4.7E-02 | *sufS* | hypothetical amintransferase |
| WT | *SL1344_1309* | 0.90 | 1.6E-05 | *ynhG* | hypothetical exported protein |
| WT | *SL1344_1323* | 1.76 | 1.2E-24 | *orf319* | hypothetical pathogenicity island protein |
| WT | *SL1344_1352* | 0.44 | 4.4E-02 | *ssaQ* | Type III secretion system protein |
| WT | *SL1344_1363* | -0.50 | 2.2E-02 | *sodB* | superoxide dismutase |
| WT | *SL1344_1372* | 0.97 | 1.5E-05 | *sodCb* | copper-zinc superoxide dismutase |
| WT | *SL1344_1379* | 1.81 | 3.8E-10 | *mliC* | lipoprotein |
| WT | *SL1344_1393* | -0.78 | 1.5E-02 | *ydgT* | conserved hypothetical protein |
| WT | *SL1344_1421* | 4.08 | 6.2E-72 | *NA* | hypothetical ABC transporter ATP/GTP-binding protein |
| WT | *SL1344_1422* | 4.22 | 3.5E-17 | *NA* | hypothetical ABC transporter membrane protein |
| WT | *SL1344_1423* | 4.85 | 7.6E-23 | *NA* | hypothetical ABC transporter periplasmic binding protein |
| WT | *SL1344_1424* | 5.65 | 5.9E-12 | *NA* | hypothetical ABC transporter membrane protein |
| WT | *SL1344_1443* | 2.69 | 1.0E-14 | *NA* | conserved hypothetical protein |
| WT | *SL1344_1444* | 1.91 | 1.1E-06 | *ydeJ* | conserved hypothetical protein |
| WT | *SL1344_1445* | 3.21 | 3.8E-17 | *ydeI* | hypothetical periplasmic protein |
| WT | *SL1344_1459* | -1.22 | 3.2E-05 | *NA* | outer membrane protein |

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|---|---|---|---|---|---|
| WT | *SL1344_1467* | -1.19 | 6.7E-04 | *hyaB2* | uptake hydrogenase-1 large subunit |
| WT | *SL1344_1468* | -1.27 | 2.5E-05 | *hyaA2* | uptake hydrogenase small subunit |
| WT | *SL1344_1484* | -1.20 | 1.3E-03 | | |
| WT | *SL1344_1488* | 1.97 | 1.5E-31 | *NA* | glycogen debranching protein |
| WT | *SL1344_1489* | 2.87 | 1.3E-24 | *NA* | hypothetical hydrolase |
| WT | *SL1344_1490* | 3.71 | 3.1E-54 | *NA* | hypothetical hydrolase |
| WT | *SL1344_1491* | 4.25 | 1.9E-59 | *NA* | hypothetical exported protein |
| WT | *SL1344_1493* | 2.67 | 7.7E-22 | *osmC* | osmotically inducible protein C |
| WT | *SL1344_1494* | 2.96 | 2.0E-10 | *yddX* | conserved hypothetical protein |
| WT | *SL1344_1495* | 2.20 | 9.7E-13 | *rpsV* | 30S ribosomal protein S22 |
| WT | *SL1344_1497* | 1.12 | 1.6E-11 | *adhP* | alcohol dehydrogenase |
| WT | *SL1344_1503* | -1.39 | 3.1E-04 | *ompD* | Outer membrane protein |
| WT | *SL1344_1504* | -1.09 | 1.1E-04 | *NA* | conserved hypothetical protein |
| WT | *SL1344_1507* | 2.04 | 1.0E-03 | *narU* | nitrite extrusion protein |
| WT | *SL1344_1508* | 1.50 | 1.2E-04 | *narZ* | respiratory nitrate reductase 2 alpha chain |
| WT | *SL1344_1509* | 1.17 | 4.5E-04 | *narY* | respiratory nitrate reductase 2 beta chain |
| WT | *SL1344_1510* | 2.14 | 4.6E-02 | *narW* | respiratory nitrate reductase 2 delta chain |
| WT | *SL1344_1515* | -0.81 | 6.7E-04 | *ansP* | L-asparagine permease |
| WT | *SL1344_1518* | 2.26 | 8.9E-41 | *yncD* | probable TonB-dependent receptor YncD precursor |
| WT | *SL1344_1519* | 2.44 | 1.7E-35 | *yncC* | hypothetical regulatory protein |
| WT | *SL1344_1520* | 1.38 | 6.7E-16 | *yncB* | hypothetical NADP-dependent oxidoreductase |
| WT | *SL1344_1524* | -2.44 | 4.8E-09 | *srfA* | virulence protein |
| WT | *SL1344_1525* | -2.53 | 5.1E-08 | *srfB* | virulence protein |
| WT | *SL1344_1526* | -2.43 | 1.3E-13 | *srfC* | virulence protein |
| WT | *SL1344_1540* | 1.16 | 1.0E-03 | *ydcK* | hypothetical transferase |
| WT | *SL1344_1556* | -3.37 | 2.4E-03 | *trg* | methyl-accepting chemotaxis protein III (mcp-iii) |
| WT | *SL1344_1563* | 1.26 | 9.5E-03 | *NA* | hypothetical periplasmic amino acid-binding protein |
| WT | *SL1344_1578* | 0.65 | 2.6E-02 | *hslJ* | heat shock protein (hslJ) |
| WT | *SL1344_1587* | 0.63 | 1.7E-03 | *zntB* | hypothetical membrane transport protein |
| WT | *SL1344_1590* | 0.53 | 2.2E-02 | *ogt* | O6-methylguanine-DNA-alkyltransferase |
| WT | *SL1344_1600* | -1.06 | 3.2E-02 | *NA* | hypothetical lipoprotein |
| WT | *SL1344_1627* | -2.09 | 1.1E-16 | *NA* | conserved hypothetical protein |
| WT | *SL1344_1634* | 0.86 | 4.1E-04 | *yciR* | conserved hypothetical protein |
| WT | *SL1344_1637* | 5.12 | 6.6E-77 | *osmB* | osmotically inducible lipoprotein B precursor |
| WT | *SL1344_1644A* | -1.10 | 4.4E-13 | *ymiA* | conserved sORF |
| WT | *SL1344_1649* | 0.69 | 9.4E-04 | *yciK* | hypothetical oxidoreductase |
| WT | *SL1344_1650* | 0.77 | 2.5E-04 | *btuR* | COB(I) alamin adenosyltransferase |
| WT | *SL1344_1659* | 3.01 | 3.3E-05 | *yciG* | conserved hypothetical protein |

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|---|---|---|---|---|---|
| WT | *SL1344_1660* | 4.02 | 4.1E-11 | *yciF* | conserved hypothetical protein |
| WT | *SL1344_1661* | 4.93 | 4.1E-11 | *yciE* | conserved hypothetical protein |
| WT | *SL1344_1662* | 1.91 | 5.6E-14 | *katN* | catalase |
| WT | *SL1344_1682* | -0.40 | 2.3E-02 | *hns* | H-NS DNA-binding protein (histone-like protein Hlp-II) |
| WT | *SL1344_1683* | 1.16 | 4.8E-07 | *galU* | glucose-1-phosphate uridylyltransferase |
| WT | *SL1344_1688* | 0.61 | 1.6E-02 | *NA* | hypothetical secreted protein |
| WT | *SL1344_1696* | 1.38 | 6.7E-14 | *ychP* | hypothetical invasin |
| WT | *SL1344_1698* | 2.68 | 2.3E-18 | *chaB* | cation transport regulator ChaB |
| WT | *SL1344_1699* | 0.61 | 1.1E-02 | *chaA* | hypothetical calcium/proton antiporter |
| WT | *SL1344_1724* | 1.00 | 3.7E-03 | *treA* | Periplasmic trehalase precursor |
| WT | *SL1344_1725* | 2.19 | 6.0E-05 | *ymgE* | hypothetical membrane protein |
| WT | *SL1344_1726* | -2.90 | 9.5E-20 | *ycgR* | conserved hypothetical protein |
| WT | *SL1344_1729* | -0.71 | 1.9E-03 | *cvrA* | Cell volume regulation protein A. Cell volume regulation protein A homolog. |
| WT | *SL1344_1732* | 2.95 | 5.4E-32 | *ycgB* | conserved hypothetical protein |
| WT | *SL1344_1747* | -0.52 | 1.4E-02 | *fadD* | long-chain-fatty-acid--CoA ligase |
| WT | *SL1344_1770* | 2.78 | 1.3E-07 | *NA* | hypothetical exported protein |
| WT | *SL1344_1778* | 0.53 | 2.3E-03 | *NA* | conserved hypothetical protein |
| WT | *SL1344_1780* | 1.45 | 2.4E-03 | *NA* | conserved hypothetical protein |
| WT | *SL1344_1784* | -3.00 | 2.4E-09 | | |
| WT | *SL1344_1811* | 0.72 | 1.9E-02 | *NA* | conserved hypothetical protein |
| WT | *SL1344_1813* | 0.47 | 3.0E-02 | *opdB* | oligopeptidase |
| WT | *SL1344_1815* | 0.68 | 4.8E-03 | *yebF* | hypothetical exported protein |
| WT | *SL1344_1846* | -1.34 | 3.7E-10 | *NA* | conserved hypothetical protein |
| WT | *SL1344_1847* | -2.00 | 3.3E-02 | *flhE* | flagellar protein FlhE precursor |
| WT | *SL1344_1848* | -2.32 | 7.7E-08 | *flhAa* | flagellar biosynthesis protein FlhA |
| WT | *SL1344_1849* | -2.38 | 7.2E-09 | *flhB* | flagellar biosynthetic protein FlhB |
| WT | *SL1344_1850* | -3.44 | 2.5E-25 | *cheZ* | chemotaxis protein CheZ |
| WT | *SL1344_1851* | -3.59 | 1.1E-24 | *cheY* | chemotaxis protein CheY |
| WT | *SL1344_1852* | -3.71 | 1.7E-19 | *cheB* | Chemotaxis response regulator protein-glutamate methylesterase |
| WT | *SL1344_1853* | -3.45 | 3.2E-17 | *cheR* | chemotaxis protein methyltransferase |
| WT | *SL1344_1854* | -3.23 | 2.5E-23 | *cheM* | methyl-accepting chemotaxis protein II |
| WT | *SL1344_1855* | -3.07 | 1.3E-14 | *cheW* | purine binding chemotaxis protein |
| WT | *SL1344_1856* | -3.25 | 8.9E-16 | *cheA* | chemotaxis protein CheA |
| WT | *SL1344_1857* | -3.24 | 1.8E-21 | *motB* | motility protein B |
| WT | *SL1344_1858* | -3.21 | 1.2E-19 | *motA* | motility protein A |
| WT | *SL1344_1859* | -2.69 | 2.1E-33 | *flhC* | flagellar transcriptional activator |
| WT | *SL1344_1860* | -1.87 | 6.2E-25 | *flhD* | Transcriptional activator flhD. |
| WT | *SL1344_1862* | 3.72 | 1.9E-74 | *otsA* | trehalose-6-phosphate synthase |

| | | | | | |
|---|---|---|---|---|---|
| WT | *SL1344_1863* | 3.97 | 6.3E-61 | *otsB* | trehalose phosphatase |
| WT | *SL1344_1865* | 1.86 | 5.4E-09 | *ftnB* | ferritin-like protein |
| WT | *SL1344_1867* | -2.99 | 3.8E-49 | *NA* | hypothetical lipoprotein |
| WT | *SL1344_1868* | -1.23 | 5.9E-03 | *ftn* | ferritin |
| WT | *SL1344_1879* | -1.29 | 8.5E-07 | *sdiA* | cell-division regulatory protein |
| WT | *SL1344_1883* | -1.04 | 5.0E-04 | *fliY* | cystine-binding periplasmic protein (FliY) |
| WT | *SL1344_1884* | -2.39 | 2.9E-09 | *fliZ* | FliZ protein |
| WT | *SL1344_1885* | -2.34 | 9.0E-07 | *fliA* | RNA polymerase sigma transcription factor for flagellar operon |
| WT | *SL1344_1886* | -3.00 | 2.6E-07 | *tnpA_2b* | transposase |
| WT | *SL1344_1887* | -3.02 | 5.6E-14 | *fliB* | lysine-N-methylase (ec 2.1.1.-) (lysine N-methyltransferase) |
| WT | *SL1344_1888* | -4.01 | 3.2E-31 | *fliC* | flagellin |
| WT | *SL1344_1889* | -2.94 | 1.5E-19 | *fliD* | flagellar hook associated protein (FliD) |
| WT | *SL1344_1890* | -2.82 | 1.1E-14 | *fliS* | flagellar protein FliS |
| WT | *SL1344_1891* | -2.89 | 1.1E-17 | *fliT* | flagellar protein FliT |
| WT | *SL1344_1892* | -0.98 | 9.1E-03 | *amyA* | cytoplasmic alpha-amylase |
| WT | *SL1344_1897* | -2.84 | 4.0E-14 | *fliE* | flagellar hook-basal body complex protein FliE |
| WT | *SL1344_1898* | -2.90 | 1.7E-19 | *fliF* | flagellar basal-body M-ring protein |
| WT | *SL1344_1899* | -2.87 | 9.8E-17 | *fliG* | flagellar motor switch protein FliG |
| WT | *SL1344_1900* | -2.95 | 1.8E-15 | *fliH* | flagellar assembly protein FliH |
| WT | *SL1344_1901* | -3.14 | 1.8E-14 | *fliI* | flagellum-specific ATP synthase |
| WT | *SL1344_1902* | -3.02 | 5.0E-14 | *fliJ* | flagellar biosynthesis protein |
| WT | *SL1344_1903* | -3.04 | 1.0E-14 | *fliK* | flagellar hook-length control protein |
| WT | *SL1344_1904* | -2.72 | 2.0E-12 | *fliL* | flagella biosynthesis protein |
| WT | *SL1344_1905* | -2.68 | 7.2E-12 | *fliM* | flagellar motor switch protein FliM |
| WT | *SL1344_1906* | -2.57 | 5.2E-09 | *fliN* | flagellar motor switch protein FliN |
| WT | *SL1344_1907* | -2.70 | 1.4E-11 | *fliO* | flagellar biosynthesis protein |
| WT | *SL1344_1908* | -2.70 | 1.1E-12 | *fliP* | flagellar biosynthetic protein FliP |
| WT | *SL1344_1909* | -2.21 | 3.2E-05 | *fliQ* | flagellar biosynthetic protein FliQ |
| WT | *SL1344_1910* | -2.60 | 2.1E-07 | *fliR* | flagellar biosynthetic protein FliR |
| WT | *SL1344_1911* | 1.72 | 9.2E-07 | *rcsA* | colanic acid capsullar biosynthesis activation protein A |
| WT | *SL1344_1914* | 1.89 | 8.7E-07 | *mngB* | Mannosyl-3-phosphoglycerate phosphatase |
| WT | *SL1344_1915* | 1.66 | 8.7E-16 | *gcpA* | Biofilm formation in nutrient-deficient medium, ATM |
| WT | *SL1344_1916* | 1.75 | 6.0E-07 | *NA* | conserved hypothetical protein |
| WT | *SL1344_1997* | -1.87 | 4.4E-02 | *cbiQ* | hypothetical cobalt transport protein |
| WT | *SL1344_1999* | -1.74 | 3.7E-02 | *cbiM* | cobalamin biosynthesis protein |
| WT | *SL1344_2002* | -1.88 | 3.6E-02 | *cbiJ* | cobalt-precorrin-6a reductase (ec 1.3.1.-) |
| WT | *SL1344_2026* | -1.83 | 9.1E-03 | *pduO* | propanediol utilization protein |
| WT | *SL1344_2027* | -1.41 | 2.2E-02 | *pduP* | hypothetical CoA-dependent proprionaldehyde dehydrogenase |

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|---|---|---|---|---|---|
| WT | *SL1344_2028* | -2.14 | 5.2E-03 | *pduQ* | hypothetical propanol dehydrogenase |
| WT | *SL1344_2043* | -1.74 | 6.3E-07 | *sopA* | Type III secretion system effector protein SopA-required for invasion |
| WT | *SL1344_2056* | 1.67 | 3.5E-13 | *wzzB* | lipopolysaccharide O-antigen chain length regulator |
| WT | *SL1344_2057* | 0.98 | 4.2E-03 | *udg* | UDP-glucose 6-dehydrogenase |
| WT | *SL1344_2075* | 0.79 | 1.9E-05 | *galF* | UTP-glucose-1-phosphate uridylyltransferase |
| WT | *SL1344_2076* | 2.22 | 2.4E-07 | *wcaM* | hypothetical exported protein |
| WT | *SL1344_2077* | 2.62 | 6.8E-07 | *wcaL* | hypothetical glycosyltransferase |
| WT | *SL1344_2078* | 2.91 | 1.2E-06 | *wcaK* | colanic acid biosynthesis protein |
| WT | *SL1344_2079* | 2.73 | 4.0E-07 | *wzx* | hypothetical transmembrane transport protein |
| WT | *SL1344_2080* | 3.19 | 8.7E-08 | *wcaJ* | hypothetical extracellular polysaccharide biosynthesis protein |
| WT | *SL1344_2081* | 4.65 | 1.0E-33 | *cpsG* | phosphomannomutase |
| WT | *SL1344_2082* | 4.70 | 6.0E-28 | *cpsB* | mannose-1-phosphate guanylyltransferase |
| WT | *SL1344_2083* | 5.42 | 2.6E-29 | *wcaI* | hypothetical glycosyltransferase |
| WT | *SL1344_2084* | 4.31 | 2.9E-12 | *gmm* | hypothetical O-antigen biosynthesis protein |
| WT | *SL1344_2085* | 4.78 | 1.7E-28 | *fcl* | GDP-fucose synthetase |
| WT | *SL1344_2086* | 4.75 | 4.0E-31 | *gmd* | GDP-mannose 4,6-dehydratase |
| WT | *SL1344_2087* | 5.88 | 5.2E-09 | *wcaF* | acetyltransferase |
| WT | *SL1344_2088* | 3.25 | 9.9E-14 | *wcaE* | glycosyltransferase |
| WT | *SL1344_2089* | 3.83 | 3.0E-18 | *wcaD* | colanic acid polymerase |
| WT | *SL1344_2090* | 1.70 | 4.7E-02 | *wcaC* | glycosyltransferase |
| WT | *SL1344_2091* | 3.55 | 1.9E-09 | *wcaB* | hypothetical acetyltransferase |
| WT | *SL1344_2092* | 3.56 | 5.9E-12 | *wcaA* | colanic acid biosynthesis glycosyl transferase |
| WT | *SL1344_2093* | 4.43 | 3.1E-15 | *wzc* | tyrosine-protein kinase |
| WT | *SL1344_2094* | 4.79 | 5.2E-08 | *wzb* | hypothetical protein-tyrosine phosphatase |
| WT | *SL1344_2095* | 4.37 | 2.7E-15 | *wza* | hypothetical polysaccharide export protein |
| WT | *SL1344_2101* | 1.66 | 1.9E-05 | *alkA* | DNA-3-methyladenine glycosidase II |
| WT | *SL1344_2108* | -0.50 | 2.9E-02 | *baeR* | hypothetical two-component system response regulator |
| WT | *SL1344_2117* | 2.90 | 8.2E-14 | *yegS* | conserved hypothetical protein |
| WT | *SL1344_2118* | 3.42 | 7.6E-24 | *fbaB* | fructose-bisphosphate aldolase class I |
| WT | *SL1344_2125* | 0.75 | 1.0E-03 | *NA* | conserved hypothetical protein |
| WT | *SL1344_2138* | 1.50 | 1.2E-03 | *yehV* | hypothetical transcriptional regulator |
| WT | *SL1344_2140* | 2.62 | 2.2E-09 | *yehW* | hypothetical permease transmembrane component |
| WT | *SL1344_2141* | 1.82 | 1.0E-10 | *yehX* | ABC transporter ATP-binding protein |
| WT | *SL1344_2142* | 1.94 | 1.2E-18 | *yehY* | hypothetical permease transmembrane component |
| WT | *SL1344_2143* | 2.17 | 9.5E-21 | *yehZ* | hypothetical periplasmic protein |
| WT | *SL1344_2145* | 0.66 | 1.6E-04 | *dld* | D-lactate dehydrogenase |
| WT | *SL1344_2149* | 1.64 | 3.9E-15 | *yohF* | hypothetical oxidoreductase |
| WT | *SL1344_2182* | -2.91 | 1.8E-02 | *fruK* | 1-phosphofructokinase |

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|---|---|---|---|---|---|
| WT | *SL1344_2183* | -3.02 | 2.9E-02 | *fruB* | pts system, fructose-specific IIA/FPR component |
| WT | *SL1344_2185* | -1.89 | 2.0E-02 | | |
| WT | *SL1344_2186* | -2.12 | 4.5E-03 | | |
| WT | *SL1344_2198* | -0.57 | 3.5E-02 | *bcr* | bicyclomycin resistance protein |
| WT | *SL1344_2208* | -1.23 | 1.5E-10 | *oafA* | hypothetical lipopolysaccharide modification acyltransferase |
| WT | *SL1344_2223A* | -4.15 | 4.7E-02 | *ccmG2* | cytochrome C-type biogenesis protein |
| WT | *SL1344_2231* | -0.93 | 3.8E-02 | *napF* | ferredoxin-type protein NapF |
| WT | *SL1344_2232* | 3.12 | 9.0E-43 | *eco* | Ecotin precursor. |
| WT | *SL1344_2235* | -0.87 | 1.5E-02 | *ada* | ADA regulatory protein |
| WT | *SL1344_2236* | -0.68 | 6.1E-03 | *apbE* | thiamine biosynthesis protein |
| WT | *SL1344_2258* | 0.77 | 1.8E-02 | *NA* | hypothetical 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase |
| WT | *SL1344_2278* | -0.80 | 2.9E-04 | *menD* | menaquinone biosynthesis protein |
| WT | *SL1344_2280* | 2.63 | 7.5E-25 | *elaB* | conserved hypothetical protein |
| WT | *SL1344_2283* | -3.32 | 9.1E-28 | *NA* | hypothetical receptor/regulator protein |
| WT | *SL1344_2298* | -1.32 | 4.0E-02 | | |
| WT | *SL1344_2299* | -1.55 | 1.4E-11 | *lrhA* | NADH dehydrogenase operon transcriptional regulator |
| WT | *SL1344_2300* | -0.53 | 2.3E-02 | *yfbQ* | hypothetical aminotransferase |
| WT | *SL1344_2306* | -0.85 | 1.9E-03 | *ackA* | acetate kinase |
| WT | *SL1344_2307* | -0.83 | 8.3E-04 | *pta* | phosphate acetyltransferase |
| WT | *SL1344_2318* | 2.41 | 2.8E-08 | *yfcG* | hypothetical glutathione-S transferase |
| WT | *SL1344_2323* | -0.66 | 8.2E-03 | *hisJ* | histidine-binding periplasmic protein |
| WT | *SL1344_2362* | 2.69 | 2.5E-12 | *yfdC* | hypothetical membrane protein |
| WT | *SL1344_2369* | 1.00 | 2.1E-05 | *lpxP* | encodes the cold shock-induced palmitoleoyl transferase |
| WT | *SL1344_2373* | 1.08 | 2.3E-03 | *NA* | hypothetical decarboxylase |
| WT | *SL1344_2375* | 2.39 | 2.0E-18 | *ypeC* | conserved hypothetical protein |
| WT | *SL1344_2392* | 0.93 | 1.9E-03 | *cysZ* | hypothetical sulfate transport protein CysZ |
| WT | *SL1344_2393* | 1.40 | 2.4E-10 | *cysK* | cysteine synthase A |
| WT | *SL1344_2403* | 0.54 | 1.9E-02 | *cysM* | cysteine synthase B |
| WT | *SL1344_2404* | 2.14 | 1.5E-16 | *cysA* | sulphate transport ATP-binding protein CysA |
| WT | *SL1344_2405* | 1.88 | 2.6E-14 | *cysW* | sulphate transport system permease protein CysW |
| WT | *SL1344_2406* | 2.35 | 2.0E-13 | *cysU* | sulphate transport system permease protein CysT |
| WT | *SL1344_2407* | 2.66 | 4.7E-37 | *cysP* | thiosulphate-binding protein precursor |
| WT | *SL1344_2436* | 2.25 | 5.3E-24 | *tal* | Transaldolase |
| WT | *SL1344_2437* | 2.32 | 1.4E-24 | *tktB* | transketolase 2 |
| WT | *SL1344_2439* | 2.29 | 4.4E-19 | *ypfG* | hypothetical exported protein |
| WT | *SL1344_2441* | 0.93 | 4.0E-02 | *NA* | hypothetical exported protein |
| WT | *SL1344_2460* | -0.68 | 2.2E-02 | *uraA* | uracil permease (uracil transporter) |
| WT | *SL1344_2465* | 0.41 | 3.1E-02 | *ppx* | exopolyphosphatase |

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|---|---|---|---|---|---|
| WT | *SL1344_2471* | -0.60 | 1.7E-02 | *guaA* | GMP synthase [glutamine-hydrolyzing] |
| WT | *SL1344_2497* | -0.42 | 3.0E-02 | *sseBb* | enhanced serine sensitivity protein |
| WT | *SL1344_2507* | -0.49 | 2.8E-03 | *NA* | hypothetical RNA methyltransferase |
| WT | *SL1344_2547* | 0.82 | 6.9E-03 | | |
| WT | *SL1344_2552* | 1.20 | 5.5E-03 | *NA* | similar to a DNA recombinase |
| WT | *SL1344_2553* | 1.51 | 1.9E-05 | *NA* | predicted bacteriophage protein |
| WT | *SL1344_2558* | 0.80 | 2.3E-02 | *NA* | predicted bacteriophage protein |
| WT | *SL1344_2560* | 1.42 | 3.2E-03 | *NA* | predicted bacteriophage protein |
| WT | *SL1344_2562* | 0.93 | 3.2E-02 | *NA* | predicted bacteriophage protein |
| WT | *SL1344_2564* | 1.15 | 1.4E-02 | *NA* | predicted bacteriophage protein |
| WT | *SL1344_2566* | 1.04 | 2.6E-02 | *NA* | predicted bacteriophage protein |
| WT | *SL1344_2568* | 2.40 | 4.5E-06 | *NA* | predicted bacteriophage protein |
| WT | *SL1344_2569* | 1.51 | 1.7E-03 | *NA* | predicted bacteriophage tail protein |
| WT | *SL1344_2570* | 0.89 | 3.6E-02 | *NA* | predicted bacteriophage protein |
| WT | *SL1344_2572* | 1.15 | 2.7E-03 | *NA* | predicted bacteriophage protein |
| WT | *SL1344_2587* | 1.03 | 2.5E-02 | *NA* | predicted bacteriophage protein |
| WT | *SL1344_2589* | 1.34 | 6.5E-04 | *NA* | predicted bacteriophage protein |
| WT | *SL1344_2590* | 1.34 | 9.9E-04 | *gpP* | predicted bacteriophage replication protein P |
| WT | *SL1344_2591* | 1.44 | 1.1E-03 | *gpO* | bacteriophage replication protein |
| WT | *SL1344_2594* | -0.50 | 4.6E-02 | *NA* | predicted bacteriophage protein |
| WT | *SL1344_2597* | 1.24 | 3.7E-03 | *recEb* | exodeoxyribonuclease VIII |
| WT | *SL1344_2619* | 1.40 | 4.5E-03 | *NA* | conserved hypothetical protein |
| WT | *SL1344_2626* | 1.13 | 7.8E-06 | *NA* | conserved hypothetical protein |
| WT | *SL1344_2643* | 0.96 | 3.1E-02 | *gpD* | bacteriophage late control gene |
| WT | *SL1344_2647* | -0.40 | 2.0E-02 | *trmD* | tRNA (guanine-N1) methyltransferase |
| WT | *SL1344_2649* | -0.45 | 3.5E-02 | *rps16* | 30S ribosomal protein S16. Chloroplast 30S ribosomal protein S16. |
| WT | *SL1344_2661* | 1.62 | 4.1E-11 | *bapA* | large repetitive protein |
| WT | *SL1344_2663* | 1.42 | 2.7E-02 | *NA* | hypothetical type I secretion protein, ATP-binding protein |
| WT | *SL1344_2674* | -4.50 | 2.1E-44 | | |
| WT | *SL1344_2675* | 1.17 | 5.7E-03 | *NA* | hypothetical bacteriophage tail fibre protein |
| WT | *SL1344_2698* | -0.56 | 6.8E-03 | *NA* | predicted bacteriophage protein |
| WT | *SL1344_2730* | -1.80 | 4.8E-03 | *NA* | hypothetical ATPase |
| WT | *SL1344_2731* | -1.67 | 4.7E-02 | *NA* | conserved hypothetical protein |
| WT | *SL1344_2741* | 3.46 | 7.8E-03 | *NA* | hypothetical glucose-6-phosphate isomerase |
| WT | *SL1344_2756* | -1.93 | 2.4E-05 | *fljB* | flagellin |
| WT | *SL1344_2757* | 1.26 | 9.0E-08 | *hin* | DNA-invertase hin |
| WT | *SL1344_2758* | -2.02 | 5.6E-08 | *iroB* | hypothetical glycosyltransferase |
| WT | *SL1344_2759* | -1.08 | 2.3E-03 | *iroC* | hypothetical ABC transporter protein |

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|---|---|---|---|---|---|
| WT | *SL1344_2763* | 0.50 | 3.0E-02 | *pipB2* | Type III secretion system effector protein, Contributes to Sif formation |
| WT | *SL1344_2774* | 1.71 | 4.9E-02 | *ygaF* | hypothetical GAB DTP gene cluster repressor |
| WT | *SL1344_2779* | 3.12 | 3.5E-74 | *ygaU* | conserved hypothetical protein |
| WT | *SL1344_2780* | 2.68 | 2.1E-10 | *yqaE* | conserved hypothetical protein |
| WT | *SL1344_2785* | 5.02 | 2.3E-54 | *ygaC* | conserved hypothetical protein |
| WT | *SL1344_2786* | 4.54 | 6.3E-62 | *ygaM* | conserved hypothetical protein |
| WT | *SL1344_2794* | 0.99 | 5.4E-03 | *proV* | glycine betaine/l-proline transport ATP-binding protein |
| WT | *SL1344_2796* | 0.86 | 3.0E-06 | *proX* | glycine betaine-binding periplasmic protein precursor |
| WT | *SL1344_2839* | 0.92 | 4.7E-04 | *fhlA* | transcriptional activator of the formate hydrogenlyase system |
| WT | *SL1344_2846* | -2.42 | 3.8E-10 | *sprB* | AraC-family transcriptional regulator |
| WT | *SL1344_2847* | -2.28 | 2.5E-19 | *hilC* | AraC-family transcriptional regulator |
| WT | *SL1344_2850* | -1.41 | 8.3E-08 | *orgA* | oxygen-regulated invasion protein |
| WT | *SL1344_2851* | -1.85 | 4.5E-23 | *prgK* | type III secretion system apparatus |
| WT | *SL1344_2852* | -2.72 | 8.7E-42 | *prgJ* | type III secretion system apparatus |
| WT | *SL1344_2853* | -2.84 | 9.1E-16 | *prgI* | type III secretion system apparatus |
| WT | *SL1344_2854* | -3.17 | 1.7E-33 | *prgH* | type III secretion apparatus component |
| WT | *SL1344_2855* | -0.66 | 6.6E-03 | *hilD* | AraC-family transcriptional regulator |
| WT | *SL1344_2856* | -1.91 | 4.5E-08 | *hilA* | invasion protein regulator |
| WT | *SL1344_2857* | -0.93 | 2.9E-02 | *iagB* | cell invasion protein |
| WT | *SL1344_2861* | -1.19 | 1.5E-17 | *sipA* | pathogenicity island 1 Type III secretion system effector protein |
| WT | *SL1344_2862* | -1.95 | 5.8E-24 | *sipD* | pathogenicity island 1 Type III secretion system apparatus-part of Translocon |
| WT | *SL1344_2863* | -2.13 | 2.1E-35 | *sipC* | pathogenicity island 1 Type III secretion system effector protein |
| WT | *SL1344_2864* | -2.25 | 2.9E-33 | *sipB* | pathogenicity island 1 Type III secretion system effector protein |
| WT | *SL1344_2865* | -2.51 | 3.5E-22 | *sicA* | type III secretion-associated chaperone |
| WT | *SL1344_2866* | -1.66 | 9.7E-13 | *spaS* | type III secretion system secretory apparatus |
| WT | *SL1344_2868* | -3.95 | 4.5E-03 | *spaQ* | type III secretion system secretory apparatus |
| WT | *SL1344_2869* | -2.02 | 6.3E-17 | *spaP* | type III secretion system secretory apparatus |
| WT | *SL1344_2870* | -2.05 | 8.2E-09 | *spaO* | surface presentation of antigens protein (associated with type III secretion ) |
| WT | *SL1344_2871* | -2.14 | 1.4E-14 | *invJ* | surface presentation of antigens protein (associated with type III secretion) |
| WT | *SL1344_2872* | -2.33 | 1.6E-19 | *invI* | type III secretion system secretory apparatus |
| WT | *SL1344_2873* | -2.10 | 4.2E-12 | *invC* | secretory apparatus ATP synthase (associated with virulence) |
| WT | *SL1344_2874* | -2.14 | 2.3E-20 | *invB* | chaperone protein for type III secretion system effectors |
| WT | *SL1344_2875* | -2.15 | 4.9E-12 | *invA* | secretory apparatus of type III secretion system |
| WT | *SL1344_2876* | -3.39 | 2.2E-30 | *invE* | cell invasion protein |
| WT | *SL1344_2877* | -3.55 | 8.6E-27 | *invG* | type III secretion system secretory apparatus |
| WT | *SL1344_2878* | -3.88 | 1.8E-26 | *invF* | AraC-family regulatory protein |
| WT | *SL1344_2879* | -1.62 | 4.1E-07 | | |
| WT | *SL1344_2887* | 2.27 | 1.5E-02 | *NA* | conserved hypothetical protein |

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|---|---|---|---|---|---|
| WT | *SL1344_2903* | 1.45 | 4.0E-15 | *rpoS* | RNA polymerase sigma subunit RpoS (sigma-38) |
| WT | *SL1344_2904* | 1.39 | 3.5E-09 | *nlpD* | lipoprotein NlpD precursor |
| WT | *SL1344_2912* | 1.70 | 4.8E-04 | *cysC* | Adenylylsulfate kinase |
| WT | *SL1344_2913* | 1.85 | 8.1E-16 | *cysN* | Sulfate adenylyltransferase subunit 1 |
| WT | *SL1344_2914* | 2.39 | 1.5E-09 | *cysD* | ATP sulfurylase (ATP:sulfate adenyltransferase) |
| WT | *SL1344_2915* | 0.94 | 1.6E-02 | *iap* | alkaline phosphatase isozyme conversion protein |
| WT | *SL1344_2925* | 2.15 | 2.3E-11 | *cysH* | Phosphoadenosine phosphosulfate reductase |
| WT | *SL1344_2926* | 2.46 | 1.6E-16 | *cysI* | sulfite reductase (NADPH) hemoprotein alpha subunit |
| WT | *SL1344_2927* | 2.77 | 2.4E-26 | *cysJ* | sulfite reductase (NADPH) flavoprotein beta subunit |
| WT | *SL1344_2963* | 3.94 | 4.7E-37 | *ygdI* | possible lipoprotein |
| WT | *SL1344_2985* | 1.82 | 7.1E-09 | *ygdR* | possible lipoprotein |
| WT | *SL1344_2986* | 0.64 | 1.3E-03 | *tas* | possible oxidoreductase |
| WT | *SL1344_2991* | 0.59 | 3.5E-02 | *lysA* | diaminopimelate decarboxylase |
| WT | *SL1344_3041* | 2.50 | 2.7E-16 | *yggE* | conserved hypothetical protein |
| WT | *SL1344_3043* | 1.24 | 1.5E-05 | *yggB* | hypothetical membrane protein |
| WT | *SL1344_3044* | -0.50 | 1.1E-02 | *fba* | fructose 1,6-bisphosphate aldolase |
| WT | *SL1344_3046* | -0.84 | 3.1E-03 | *epd* | D-erythrose 4-phosphate dehydrogenase |
| WT | *SL1344_3053* | 1.69 | 5.0E-16 | *yggG* | conserved hypothetical protein |
| WT | *SL1344_3112* | -3.28 | 2.5E-73 | *NA* | annotation |
| WT | *SL1344_3114* | 0.71 | 1.1E-02 | *yghU* | possible transferase |
| WT | *SL1344_3117* | -1.15 | 9.5E-06 | *hybG* | hydrogenase-2 component protein |
| WT | *SL1344_3118* | -1.44 | 6.8E-05 | *hybF* | hydrogenase-2 component protein |
| WT | *SL1344_3119* | -1.11 | 3.7E-03 | *hybE* | hydrogenase-2 component protein |
| WT | *SL1344_3120* | -1.20 | 1.0E-05 | *hybD* | hydrogenase-2 component protein |
| WT | *SL1344_3121* | -1.16 | 4.3E-10 | *hybC* | hydrogenase-2 large subunit |
| WT | *SL1344_3122* | -1.72 | 1.9E-09 | *hybB* | probable hydrogenase-2 cytochrome b subunit |
| WT | *SL1344_3123* | -2.45 | 1.1E-08 | *hybA* | hydrogenase-2 small subunit |
| WT | *SL1344_3124* | -1.78 | 9.4E-13 | *hypO* | hydrogenase-2 small chain protein |
| WT | *SL1344_3125* | -3.20 | 1.5E-28 | *yghW* | conserved hypothetical protein |
| WT | *SL1344_3126* | -3.13 | 1.0E-23 | *NA* | methyl-accepting chemotaxis protein |
| WT | *SL1344_3128* | -1.79 | 1.3E-12 | *NA* | exported protein |
| WT | *SL1344_3129* | -1.86 | 1.1E-28 | *NA* | annotation |
| WT | *SL1344_3130* | -1.88 | 2.5E-16 | *NA* | annotation |
| WT | *SL1344_3131* | 1.15 | 2.3E-08 | *yghA* | possible oxidoreductase |
| WT | *SL1344_3141* | 0.69 | 3.8E-03 | *NA* | conserved hypothetical protein |
| WT | *SL1344_3176* | 0.96 | 4.4E-10 | *ygiM* | hypothetical signal transduction protein |
| WT | *SL1344_3177* | 0.58 | 2.5E-03 | *cca* | tRNA nucleotidyltransferase |
| WT | *SL1344_3189* | -3.98 | 2.0E-21 | *NA* | methyl-accepting chemotaxis protein II |

| | | | | | |
|---|---|---|---|---|---|
| WT | *SL1344_3190* | -3.34 | 3.3E-03 | *aer* | aerotaxis receptor protein |
| WT | *SL1344_3191* | 0.90 | 3.2E-02 | *oat* | probable aminotransferase |
| WT | *SL1344_3201* | 1.15 | 6.8E-10 | *yqjC* | hypothetical exported protein |
| WT | *SL1344_3202* | 1.14 | 2.8E-07 | *yqjE* | hypothetical membrane protein |
| WT | *SL1344_3203* | 1.76 | 9.0E-03 | *yqjK* | conserved hypothetical protein |
| WT | *SL1344_3205* | 1.19 | 8.6E-06 | *yqjG* | conserved hypothetical protein |
| WT | *SL1344_3206* | 0.81 | 1.3E-02 | *yhaH* | hypothetical membrane protein |
| WT | *SL1344_3212* | -1.18 | 3.5E-04 | *tdcG* | L-serine dehydratase |
| WT | *SL1344_3213* | -2.06 | 6.0E-10 | *tdcE* | probable formate acetyltransferase |
| WT | *SL1344_3214* | -2.15 | 1.7E-04 | *tdcD* | propionate kinase |
| WT | *SL1344_3215* | -1.58 | 1.1E-08 | *tdcC* | threonine/serine transporter |
| WT | *SL1344_3216* | -1.15 | 1.1E-04 | *tdcB* | catabolic threonine dehydratase |
| WT | *SL1344_3241* | 0.99 | 7.4E-03 | *yraR* | conserved hypothetical protein |
| WT | *SL1344_3242* | 5.17 | 5.2E-22 | *yhbO* | conserved hypothetical protein |
| WT | *SL1344_3249* | 0.77 | 1.9E-02 | *yhbW* | possible monooxygenase |
| WT | *SL1344_3278* | 0.84 | 7.6E-03 | *nlp* | Ner-like regulatory protein |
| WT | *SL1344_3281* | 0.74 | 7.3E-03 | *yrbB* | possible anti-sigma factor antagonist |
| WT | *SL1344_3282* | 0.64 | 9.5E-06 | *yrbC* | possible exported protein |
| WT | *SL1344_3335* | 1.86 | 1.4E-25 | *yhcO* | conserved hypothetical protein |
| WT | *SL1344_3365* | 2.31 | 7.4E-22 | *yhdV* | possible lipoprotein |
| WT | *SL1344_3366* | 1.18 | 2.7E-06 | *yrdA* | hypothetical transferase |
| WT | *SL1344_3377* | 0.60 | 1.8E-02 | *mscL* | large-conductance mechanosensitive channel |
| WT | *SL1344_3387* | -0.46 | 3.3E-02 | *prlA* | preprotein translocase subunit |
| WT | *SL1344_3393* | -0.46 | 5.0E-02 | *rpsH* | 30S ribosomal subunit protein S8 |
| WT | *SL1344_3399* | -0.50 | 4.0E-02 | *rpmC* | 50S ribosomal subunit protein L29 |
| WT | *SL1344_3400* | -0.53 | 2.7E-03 | *rplP* | 50S ribosomal subunit protein L16 |
| WT | *SL1344_3403* | -0.54 | 3.4E-02 | *rpsS* | 30S ribosomal subunit protein S19 |
| WT | *SL1344_3404* | -0.54 | 3.3E-02 | *rplB* | 50S ribosomal subunit protein L2 |
| WT | *SL1344_3405* | -0.55 | 4.6E-02 | *rplW* | 50S ribosomal subunit protein L23 |
| WT | *SL1344_3407* | -0.61 | 1.8E-02 | *rplC* | 50S ribosomal subunit protein L3 |
| WT | *SL1344_3410* | 1.30 | 1.1E-05 | *bfr* | bacterioferritin |
| WT | *SL1344_3412* | -0.40 | 3.7E-02 | *tufA* | elongation factor Tu |
| WT | *SL1344_3415* | -0.44 | 2.9E-02 | *rpsL* | 30S ribosomal subunit protein S12 |
| WT | *SL1344_3437* | 1.43 | 2.9E-08 | *fic* | cell filamentation protein Fic |
| WT | *SL1344_3438* | 1.56 | 2.6E-04 | *yhfG* | conserved hypothetical protein |
| WT | *SL1344_3495* | 0.55 | 1.4E-02 | *NA* | hypothetical membrane protein |
| WT | *SL1344_3501* | 0.99 | 6.6E-05 | *glgP* | glycogen phosphorylase |
| WT | *SL1344_3502* | 1.43 | 1.0E-05 | *glgA* | glycogen synthase |

| | | | | | |
|---|---|---|---|---|---|
| WT | *SL1344_3503* | 1.38 | 3.9E-05 | *glgC* | glucose-1-phosphate adenylyltransferase |
| WT | *SL1344_3504* | 1.91 | 5.3E-14 | *glgX* | glycogen operon protein |
| WT | *SL1344_3505* | 1.89 | 8.6E-25 | *glgB* | 1,4-alpha-glucan branching enzyme |
| WT | *SL1344_3517* | 1.05 | 5.0E-06 | *ggt* | gamma-glutamyltranspeptidase precursor |
| WT | *SL1344_3522* | 1.60 | 2.1E-02 | *ugpA* | glycerol-3-phosphate transport system permease protein |
| WT | *SL1344_3523* | 1.42 | 5.0E-06 | *ugpB* | glycerol-3-phosphate-binding periplasmic protein |
| WT | *SL1344_3542* | -3.07 | 2.9E-12 | *tcp* | methyl-accepting chemotaxis citrate transducer |
| WT | *SL1344_3545* | 0.68 | 5.9E-03 | *NA* | hypothetical lipoprotein |
| WT | *SL1344_3547* | 1.29 | 5.5E-05 | *yhhT* | hypothetical membrane protein |
| WT | *SL1344_3555* | 0.77 | 3.7E-02 | *uspB* | universal stress protein B |
| WT | *SL1344_3569* | -1.05 | 1.5E-03 | *NA* | hypothetical membrane protein |
| WT | *SL1344_3573* | 1.07 | 7.4E-03 | *yhjD* | hypothetical membrane protein |
| WT | *SL1344_3576* | -3.86 | 7.5E-30 | *yhjH* | conserved hypothetical protein |
| WT | *SL1344_3582* | 0.57 | 8.1E-03 | *bcsC* | probable endoglucanase precursor |
| WT | *SL1344_3583* | 0.66 | 2.1E-03 | *yhjN* | hypothetical polysaccharide biosynthesis protein subunit B |
| WT | *SL1344_3584* | 0.58 | 2.6E-02 | *bcsA* | hypothetical polysaccharide biosynthesis protein catalytic subunit |
| WT | *SL1344_3585* | 0.57 | 6.6E-03 | *yhjQ* | conserved hypothetical protein |
| WT | *SL1344_3589* | 0.80 | 4.2E-05 | *yhjU* | hypothetical membrane protein |
| WT | *SL1344_3611* | 2.72 | 1.1E-63 | *yiaD* | hypothetical outer membrane protein |
| WT | *SL1344_3614* | 3.78 | 8.2E-42 | *yiaG* | hypothetical HTH-type transcriptional regulator |
| WT | *SL1344_3622* | 2.00 | 7.1E-13 | *NA* | hypothetical lipoprotein |
| WT | *SL1344_3628* | 0.89 | 1.0E-03 | *bax* | hypothetical exported amidase |
| WT | *SL1344_3632* | 0.48 | 3.4E-02 | *yiaJ* | hypothetical transcriptional regulator |
| WT | *SL1344_3646* | 1.80 | 3.2E-10 | *NA* | hypothetical sugar kinase |
| WT | *SL1344_3649* | 0.71 | 3.4E-04 | *yibF* | hypothetical glutathione transferase |
| WT | *SL1344_3653* | 1.58 | 5.1E-05 | *NA* | annotation |
| WT | *SL1344_3656* | 0.63 | 8.0E-03 | *sadA* | autotransporter |
| WT | *SL1344_3678* | -0.41 | 4.0E-02 | *rfaC* | lipopolysaccharide heptosyltransferase-1 |
| WT | *SL1344_3684* | -0.55 | 3.2E-02 | *rfaI* | lipopolysaccharide 1,3-galactosyltransferase |
| WT | *SL1344_3727* | 1.96 | 6.2E-12 | *cigR* | hypothetical inner membrane protein |
| WT | *SL1344_3731* | 0.57 | 1.1E-02 | *NA* | conserved hypothetical protein |
| WT | *SL1344_3739* | 3.85 | 5.9E-23 | *NA* | hypothetical secreted protein |
| WT | *SL1344_3817* | 1.03 | 2.0E-05 | *yieF* | conserved hypothetical protein |
| WT | *SL1344_3859* | -0.47 | 3.0E-02 | *yifE* | conserved hypothetical protein |
| WT | *SL1344_3880* | 0.40 | 3.7E-02 | *rffD* | UDP-ManNAc dehydrogenase |
| WT | *SL1344_3881* | 0.44 | 7.0E-03 | *rffG* | UDP-N-acetylglucosamine epimerase (UDP-GlcNAc-2-epimerase) |
| WT | *SL1344_3883* | 0.45 | 2.6E-02 | *rffC* | lipopolysaccharide biosynthesis protein |
| WT | *SL1344_3921* | 2.08 | 2.0E-22 | *dlhH* | hypothetical hydrolase |

| | | | | | |
|---|---|---|---|---|---|
| WT | *SL1344_3951* | -0.39 | 3.3E-02 | *hemN* | oxygen-independent coproporphyrinogen III oxidase |
| WT | *SL1344_3952* | -0.77 | 2.0E-03 | *glnG* | Two-component system, response regulator |
| WT | *SL1344_3953* | -0.85 | 1.9E-03 | *glnL* | Two-component system sensory histidine kinase |
| WT | *SL1344_3954* | -1.17 | 6.6E-03 | *glnA* | glutamine synthetase |
| WT | *SL1344_4009* | 1.50 | 9.7E-13 | *cpxP* | extracytoplasmic stress protein for protein-mediated toxicities |
| WT | *SL1344_4012* | 1.49 | 1.7E-05 | *sbp* | periplasmic sulphate binding protein |
| WT | *SL1344_4039* | -0.47 | 2.3E-02 | *menA* | menaquinone biosynthetic protein |
| WT | *SL1344_4093* | -0.35 | 2.3E-02 | *rpoC* | DNA-directed RNA polymerase, beta'-subunit |
| WT | *SL1344_4105* | 0.51 | 4.0E-02 | *nudC* | conserved hypothetical protein |
| WT | *SL1344_4107* | 0.60 | 1.7E-02 | *nfi* | hypothetical endonuclease |
| WT | *SL1344_4145* | 0.72 | 4.9E-02 | *NA* | predicted bacteriophage protein |
| WT | *SL1344_4158* | 4.88 | 7.3E-25 | *yjbE* | hypothetical exported protein |
| WT | *SL1344_4159* | 3.19 | 1.6E-20 | *yjbF* | hypothetical lipoprotein |
| WT | *SL1344_4160* | 3.39 | 1.0E-21 | *yjbG* | hypothetical exported protein |
| WT | *SL1344_4161* | 1.86 | 3.3E-13 | *yjbH* | hypothetical lipoprotein |
| WT | *SL1344_4176* | 2.35 | 7.5E-12 | *yjbJ* | conserved hypothetical protein |
| WT | *SL1344_4178* | 2.06 | 2.9E-41 | *NA* | hypothetical exported protein |
| WT | *SL1344_4181* | 1.14 | 1.1E-04 | *qor* | quinone oxidoreductase |
| WT | *SL1344_4193* | -2.39 | 1.3E-09 | *siiA* | type I secretion-related protein |
| WT | *SL1344_4194* | -2.99 | 8.5E-17 | *siiB* | hypothetical integral membrane protein |
| WT | *SL1344_4196* | -2.54 | 2.3E-06 | *siiD* | hypothetical type-I secretion protein |
| WT | *SL1344_4203* | 1.05 | 6.2E-03 | *NA* | hypothetical glutathione S transferase |
| WT | *SL1344_4205* | 0.77 | 6.1E-04 | *yjcE* | hypothetical sodium/hydrogen exchanger family protein |
| WT | *SL1344_4214* | -2.35 | 6.2E-15 | *nrfB* | penta-heme cytochrome c , subunit of nitrite reductase complex |
| WT | *SL1344_4227* | 1.50 | 1.7E-08 | *proP* | hypothetical amino acid permease |
| WT | *SL1344_4237* | -1.17 | 1.4E-02 | *fumB* | fumarate hydratase class I |
| WT | *SL1344_4238* | -1.32 | 2.7E-02 | *dcuB* | anaerobic C4-dicarboxylate transporter |
| WT | *SL1344_4239* | -1.64 | 1.3E-02 | | |
| WT | *SL1344_4247* | -0.81 | 1.6E-02 | *NA* | hypothetical membrane protein |
| WT | *SL1344_4249* | -2.03 | 9.9E-05 | | |
| WT | *SL1344_4250* | -3.94 | 2.7E-09 | *rtsB* | Regulator of flhDC |
| WT | *SL1344_4251* | -4.34 | 5.2E-19 | *rtsA* | Regulator of SPI-1 |
| WT | *SL1344_4259* | 0.86 | 9.6E-04 | *yjdC* | hypothetical transcriptional regulator |
| WT | *SL1344_4271* | -0.49 | 2.0E-03 | *efp* | elongation factor P |
| WT | *SL1344_4273* | 1.59 | 3.0E-08 | *ecnB* | entericidin B precursor |
| WT | *SL1344_4274* | -1.98 | 1.9E-18 | *ecnR* | transcriptional regulatory protein |
| WT | *SL1344_4276* | 1.94 | 1.6E-09 | *blc* | hypothetical lipoprotein |
| WT | *SL1344_4313* | 0.56 | 4.8E-02 | *yjfP* | conserved hypothetical protein |

| | | | | | |
|---|---|---|---|---|---|
| WT | *SL1344_4324* | -0.56 | 8.2E-03 | *rpsF* | 30s ribosomal protein S6 |
| WT | *SL1344_4337* | 0.54 | 3.7E-02 | *cysQ* | cysQ protein |
| WT | *SL1344_4339* | 1.72 | 5.9E-09 | *ytfK* | conserved hypothetical protein |
| WT | *SL1344_4416* | 3.23 | 3.5E-18 | *yjgB* | hypothetical alcohol dehydrogenase |
| WT | *SL1344_4440* | 0.93 | 1.8E-04 | *NA* | conserved hypothetical protein |
| WT | *SL1344_4450* | 3.32 | 7.5E-57 | *NA* | hypothetical aldehyde dehydrogenase |
| WT | *SL1344_4464* | -3.70 | 6.0E-21 | *tsr* | methyl-accepting chemotaxis protein |
| WT | *SL1344_4465* | -1.81 | 2.6E-03 | *NA* | hypothetical transcriptional regulatory protein |
| WT | *SL1344_4480* | 0.54 | 2.4E-02 | *NA* | conserved hypothetical protein |
| WT | *SL1344_4489* | 4.78 | 1.7E-188 | *osmY* | Putative periplasmic protein |
| WT | *SL1344_4490* | 1.05 | 8.2E-05 | *yjjU* | conserved hypothetical protein |
| WT | *SL1344_4509* | 0.65 | 1.5E-03 | *slt* | lytic murein transglycosylase |
| D56A | *SL1344_1029* | 1.69 | 6.0E-06 | *pipC* | cell invasion protein |
| D56A | *SL1344_1731* | 0.98 | 3.5E-02 | *dadA* | D-amino acid dehydrogenase small subunit |
| D56A | *SL1344_1784* | 1.62 | 1.8E-02 | | |
| D56A | *SL1344_1888* | -4.05 | 2.9E-68 | *fliC* | flagellin |
| D56A | *SL1344_2755* | 7.09 | 1.5E-122 | *fljA* | repressor of phase 1 flagellin gene |
| D56A | *SL1344_2756* | 7.34 | 1.6E-79 | *fljB* | flagellin |
| D56A | *SL1344_2758* | -2.70 | 1.1E-05 | *iroB* | hypothetical glycosyltransferase |
| D56A | *SL1344_2863* | 1.30 | 1.8E-02 | *sipC* | pathogenicity island 1 Type III secretion system effector protein |
| D56A | *SL1344_3088* | 1.37 | 1.2E-02 | *nupG* | nucleoside permease nupg (nucleoside-transport system protein) |
| D56A | *SL1344_3659* | 1.11 | 3.0E-02 | *lctD* | hypothetical L-lactate dehydrogenase |
| D56A | *SL1344_3850* | 1.50 | 2.6E-02 | *rbsC* | high affinity ribose transport protein |
| D56A | *SL1344_3852* | 1.13 | 1.8E-02 | *rbsK* | ribokinase |
| D56A | *SL1344_3853* | 1.19 | 1.1E-02 | *rbsR* | ribose operon repressor |
| D56A | *SL1344_4196* | 1.12 | 4.1E-02 | *siiD* | hypothetical type-I secretion protein |
| D56A | *SL1344_4461* | 0.86 | 1.9E-02 | *yjiA* | conserved hypothetical protein |
| D56A | *SL1344_4495* | 0.98 | 1.8E-02 | *deoA* | thymidine phosphorylase |
| M88A | *SL1344_0012* | -1.87 | 7.5E-05 | *dnaK* | Chaperone protein dnaK |
| M88A | *SL1344_0013* | -1.62 | 2.7E-04 | *dnaJ* | DnaJ protein |
| M88A | *SL1344_0192* | 1.51 | 1.8E-02 | *fhuA* | ferrichrome-iron receptor |
| M88A | *SL1344_0193* | 1.93 | 5.4E-04 | *fhuC* | ferrichrome transport ATP-binding protein FhuC |
| M88A | *SL1344_0194* | 1.94 | 3.5E-04 | *fhuD* | ferrichrome-binding periplasmic protein precursor |
| M88A | *SL1344_0195* | 1.75 | 7.0E-04 | *fhuB* | ferrichrome transport protein FhuB precursor |
| M88A | *SL1344_0444* | -1.13 | 6.7E-03 | *lon* | Lon protease |
| M88A | *SL1344_0480* | -1.82 | 5.8E-03 | *htpG* | heat shock protein HtpG |
| M88A | *SL1344_0573* | 2.50 | 1.4E-05 | *fepA* | ferrienterobactin receptor precursor |
| M88A | *SL1344_0574* | 2.43 | 9.2E-08 | *fes* | enterochelin esterase |

| | | | | | |
|---|---|---|---|---|---|
| M88A | *SL1344_0575* | 2.60 | 7.9E-03 | *ybdZ* | conserved hypothetical protein |
| M88A | *SL1344_0576* | 1.72 | 4.0E-04 | *entF* | enterobactin synthetase component F |
| M88A | *SL1344_0578* | 2.20 | 2.3E-02 | *fepC* | ferric enterobactin transport ATP-binding protein FepC |
| M88A | *SL1344_0580* | 2.05 | 1.7E-02 | *fepD* | ferric enterobactin transport protein FepD |
| M88A | *SL1344_0581* | 2.16 | 5.1E-04 | *ybdA* | hypothetical membrane protein p43 |
| M88A | *SL1344_0584* | 1.18 | 4.1E-02 | *entE* | 2,3-dihydroxybenzoate-AMP ligase |
| M88A | *SL1344_0622* | 0.96 | 4.9E-02 | *ybeF* | lysR-family transcriptional regulator |
| M88A | *SL1344_1109* | -1.38 | 8.2E-07 | *flgM* | negative regulator of flagellin synthesis (anti-sigma factor) |
| M88A | *SL1344_1141* | 1.86 | 2.4E-02 | *fhuE* | outer-membrane receptor for Fe(iii)-coprogen, fe(iii)-ferrioxamine b and fe(iii) |
| M88A | *SL1344_1149* | 1.50 | 9.8E-03 | *ycfJ* | hypothetical secreted protein |
| M88A | *SL1344_1181* | 1.42 | 1.2E-05 | *envE* | hypothetical lipoprotein |
| M88A | *SL1344_1182* | 1.37 | 1.6E-02 | *cspH* | cold shock protein (CspH) |
| M88A | *SL1344_1185* | 1.61 | 3.4E-02 | *pliC* | hypothetical secreted protein |
| M88A | *SL1344_1201* | 1.24 | 3.2E-02 | *NA* | hypothetical transcriptional regulator |
| M88A | *SL1344_1225* | -0.82 | 5.0E-02 | *gapA* | glyceraldehyde 3-phosphate dehydrogenase A |
| M88A | *SL1344_1235* | -1.43 | 4.5E-04 | *NA* | hypothetical exported protein |
| M88A | *SL1344_1280* | 1.43 | 6.1E-03 | *ydiE* | conserved hypothetical protein |
| M88A | *SL1344_1467* | -1.56 | 6.7E-03 | *hyaB2* | uptake hydrogenase-1 large subunit |
| M88A | *SL1344_1516* | 1.36 | 2.5E-02 | *NA* | hypothetical lipoprotein |
| M88A | *SL1344_1517* | 1.26 | 1.8E-02 | *NA* | possible ATP-binding protein |
| M88A | *SL1344_1637* | 2.47 | 1.1E-03 | *osmB* | osmotically inducible lipoprotein B precursor |
| M88A | *SL1344_1696* | 1.01 | 3.1E-02 | *ychP* | hypothetical invasin |
| M88A | *SL1344_1726* | -1.17 | 1.1E-03 | *ycgR* | conserved hypothetical protein |
| M88A | *SL1344_1765* | 1.12 | 1.2E-02 | *ftsI2* | penicillin-binding protein |
| M88A | *SL1344_1802* | 1.18 | 3.4E-02 | *NA* | hypothetical bacteriophage membrane protein |
| M88A | *SL1344_1842* | 1.50 | 8.4E-03 | *cutC* | hypothetical copper homeostasis protein |
| M88A | *SL1344_1855* | -1.05 | 3.2E-02 | *cheW* | purine binding chemotaxis protein |
| M88A | *SL1344_1858* | -1.10 | 2.9E-02 | *motA* | motility protein A |
| M88A | *SL1344_1859* | -0.97 | 2.2E-02 | *flhC* | flagellar transcriptional activator |
| M88A | *SL1344_1863* | 1.33 | 3.6E-02 | *otsB* | trehalose phosphatase |
| M88A | *SL1344_1868* | -1.71 | 1.3E-03 | *ftn* | ferritin |
| M88A | *SL1344_1888* | -1.24 | 9.6E-06 | *fliC* | flagellin |
| M88A | *SL1344_1924* | 1.79 | 2.3E-03 | *cspB* | cold shock protein |
| M88A | *SL1344_2080* | 2.77 | 1.9E-02 | *wcaJ* | hypothetical extracellular polysaccharide biosynthesis protein |
| M88A | *SL1344_2081* | 3.80 | 1.2E-04 | *cpsG* | phosphomannomutase |
| M88A | *SL1344_2082* | 3.45 | 5.1E-04 | *cpsB* | mannose-1-phosphate guanylyltransferase |
| M88A | *SL1344_2083* | 3.75 | 1.1E-03 | *wcaI* | hypothetical glycosyltransferase |
| M88A | *SL1344_2089* | 2.38 | 3.2E-02 | *wcaD* | colanic acid polymerase |

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|---|---|---|---|---|---|
| M88A | *SL1344_2092* | 1.98 | 4.3E-02 | *wcaA* | colanic acid biosynthesis glycosyl transferase |
| M88A | *SL1344_2176* | 1.98 | 3.2E-04 | *cirA* | colicin I receptor precursor |
| M88A | *SL1344_2265* | 0.90 | 1.9E-02 | *ais* | hypothetical protein (protein induced by aluminum) |
| M88A | *SL1344_2283* | -1.44 | 9.6E-06 | *NA* | hypothetical receptor/regulator protein |
| M88A | *SL1344_2369* | 1.98 | 4.9E-07 | *lpxP* | encodes the cold shock-induced palmitoleoyl transferase |
| M88A | *SL1344_2404* | 1.78 | 8.1E-04 | *cysA* | sulphate transport ATP-binding protein CysA |
| M88A | *SL1344_2405* | 1.65 | 1.2E-02 | *cysW* | sulphate transport system permease protein CysW |
| M88A | *SL1344_2620* | -1.26 | 2.3E-02 | *clpB* | ClpB protein (heat shock protein f84.1) |
| M88A | *SL1344_2654* | -1.05 | 9.6E-03 | *grpE* | heat shock protein GrpE (heat shock protein b25.3) (hsp24) |
| M88A | *SL1344_2656* | -0.84 | 2.5E-02 | *recN* | DNA repair protein |
| M88A | *SL1344_2785* | 2.66 | 4.0E-04 | *ygaC* | conserved hypothetical protein |
| M88A | *SL1344_2794* | 1.53 | 1.4E-02 | *proV* | glycine betaine/l-proline transport ATP-binding protein |
| M88A | *SL1344_2925* | 2.15 | 2.7E-04 | *cysH* | Phosphoadenosine phosphosulfate reductase |
| M88A | *SL1344_2926* | 1.99 | 4.0E-04 | *cysI* | sulfite reductase (NADPH) hemoprotein alpha subunit |
| M88A | *SL1344_2927* | 2.00 | 7.9E-03 | *cysJ* | sulfite reductase (NADPH) flavoprotein beta subunit |
| M88A | *SL1344_2991* | 1.22 | 2.3E-02 | *lysA* | diaminopimelate decarboxylase |
| M88A | *SL1344_3112* | -2.20 | 4.3E-08 | *NA* | annotation |
| M88A | *SL1344_3132* | 1.07 | 5.0E-02 | *exbD* | biopolymer transport ExbD protein |
| M88A | *SL1344_3189* | -1.38 | 1.1E-03 | *NA* | methyl-accepting chemotaxis protein II |
| M88A | *SL1344_3410* | 1.21 | 2.9E-02 | *bfr* | bacterioferritin |
| M88A | *SL1344_3473* | 1.33 | 9.9E-03 | *feoB* | ferrous iron transport protein B |
| M88A | *SL1344_3474* | 1.52 | 5.1E-04 | *yhgG* | conserved hypothetical protein |
| M88A | *SL1344_3576* | -1.40 | 5.8E-04 | *yhjH* | conserved hypothetical protein |
| M88A | *SL1344_3614* | 1.77 | 7.9E-03 | *yiaG* | hypothetical HTH-type transcriptional regulator |
| M88A | *SL1344_3775* | -1.98 | 2.9E-11 | *hslS* | heat shock protein B |
| M88A | *SL1344_3776* | -1.85 | 3.9E-05 | *hslT* | heat shock protein A |
| M88A | *SL1344_3859* | -1.10 | 4.5E-03 | *yifE* | conserved hypothetical protein |
| M88A | *SL1344_3987* | 1.43 | 2.5E-02 | *NA* | hypothetical lipoprotein |
| M88A | *SL1344_4009* | 2.43 | 1.5E-04 | *cpxP* | extracytoplasmic stress protein for protein-mediated toxicities |
| M88A | *SL1344_4040* | -1.16 | 1.4E-02 | *hslU* | heat shock protein |
| M88A | *SL1344_4041* | -1.17 | 4.2E-03 | *hslV* | heat shock protein |
| M88A | *SL1344_4251* | -1.40 | 2.4E-02 | *rtsA* | Regulator of SPI-1 |
| M88A | *SL1344_4464* | -1.03 | 2.5E-02 | *tsr* | methyl-accepting chemotaxis protein |
| M88A | *SL1344_4481* | 1.48 | 2.5E-02 | *fhuF* | ferric iron reductase protein |
| M88A | *SL1344_4489* | 1.54 | 1.5E-02 | *osmY* | Putative periplasmic protein |
| L108A | *SL1344_0012* | -1.74 | 7.6E-04 | *dnaK* | Chaperone protein dnaK |
| L108A | *SL1344_0013* | -1.58 | 2.0E-02 | *dnaJ* | DnaJ protein |
| L108A | *SL1344_0170* | 1.34 | 8.6E-04 | *gcd* | glucose dehydrogenase |

| | | | | | |
|---|---|---|---|---|---|
| L108A | *SL1344_0195* | 1.82 | 4.3E-02 | *fhuB* | ferrichrome transport protein FhuB precursor |
| L108A | *SL1344_0407* | -1.72 | 3.5E-06 | *tsx* | nucleoside-specific channel-forming protein tsx precursor |
| L108A | *SL1344_0497* | -1.18 | 1.8E-02 | *ybbN* | thioredoxin-like protein |
| L108A | *SL1344_0649* | -1.61 | 4.5E-05 | *NA* | hypothetical conserved hypothetical protein |
| L108A | *SL1344_0650* | -1.88 | 4.3E-03 | *rihA* | probable nucleoside hydrolase |
| L108A | *SL1344_0667* | -0.91 | 2.5E-02 | *nagE* | pts system, N-acetylglucosamine-specific IIABC component |
| L108A | *SL1344_0681* | -5.01 | 2.0E-02 | *NA* | possible 5-nitroimidazole antibiotic resistance |
| L108A | *SL1344_0682* | -6.00 | 7.1E-03 | *potE* | putrescine-ornithine antiporter |
| L108A | *SL1344_0683* | -6.09 | 1.1E-02 | *speF* | ornithine decarboxylase, inducible (ec 4.1.1.17) |
| L108A | *SL1344_0716* | -1.24 | 1.5E-03 | *sdhA* | succinate dehydrogenase flavoprotein subunit |
| L108A | *SL1344_0717* | -1.28 | 1.6E-03 | *sdhB* | succinate dehydrogenase iron-sulfur protein |
| L108A | *SL1344_0718* | -1.13 | 1.7E-02 | *sucA* | 2-oxoglutarate dehydrogenase E1 component |
| L108A | *SL1344_0720* | -1.07 | 2.6E-02 | *sucC* | succinyl-CoA synthetase beta chain |
| L108A | *SL1344_0721* | -1.02 | 2.6E-02 | *sucD* | succinyl-CoA synthetase alpha chain |
| L108A | *SL1344_0736* | 1.52 | 2.4E-02 | *ybgS* | hypothetical exported protein |
| L108A | *SL1344_0758* | -1.67 | 1.0E-04 | *modA* | molybdate-binding periplasmic protein precursor |
| L108A | *SL1344_0759* | -1.57 | 3.1E-04 | *modB* | molybdenum transport system permease protein ModB |
| L108A | *SL1344_0760* | -1.88 | 3.4E-06 | *modC* | molybdenum transport ATP-binding protein ModC |
| L108A | *SL1344_0767* | -1.17 | 4.5E-02 | *hutU* | urocanate hydratase |
| L108A | *SL1344_1029* | -1.94 | 2.1E-08 | *pipC* | cell invasion protein |
| L108A | *SL1344_1030* | -2.44 | 4.3E-11 | *sopB* | Type III secretion system effector protein. |
| L108A | *SL1344_1062* | -1.33 | 1.7E-03 | *putA* | proline dehydrogenase (proline oxidase) |
| L108A | *SL1344_1108* | -2.06 | 4.6E-12 | *flgN* | flagella synthesis protein FlgN |
| L108A | *SL1344_1109* | -2.28 | 2.8E-09 | *flgM* | negative regulator of flagellin synthesis (anti-sigma factor) |
| L108A | *SL1344_1111* | -1.19 | 8.2E-03 | *flgB* | hypothetical flagellar basal-body rod protein FlgB (proximal rod protein) |
| L108A | *SL1344_1112* | -1.08 | 1.7E-02 | *flgC* | hypothetical flagellar basal-body rod protein FlgC (proximal rod protein) |
| L108A | *SL1344_1113* | -1.08 | 5.8E-04 | *flgD* | flagellar hook formation protein FlgD |
| L108A | *SL1344_1114* | -1.27 | 7.6E-03 | *flgE* | flagellar hook protein FlgE |
| L108A | *SL1344_1115* | -1.25 | 2.3E-05 | *flgF* | hypothetical flagellar basal-body rod protein FlgF (proximal rod protein) |
| L108A | *SL1344_1116* | -1.24 | 1.9E-05 | *flgG* | flagellar basal-body rod protein FlgG (distal rod protein) |
| L108A | *SL1344_1117* | -1.04 | 7.0E-03 | *flgH* | Flagellar L-ring protein precursor |
| L108A | *SL1344_1118* | -0.91 | 2.4E-02 | *flgI* | Flagellar P-ring protein precursor |
| L108A | *SL1344_1120* | -2.00 | 9.1E-08 | *flgK* | flagellar hook-associated protein 1 |
| L108A | *SL1344_1121* | -1.90 | 2.2E-06 | *flgL* | flagellar hook-associated protein 3 |
| L108A | *SL1344_1181* | 2.08 | 3.7E-04 | *envE* | hypothetical lipoprotein |
| L108A | *SL1344_1235* | -2.97 | 1.7E-08 | *NA* | hypothetical exported protein |
| L108A | *SL1344_1263* | -1.50 | 3.7E-03 | *NA* | hypothetical outer membrane protein |
| L108A | *SL1344_1435* | -1.72 | 2.5E-04 | *rspA* | starvation sensing protein RspA |

| | | | | | |
|---|---|---|---|---|---|
| L108A | *SL1344_1490* | 1.40 | 4.0E-02 | *NA* | hypothetical hydrolase |
| L108A | *SL1344_1491* | 1.80 | 1.8E-02 | *NA* | hypothetical exported protein |
| L108A | *SL1344_1503* | -1.24 | 1.8E-02 | *ompD* | Outer membrane protein |
| L108A | *SL1344_1524* | -1.40 | 1.2E-04 | *srfA* | virulence protein |
| L108A | *SL1344_1525* | -1.16 | 1.3E-03 | *srfB* | virulence protein |
| L108A | *SL1344_1526* | -1.11 | 6.5E-04 | *srfC* | virulence protein |
| L108A | *SL1344_1556* | -3.37 | 4.4E-11 | *trg* | methyl-accepting chemotaxis protein III (mcp-iii) |
| L108A | *SL1344_1663* | -2.38 | 1.6E-02 | *ompW* | hypothetical outer membrane protein |
| L108A | *SL1344_1726* | -1.90 | 1.0E-05 | *ycgR* | conserved hypothetical protein |
| L108A | *SL1344_1730* | -1.03 | 9.2E-03 | *alr-a* | Alanine racemase |
| L108A | *SL1344_1731* | -1.13 | 1.8E-02 | *dadA* | D-amino acid dehydrogenase small subunit |
| L108A | *SL1344_1784* | -1.74 | 3.9E-02 | | |
| L108A | *SL1344_1849* | -1.08 | 5.2E-04 | *flhB* | flagellar biosynthetic protein FlhB |
| L108A | *SL1344_1850* | -2.13 | 6.7E-05 | *cheZ* | chemotaxis protein CheZ |
| L108A | *SL1344_1851* | -2.37 | 1.7E-06 | *cheY* | chemotaxis protein CheY |
| L108A | *SL1344_1852* | -2.55 | 4.9E-09 | *cheB* | Chemotaxis response regulator protein-glutamate methylesterase |
| L108A | *SL1344_1853* | -1.99 | 7.4E-06 | *cheR* | chemotaxis protein methyltransferase |
| L108A | *SL1344_1854* | -1.94 | 8.9E-05 | *cheM* | methyl-accepting chemotaxis protein II |
| L108A | *SL1344_1855* | -2.08 | 1.8E-04 | *cheW* | purine binding chemotaxis protein |
| L108A | *SL1344_1856* | -2.08 | 1.1E-05 | *cheA* | chemotaxis protein CheA |
| L108A | *SL1344_1857* | -2.25 | 3.1E-06 | *motB* | motility protein B |
| L108A | *SL1344_1858* | -2.07 | 8.9E-05 | *motA* | motility protein A |
| L108A | *SL1344_1859* | -1.58 | 1.6E-02 | *flhC* | flagellar transcriptional activator |
| L108A | *SL1344_1867* | -2.00 | 7.1E-05 | *NA* | hypothetical lipoprotein |
| L108A | *SL1344_1879* | -1.49 | 4.1E-03 | *sdiA* | cell-division regulatory protein |
| L108A | *SL1344_1883* | -0.98 | 1.5E-02 | *fliY* | cystine-binding periplasmic protein (FliY) |
| L108A | *SL1344_1884* | -1.36 | 7.6E-06 | *fliZ* | FliZ protein |
| L108A | *SL1344_1885* | -1.37 | 1.6E-02 | *fliA* | RNA polymerase sigma transcription factor for flagellar operon |
| L108A | *SL1344_1887* | -1.74 | 1.6E-09 | *fliB* | lysine-N-methylase (ec 2.1.1.-) (lysine N-methyltransferase) |
| L108A | *SL1344_1888* | -2.74 | 7.2E-14 | *fliC* | flagellin |
| L108A | *SL1344_1889* | -1.99 | 5.5E-13 | *fliD* | flagellar hook associated protein (FliD) |
| L108A | *SL1344_1890* | -1.84 | 6.2E-10 | *fliS* | flagellar protein FliS |
| L108A | *SL1344_1891* | -1.62 | 1.8E-06 | *fliT* | flagellar protein FliT |
| L108A | *SL1344_1897* | -1.80 | 3.0E-04 | *fliE* | flagellar hook-basal body complex protein FliE |
| L108A | *SL1344_1898* | -1.29 | 5.8E-05 | *fliF* | flagellar basal-body M-ring protein |
| L108A | *SL1344_1899* | -1.00 | 2.4E-02 | *fliG* | flagellar motor switch protein FliG |
| L108A | *SL1344_1900* | -1.21 | 2.6E-03 | *fliH* | flagellar assembly protein FliH |
| L108A | *SL1344_1901* | -1.02 | 4.1E-02 | *fliI* | flagellum-specific ATP synthase |

| | | | | | |
|---|---|---|---|---|---|
| L108A | *SL1344_1903* | -1.11 | 1.7E-03 | *fliK* | flagellar hook-length control protein |
| L108A | *SL1344_1904* | -1.18 | 1.4E-03 | *fliL* | flagella biosynthesis protein |
| L108A | *SL1344_1905* | -1.12 | 6.4E-03 | *fliM* | flagellar motor switch protein FliM |
| L108A | *SL1344_1907* | -1.08 | 9.2E-03 | *fliO* | flagellar biosynthesis protein |
| L108A | *SL1344_1924* | 2.30 | 7.9E-03 | *cspB* | cold shock protein |
| L108A | *SL1344_1978* | 2.32 | 2.2E-02 | *NA* | hypothetical bacteriophage integrase |
| L108A | *SL1344_1999* | -2.11 | 1.1E-02 | *cbiM* | cobalamin biosynthesis protein |
| L108A | *SL1344_2000* | -3.28 | 1.2E-03 | *cbiL* | cobalt-precorrin-2 C(20)-methyltransferase |
| L108A | *SL1344_2001* | -2.40 | 1.1E-02 | *cbiK* | sirohydrochlorin cobaltochelatase (ec 4.99.1.3) |
| L108A | *SL1344_2041* | -1.62 | 2.3E-03 | *phsA* | thiosulfate reductase precursor |
| L108A | *SL1344_2136* | -1.01 | 3.4E-03 | *yehT* | hypothetical two-component system response regulator |
| L108A | *SL1344_2137* | -1.19 | 4.0E-03 | *yehU* | hypothetical two-component system sensor kinase |
| L108A | *SL1344_2166* | -2.98 | 5.6E-04 | *mglA* | galactoside transport atp-binding protein mgla |
| L108A | *SL1344_2167* | -2.39 | 9.3E-09 | *mglB* | D-galactose-binding periplasmic protein precursor |
| L108A | *SL1344_2223* | -2.17 | 2.0E-02 | *ccmH2* | cytochrome C-type biogenesis protein H2 |
| L108A | *SL1344_2226* | -1.12 | 2.3E-02 | *napB* | cytochrome c-type protein NapB precursor |
| L108A | *SL1344_2230* | -1.60 | 2.3E-02 | *napD* | hypothetical napAB assembly protein |
| L108A | *SL1344_2232* | 1.09 | 3.1E-03 | *eco* | Ecotin precursor. |
| L108A | *SL1344_2251* | -1.96 | 6.5E-07 | *glpQ* | glycerophosphoryl diester phosphodiesterase periplasmic precursor |
| L108A | *SL1344_2252* | -2.17 | 3.9E-11 | *glpT* | glycerol-3-phosphate transporter |
| L108A | *SL1344_2253* | -2.36 | 3.8E-10 | *glpA* | anaerobic glycerol-3-phosphate dehydrogenase subunit A |
| L108A | *SL1344_2254* | -1.90 | 9.8E-06 | *glpB* | Anaerobic glycerol-3-phosphate dehydrogenase subunit B |
| L108A | *SL1344_2255* | -1.47 | 1.3E-03 | *glpC* | anaerobic glycerol-3-phosphate dehydrogenase subunit C |
| L108A | *SL1344_2283* | -2.93 | 7.3E-17 | *NA* | hypothetical receptor/regulator protein |
| L108A | *SL1344_2359* | -1.06 | 4.8E-02 | *yfcZ* | conserved hypothetical protein |
| L108A | *SL1344_2369* | 2.20 | 2.1E-02 | *lpxP* | encodes the cold shock-induced palmitoleoyl transferase |
| L108A | *SL1344_2377* | -1.61 | 9.7E-04 | *nupC* | nucleoside permease NupC |
| L108A | *SL1344_2408* | -1.24 | 1.8E-02 | *ucpA* | hypothetical oxidoreductase |
| L108A | *SL1344_2444A* | -2.13 | 8.4E-04 | | |
| L108A | *SL1344_2620* | -1.46 | 9.4E-04 | *clpB* | ClpB protein (heat shock protein f84.1) |
| L108A | *SL1344_2654* | -1.03 | 4.2E-02 | *grpE* | heat shock protein GrpE (heat shock protein b25.3) (hsp24) |
| L108A | *SL1344_2674* | -2.46 | 6.8E-05 | | |
| L108A | *SL1344_2756* | -1.38 | 2.1E-02 | *fljB* | flagellin |
| L108A | *SL1344_2769* | -1.67 | 4.5E-04 | *tctD* | transcriptional regulator |
| L108A | *SL1344_2795* | 1.26 | 2.8E-02 | *proW* | glycine betaine/L-proline transport system permease protein P |
| L108A | *SL1344_2796* | 1.20 | 2.1E-02 | *proX* | glycine betaine-binding periplasmic protein precursor |
| L108A | *SL1344_2851* | -1.28 | 4.4E-02 | *prgK* | type III secretion system apparatus |
| L108A | *SL1344_2852* | -1.71 | 2.0E-03 | *prgJ* | type III secretion system apparatus |

| | | | | | |
|---|---|---|---|---|---|
| L108A | *SL1344_2853* | -1.78 | 1.9E-02 | *prgI* | type III secretion system apparatus |
| L108A | *SL1344_2856* | -2.08 | 6.1E-04 | *hilA* | invasion protein regulator |
| L108A | *SL1344_2861* | -1.08 | 2.5E-02 | *sipA* | pathogenicity island 1 Type III secretion system effector protein |
| L108A | *SL1344_2862* | -1.75 | 2.3E-05 | *sipD* | pathogenicity island 1 Type III secretion system apparatus-part of Translocon |
| L108A | *SL1344_2863* | -1.88 | 5.9E-11 | *sipC* | pathogenicity island 1 Type III secretion system effector protein |
| L108A | *SL1344_2864* | -2.22 | 3.5E-14 | *sipB* | pathogenicity island 1 Type III secretion system effector protein |
| L108A | *SL1344_2865* | -2.52 | 9.8E-07 | *sicA* | type III secretion-associated chaperone |
| L108A | *SL1344_2866* | -1.49 | 7.1E-03 | *spaS* | type III secretion system secretory apparatus |
| L108A | *SL1344_2869* | -1.85 | 1.3E-03 | *spaP* | type III secretion system secretory apparatus |
| L108A | *SL1344_2870* | -1.96 | 6.9E-06 | *spaO* | surface presentation of antigens protein (associated with type III secretion) |
| L108A | *SL1344_2871* | -2.34 | 3.8E-10 | *invJ* | surface presentation of antigens protein (associated with type III secretion) |
| L108A | *SL1344_2872* | -2.28 | 9.8E-06 | *invI* | type III secretion system secretory apparatus |
| L108A | *SL1344_2873* | -1.72 | 3.0E-05 | *invC* | secretory apparatus ATP synthase (associated with virulence) |
| L108A | *SL1344_2874* | -2.38 | 9.3E-09 | *invB* | chaperone protein for type III secretion system effectors |
| L108A | *SL1344_2875* | -2.11 | 5.4E-05 | *invA* | secretory apparatus of type III secretion system |
| L108A | *SL1344_2876* | -2.09 | 1.2E-02 | *invE* | cell invasion protein |
| L108A | *SL1344_2877* | -2.46 | 6.1E-05 | *invG* | type III secretion system secretory apparatus |
| L108A | *SL1344_2878* | -2.41 | 2.6E-03 | *invF* | AraC-family regulatory protein |
| L108A | *SL1344_2879* | -1.40 | 7.1E-03 | | |
| L108A | *SL1344_2927* | 1.06 | 2.2E-02 | *cysJ* | sulfite reductase (NADPH) flavoprotein beta subunit |
| L108A | *SL1344_2950* | -2.03 | 2.0E-09 | *sdaC* | serine transporter |
| L108A | *SL1344_2951* | -1.56 | 1.8E-06 | *sdaB* | L-serine dehydratase 2 (L-serine deaminase 2) |
| L108A | *SL1344_2997* | -1.25 | 4.4E-03 | *yqeF* | probable acetyl-CoA acetyltransferase |
| L108A | *SL1344_3088* | -1.33 | 3.4E-02 | *nupG* | nucleoside permease nupg (nucleoside-transport system protein) |
| L108A | *SL1344_3109* | -1.00 | 2.0E-02 | *uxuA* | D-mannonate hydrolase |
| L108A | *SL1344_3112* | -2.25 | 7.1E-03 | *NA* | annotation |
| L108A | *SL1344_3117* | -1.14 | 2.8E-02 | *hybG* | hydrogenase-2 component protein |
| L108A | *SL1344_3118* | -1.21 | 3.8E-03 | *hybF* | hydrogenase-2 component protein |
| L108A | *SL1344_3120* | -1.20 | 1.2E-03 | *hybD* | hydrogenase-2 component protein |
| L108A | *SL1344_3121* | -1.00 | 9.3E-03 | *hybC* | hydrogenase-2 large subunit |
| L108A | *SL1344_3123* | -1.76 | 7.6E-04 | *hybA* | hydrogenase-2 small subunit |
| L108A | *SL1344_3125* | -2.15 | 9.1E-06 | *yghW* | conserved hypothetical protein |
| L108A | *SL1344_3126* | -2.44 | 4.9E-09 | *NA* | methyl-accepting chemotaxis protein |
| L108A | *SL1344_3128* | -1.49 | 1.8E-04 | *NA* | exported protein |
| L108A | *SL1344_3130* | -1.45 | 9.7E-03 | *NA* | annotation |
| L108A | *SL1344_3189* | -3.04 | 3.0E-05 | *NA* | methyl-accepting chemotaxis protein II |
| L108A | *SL1344_3190* | -3.36 | 7.6E-12 | *aer* | aerotaxis receptor protein |
| L108A | *SL1344_3212* | -1.42 | 6.9E-04 | *tdcG* | L-serine dehydratase |

| | | | | | |
|---|---|---|---|---|---|
| L108A | *SL1344_3213* | -1.95 | 3.8E-05 | *tdcE* | probable formate acetyltransferase |
| L108A | *SL1344_3214* | -2.36 | 9.1E-08 | *tdcD* | propionate kinase |
| L108A | *SL1344_3215* | -2.05 | 1.5E-06 | *tdcC* | threonine/serine transporter |
| L108A | *SL1344_3216* | -1.66 | 1.2E-04 | *tdcB* | catabolic threonine dehydratase |
| L108A | *SL1344_3242* | 2.63 | 1.3E-02 | *yhbO* | conserved hypothetical protein |
| L108A | *SL1344_3416* | -0.92 | 3.5E-02 | *yheL* | conserved hypothetical protein |
| L108A | *SL1344_3542* | -2.19 | 5.3E-05 | *tcp* | methyl-accepting chemotaxis citrate transducer |
| L108A | *SL1344_3569* | -1.21 | 1.2E-03 | *NA* | hypothetical membrane protein |
| L108A | *SL1344_3575* | -1.21 | 2.9E-02 | *yhjG* | hypothetical membrane protein |
| L108A | *SL1344_3576* | -2.92 | 3.0E-13 | *yhjH* | conserved hypothetical protein |
| L108A | *SL1344_3579* | -2.21 | 4.2E-06 | *dctA* | C4-dicarboxylate transport protein |
| L108A | *SL1344_3614* | 1.98 | 8.1E-04 | *yiaG* | hypothetical HTH-type transcriptional regulator |
| L108A | *SL1344_3775* | -2.07 | 6.2E-09 | *hslS* | heat shock protein B |
| L108A | *SL1344_3776* | -1.73 | 1.3E-04 | *hslT* | heat shock protein A |
| L108A | *SL1344_3848* | -2.53 | 3.2E-06 | *rbsD* | high affinity ribose transport protein RbsD |
| L108A | *SL1344_3849* | -2.23 | 2.5E-03 | *rbsA* | high affinity ribose transport protein |
| L108A | *SL1344_3850* | -1.91 | 3.2E-04 | *rbsC* | high affinity ribose transport protein |
| L108A | *SL1344_3851* | -1.89 | 5.4E-09 | *rbsB* | D-ribose-binding periplasmic protein |
| L108A | *SL1344_3852* | -1.74 | 5.2E-06 | *rbsK* | ribokinase |
| L108A | *SL1344_3853* | -1.45 | 4.1E-04 | *rbsR* | ribose operon repressor |
| L108A | *SL1344_4009* | 3.05 | 2.1E-04 | *cpxP* | extracytoplasmic stress protein for protein-mediated toxicities |
| L108A | *SL1344_4012* | 1.90 | 3.9E-02 | *sbp* | periplasmic sulphate binding protein |
| L108A | *SL1344_4035* | -1.85 | 6.3E-09 | *glpK* | glycerol kinase |
| L108A | *SL1344_4036* | -1.94 | 5.1E-04 | *glpF* | glycerol uptake facilitator protein |
| L108A | *SL1344_4040* | -1.21 | 7.6E-03 | *hslU* | heat shock protein |
| L108A | *SL1344_4041* | -1.17 | 2.0E-03 | *hslV* | heat shock protein |
| L108A | *SL1344_4166* | -2.93 | 8.5E-04 | *malE* | periplasmic maltose-binding protein |
| L108A | *SL1344_4167* | -3.85 | 1.7E-04 | *malK* | maltose/maltodextrin transport ATP-binding protein |
| L108A | *SL1344_4168* | -2.78 | 2.1E-03 | *lamB* | maltoporin precursor |
| L108A | *SL1344_4194* | -2.15 | 8.4E-06 | *siiB* | hypothetical integral membrane protein |
| L108A | *SL1344_4196* | -1.52 | 6.4E-03 | *siiD* | hypothetical type-I secretion protein |
| L108A | *SL1344_4214* | -2.38 | 1.7E-06 | *nrfB* | penta-heme cytochrome c , subunit of nitrite reductase complex |
| L108A | *SL1344_4227* | 1.19 | 3.2E-03 | *proP* | hypothetical amino acid permease |
| L108A | *SL1344_4234* | -1.22 | 2.1E-02 | *melR* | melibiose operon regulatory protein |
| L108A | *SL1344_4238* | -1.15 | 1.7E-02 | *dcuB* | anaerobic C4-dicarboxylate transporter |
| L108A | *SL1344_4247* | -1.22 | 2.1E-02 | *NA* | hypothetical membrane protein |
| L108A | *SL1344_4250* | -3.01 | 1.2E-03 | *rtsB* | Regulator of flhDC |
| L108A | *SL1344_4251* | -3.32 | 8.9E-10 | *rtsA* | Regulator of SPI-1 |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| L108A | *SL1344_4263* | -1.97 | 2.6E-03 | *aspA* | aspartate ammonia-lyase |
| L108A | *SL1344_4274* | -1.23 | 1.6E-03 | *ecnR* | transcriptional regulatory protein |
| L108A | *SL1344_4300* | 1.56 | 4.9E-02 | *nsrR* | nitric oxide sensitive transcriptional repressor |
| L108A | *SL1344_4336* | -1.28 | 3.4E-02 | *cpdB* | 2',3'-cyclic-nucleotide 2'-phosphodiesterase |
| L108A | *SL1344_4464* | -2.70 | 7.3E-11 | *tsr* | methyl-accepting chemotaxis protein |
| L108A | *SL1344_4465* | -1.56 | 2.3E-02 | *NA* | hypothetical transcriptional regulatory protein |
| L108A | *SL1344_4489* | 1.80 | 6.4E-03 | *osmY* | Putative periplasmic protein |

**Suplementary Table S7**. RcsB boxes (motifs) predicted *in silico* in the genome of *S.* Typhimurium SL1344 (GenBank: NC_016810.1)

(*) *Log2 of fold change values respect empty-vector*

🟩 *positions higlighted in green indicates RcsB motif within bidirectional promoter regions*

| ID | Genome coordenates | predicted target (Locus ID) | Gene | Site (as in Fig. 6A) | distance to start ATG (bp) | distance to mapped TSS (bp) | Motif (positive strand 5'-3') |
|---|---|---|---|---|---|---|---|
| **1** | 12815 | *SL1344_0012* | *dnaK* | Intra-CDS | 1223 | | TGAGAGAGTTCTGA |
| **2** | 17417 | *SL1344_0017* | | Intra-CDS | 69 | | TGAGACCGTCCTCA |
| **3** | 20650 | *SL1344_0019* | | Intra-CDS | 593 | | TCAGACGTTACTGA |
| **4** | 31355 | *SL1344_0028* | *bcfH* | Intra-CDS | 82 | | TCAGACGAATCTGA |
| **5** | 32270 | *SL1344_0029* | | Intra-CDS | 113 | | TAGGAACCTCCTCA |
| **6** | 45554 | *SL1344_0040* | *nhaA* | Intra-CDS | -636 | -334 | TAAGATTTTCCTCA |
| **7** | 55540 | *SL1344_0047* | *ileS* | Intra-CDS | 1686 | | TTGGAGTTAACTCA |
| **8** | 66546 | *SL1344_0056* | | Intra-CDS | 91 | | TTGGAAATATCTCA |
| **9** | 86206 | *SL1344_0074* | *caiA* | Intra-CDS | 448 | | TGAGATAAACCTTA |
| **10** | 100989 | *SL1344_0088* | *folA* | Intra-CDS | 148 | | TCGGACGCCCCTTA |
| **11** | 153297 | *SL1344_0131* | *ftsQ* | Intra-CDS | -239 | 44 | TTAGATGCGTCCCA |
| **12** | 158316 | *SL1344_0135* | *yacA* | Intra-CDS | 210 | | TTAGAAGCCTCTAA |
| **13** | 177662 | *SL1344_0152* | *aceE* | Intra-CDS | 1419 | | TTAGAGCTGCCTCA |
| **14** | 211533 | *SL1344_0181* | *panD* | Intra-CDS | -126 | -14 | TCAGACGCGCCTGA |
| **15** | 265900 | *SL1344_0227* | *lpxD* | internalTSS | | -179 | TGAGAATTGCCTGA |
| **16** | 426348 | *SL1344_0368* | *yaiU* | Intra-CDS | 1698 | | TGGGATACCACTCA |
| **17** | 437145 | *SL1344_0379* | *psiF* | 5-UTR | -57 | 7 | TGGGATATTTCCCA |
| **18** | 437145 | *STnc4150* | | promoter | -63 | -63 | TGGGATATTTCCCA |
| **19** | 580329 | *SL1344_0513* | | Intra-CDS | 704 | | TCAGAAAGACCTTA |
| **20** | 590090 | *SL1344_0521* | *allD* | Intra-CDS | 427 | | TAGGATCGGACTGA |
| **21** | 603317 | *SL1344_0536* | *fimA* | promoter | -285 | | TTAGACCCTTCTTA |
| **22** | 603317 | *SL1344_0535* | *folD* | 5-UTR | -261 | 23 | TTAGACCCTTCTTA |
| **23** | 643966 | *SL1344_0574* | *fes* | Intra-CDS | 477 | | TGGGATCGTCCTGA |
| **24** | 649004 | *SL1344_0577* | *fepE* | promoter | -79 | -36 | TCGGATAATTCTGA |
| **25** | 684173 | *SL1344_0609* | *citF* | Intra-CDS | 673 | | TCAGATCAACCTGA |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| **26** | 692950 | *SL1344_0618* | *ccrB* | Intra-CDS | 103 | | TGGGAATCGCCTGA |
| **27** | 695251 | *SL1344_0621* | *lipA* | Intra-CDS | 64 | | TAAGAGCCATCTTA |
| **28** | 695972 | *SL1344_0622* | *ybeF* | internalTSS | | -242 | TGAGATCGGTCTGA |
| **29** | 801182 | *SL1344_0718* | *sucA* | Intra-CDS | 27 | | TTGGACTCTTCTTA |
| **30** | 844864 | *SL1344_0758* | *modA* | 5-UTR | -64 | 29 | TGGGAAACCCCTGA |
| **31** | 866144 | *SL1344_0776* | *slrP* | promoter | -55 | -33 | TGAGAATATCCTTA |
| **32** | 870623 | *SL1344_0779* | *moaB* | Intra-CDS | -281 | | TGAGATCGGCCTCA |
| **33** | 919302 | *SL1344_0825* | *yliB* | Intra-CDS | 37 | | TGGGACTGGCCTCA |
| **34** | 930285 | *SL1344_0834* | | Intra-CDS | 693 | | TCAGACCAGTCCCA |
| **35** | 934562 | *SL1344_0839* | *dacC* | promoter | -195 | -16 | TGAGATAAACCTAA |
| **36** | 934562 | *SL1344_0838* | *yliJ* | 5-UTR | -48 | 1 | TGAGATAAACCTAA |
| **37** | 940457 | *SL1344_0844* | | Intra-CDS | 608 | | TGAGAATCTTCCGA |
| **38** | 958877 | *SL1344_0864* | *artM* | Intra-CDS | 46 | | TGAGAATGTACTGA |
| **39** | 974561 | *SL1344_0880* | *ybjY* | Intra-CDS | -587 | -83 | TGAGACCAGACTGA |
| **40** | 1010436 | *SL1344_0908* | | Intra-CDS | 61 | | TCAGATGTGTCCAA |
| **41** | 1063046 | *SL1344_0952* | | Intra-CDS | 236 | | TAAGACAACACTGA |
| **42** | 1132878 | *SL1344_1026* | *pipA* | Intra-CDS | -328 | | TTAGAGCTATCTTA |
| **43** | 1211871 | *SL1344_1107* | *mviN* | Intra-CDS | 728 | | TCAGATCTCCCTTA |
| **44** | 1213583 | *SL1344_1109* | *flgM* | Intra-CDS | 649 | -17 | TAAGAATATTCCCA |
| **45** | 1231245 | *SL1344_1126* | *maf-a* | 5-UTR | -28 | -1 | TGAGAGCCATCTTA |
| **46** | 1231245 | *SL1344_1127* | *yceD* | promoter | -169 | -168 | TGAGAGCCATCTTA |
| **47** | 1239478 | *SL1344_1137* | *tmK* | Intra-CDS | -288 | -53 | TCAGACCGATCCCA |
| **48** | 1251955 | *SL1344_1149* | *ycfJ* | promoter | -123 | -100 | TCGGAGTTGTCCGA |
| **49** | 1282634 | *SL1344_1177* | | promoter | -301 | -117 | TGAGACCCCCCTGA |
| **50** | 1282634 | *STnc150* | | Intra-CDS | | -43 | TGAGACCCCCCTGA |
| **51** | 1310949 | *SL1344_1212* | | promoter-5-UTR | -42 | -6 | TAAGAACAATCTGA |
| **52** | 1337038 | *SL1344_1235* | | promoter-5-UTR | -32 | -6 | TGAGAATATACTTA |
| **53** | 1337038 | *SL1344_1234* | *gdhA* | promoter | -206 | -141 | TGAGAATATACTTA |
| **54** | 1345834 | *STnc1640* | | internalTSS | | -49 | TGAGAAGCGTCTGA |
| **55** | 1359181 | *SL1344_1256* | *ydjM* | promoter | -126 | | TCGGAAACATCTTA |
| **56** | 1359181 | *STnc3570* | *STnc3570* | 5-UTR | | 2 | TCGGAAACATCTTA |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| **57** | 1401825 | *rprA* | *rprA* | promoter | -35 | | TCAGATTCGTCTCA |
| **58** | 1416552 | *SL1344_1311* | *lpp* | promoter | -85 | -47 | TGGGAATGCACTTA |
| **59** | 1416643 | *SL1344_1311* | *lpp* | promoter | -176 | -138 | TCGGATTCTTCTTA |
| **60** | 1471842 | *SL1344_1371* | *ydhF* | intragenic | 84 | | TCGGAAGATCCTCA |
| **61** | 1474438 | *SL1344_1373* | *asSL1373* | internalTSS | | -51 | TCAGATATAACTGA |
| **62** | 1479070 | *SL1344_1379* | *mliC* | Intra-CDS | -98 | -15 | TCAGAGTTAACTGA |
| **63** | 1554214 | *SL1344_1449* | *marA* | Intra-CDS | 167 | | TTGGAATATCCTGA |
| **64** | 1601764 | *SL1344_1493* | *osmC* | promoter | -243 | -21 | TGAGATTTATCCTA |
| **66** | 1601764 | *SL1344_1494* | *yddX* | promoter-5-UTR | -269 | -9 | TGAGATTTATCCTA |
| **67** | 1602545 | *SL1344_1496* | *sfcA* | promoter | -118 | -43 | TAGGAATGACCTTA |
| **68** | 1621296 | *SL1344_1509* | *narY* | Intra-CDS | 20 | | TGGGATGGTACTGA |
| **69** | 1632569 | *SL1344_1518* | *yncD* | Intra-CDS | 1807 | | TGGGATTCGCCTCA |
| **70** | 1662450 | *SL1344_1546* | | Intra-CDS | 128 | | TGAGAACACCCTTA |
| **71** | 1680187 | *SL1344_1563* | *PBPb* | Intra-CDS | -556 | -205 | TCAGATATTTCTGA |
| **72** | 1680187 | *SL1344_1562* | | promoter | -350 | | TCAGATATTTCTGA |
| **73** | 1682336 | *SL1344_1565* | | Intra-CDS | 153 | | TTAGAAGAACCTGA |
| **74** | 1703022 | *SL1344_1582* | *ynaF* | Intra-CDS | 39 | | TCAGAATTAACTCA |
| **75** | 1727732 | *SL1344_1607* | | 5-UTR | -26 | 1 | TCAGAACAGTCTAA |
| **76** | 1727732 | *SL1344_1608* | | promoter | -92 | | TCAGAACAGTCTAA |
| **77** | 1756560 | *SL1344_1637* | *osmB* | promoter | -215 | -73 | TAAGACTTTTCTGA |
| **78** | 1759317 | *SL1344_1640* | *yciM* | Intra-CDS | 220 | | TGAGATGAGCCTCA |
| **79** | 1765036 | *SL1344_1644A* | *ymiA* | 5-UTR | -36 | 1 | TGAGACAAATCCTA |
| **80** | 1776364 | *SL1344_1654* | *trpE* | Intra-CDS | 962 | | TGAGATTTATCCCA |
| **81** | 1782070 | *SL1344_1659* | *yciG* | promoter | -340 | -55 | TAAGAAAACTCCTA |
| **82** | 1916625 | *SL1344_1792* | | promoter | -168 | | TCAGAGCTTCCTGA |
| **83** | 1916625 | *SL1344_1793* | *pagO* | promoter | -449 | -429 | TCAGAGCTTCCTGA |
| **84** | 1916702 | *SL1344_1792* | | promoter | -245 | | TGAGAATTTACTCA |
| **85** | 1916702 | *SL1344_1793* | *pagO* | promoter | -372 | -352 | TGAGAATTTACTCA |
| **86** | 1954449 | *SL1344_1836* | *aspS* | Intra-CDS | 1 | | TGAGATATCCCTTA |
| **87** | 1977672 | *SL1344_1857* | *motB* | internalTSS | 22 | -170 | TGGGATGAGCCTGA |
| **88** | 1979777 | *SL1344_1860* | *flhD* | 5-UTR | -143 | 60 | TGAGATTCGCCTTA |

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|---|---|---|---|---|---|---|---|
| **89** | 1979819 | *SL1344_1860* | *flhD* | 5-UTR | -185 | 18 | TAAGATTTTTCCTA |
| **90** | 1983384 | *SL1344_1863* | *otsB* | promoter | -318 | -267 | TGAGACTTTTCCGA |
| **91** | 2006994 | *SL1344_1889* | *fliD* | Intra-CDS | 25 | | TGGGATCAAACTTA |
| **92** | 2025283 | *SL1344_1911* | *rcsA* | Intra-CDS | 289 | | TAAGACAAAACTTA |
| **93** | 2026300 | *DsrA* | *DsrA* | 5-UTR | | 1 | TGAGATTTACCTTA |
| **94** | 2048422 | *SL1344_1937* | | Intra-CDS | 500 | | TCAGAAATACCTGA |
| **95** | 2074739 | *SL1344_1969* | | Intra-CDS | 557 | | TAAGAAATCCCTTA |
| **96** | 2086224 | *SL1344_1983* | | Intra-CDS | -163 | | TGAGAAAGACCTCA |
| **97** | 2156706 | *SL1344_2057* | *udg* | Intra-CDS | 133 | | TCGGAGATATCCGA |
| **98** | 2156848 | *SL1344_2057* | *udg* | 5-UTR | -9 | 111 | TCAGAATTAACTTA |
| **99** | 2181905 | *SL1344_2078* | *wcaK* | Intra-CDS | 251 | | TGAGAATATACTGA |
| **100** | 2198160 | *SL1344_2093* | *wzc* | Intra-CDS | 615 | | TGAGAATTTACTCA |
| **101** | 2212782 | *SL1344_2103* | | Intra-CDS | 783 | | TGGGATCGGACTAA |
| **102** | 2239784 | *SL1344_2125* | *rcnB* | promoter | -186 | -86 | TCAGATAGTTCTCA |
| **103** | 2239784 | *SL1344_2124* | *thiM* | promoter | -223 | -71 | TCAGATAGTTCTCA |
| **104** | 2261017 | *SL1344_2144* | *bglX* | Intra-CDS | 169 | | TCAGACGTAACTGA |
| **105** | 2330516 | *SL1344_2208* | *oafA* | Intra-CDS | 671 | | TGGGATAGTCCTCA |
| **106** | 2355348 | *SL1344_2229* | *asnapA* | internalTSS | | -474 | TGAGAAGGTTCCCA |
| **107** | 2477178 | *SL1344_2335* | *accD* | Intra-CDS | 142 | | TAGGACAGACCTCA |
| **108** | 2493700 | *SL1344_2353* | *aroC* | Intra-CDS | 358 | -202 | TCAGATCGTACTGA |
| **109** | 2511819 | *SL1344_2368* | | promoter-5-UTR | -64 | -5 | TAAGATAAACCTTA |
| **110** | 2520241 | *SL1344_2374* | | Intra-CDS | 306 | | TGGGATGGCCCTTA |
| **111** | 2560958 | *SL1344_2416* | | Intra-CDS | 660 | | TGGGAGCTCACTGA |
| **112** | 2579898 | *SL1344_2435* | *maeB* | Intra-CDS | 76 | | TCGGAGAAACCTGA |
| **113** | 2587150 | *RS27105* | | promoter | -66 | | TAAGATTGTCCTCA |
| **114** | 2608273 | *SL1344_2459* | *yfgE* | Intra-CDS | 28 | | TCAGAGATACCTCA |
| **115** | 2610796 | *SL1344_2462* | *purM* | Intra-CDS | 8 | | TAAGACCTCTCTTA |
| **116** | 2630608 | *SL1344_2474* | *shdA* | Intra-CDS | 850 | | TAAGAGCGGCCTTA |
| **117** | 2656642 | *SL1344_2486* | *yfgA* | Intra-CDS | -521 | -355 | TCAGATTAATCTTA |
| **118** | 2670216 | *SL1344_2494* | | Intra-CDS | 197 | | TCGGAGGCGTCTAA |
| **119** | 2696144 | *SL1344_2520* | *cadB* | promoter | -108 | -38 | TAGGACTTATCTCA |

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|---|---|---|---|---|---|---|---|
| **120** | 2719393 | *SL1344_2538* | *yfhL* | promoter | -13 | 17 | TGAGAATTTCCTGA |
| **121** | 2727871 | *SL1344_2546* | *gogB* | Intra-CDS | 1179 | | TCAGACTTATCCAA |
| **122** | 2763310 | *SL1344_2584* | | Intra-CDS | 145 | | TCAGACCATCCTGA |
| **123** | 2816682 | *SL1344_2632* | | Intra-CDS | 112 | | TTAGAGGCCACTTA |
| **124** | 2874291 | *SL1344_2693* | | promoter | -13 | | TTAGAAATAACTTA |
| **125** | 2881179 | *SL1344_2700* | | promoter | -106 | -53 | TTAGATAGCCCTGA |
| **126** | 2909864 | *SL1344_2731* | | Intra-CDS | -102 | | TGGGATATAACTTA |
| **127** | 2926302 | *SL1344_2746* | | Intra-CDS | 1161 | | TGGGATCTTACTAA |
| **128** | 2933241 | *SL1344_2752* | | promoter | -263 | | TAAGAGGTGACTCA |
| **129** | 2968579 | *SL1344_2780* | | promoter | -145 | -88 | TTAGAATTAACTAA |
| **130** | 2968595 | *SL1344_2780* | | promoter | -161 | -104 | TTAGAAAATACTTA |
| **131** | 2982325 | *SL1344_2797* | | Intra-CDS | 310 | | TCGGAACGGCCTTA |
| **132** | 2994134 | *SL1344_2806* | *csrA* | Intra-CDS | -422 | -295 | TCAGAGAAACCTTA |
| **133** | 3037755 | *SL1344_2850* | *orgA* | Intra-CDS | 575 | | TCAGAACGTTCTGA |
| **134** | 3040998 | *SL1344_2855* | *hilD* | Intra-CDS | 587 | | TGAGATCATCCTTA |
| **135** | 3089909 | *SL1344_2904* | *nlpD* | Intra-CDS | 334 | | TCGGAATATTCCCA |
| **136** | 3123330 | *SL1344_2933* | *mazG* | promoter | -457 | -370 | TAAGAATATACTCA |
| **137** | 3123330 | *SL1344_2934* | *SteA* | promoter | -148 | | TAAGAATATACTCA |
| **138** | 3132339 | *SL1344_2941* | *gudD* | Intra-CDS | 1003 | | TCAGACCGAACTCA |
| **139** | 3137011 | *SL1344_2944* | | Intra-CDS | -23 | 6 | TCAGATGAGTCTCA |
| **140** | 3138696 | *ST4-CrsA* | *CsrA* | promoter | -174 | | TAAGAGATCTCTCA |
| **141** | 3159157 | *SL1344_2966* | | promoter | -208 | | TCAGATTTCCCTGA |
| **142** | 3205856 | *SL1344_3002* | *yohM* | Intra-CDS | 218 | | TGGGATGTATCTTA |
| **143** | 3213312 | *SL1344_3008* | *stdA* | promoter | -50 | | TAAGAAAATTCTTA |
| **144** | 3225752 | *SL1344_3020* | *xerD* | Intra-CDS | 289 | | TCGGATCATCCTCA |
| **145** | 3250037 | *SL1344_3043* | *yggB* | 5-UTR | -33 | 24 | TGAGATCATTCTCA |
| **146** | 3250037 | *STnc3030* | *STnc3030* | promoter | -69 | | TGAGATCATTCTCA |
| **147** | 3351250 | *SL1344_3142* | *ygiR* | Intra-CDS | 563 | | TTGGAATCGACTAA |
| **148** | 3388439 | *SL1344_3175* | *ygiF* | Intra-CDS | 568 | | TCAGACTGCCCTGA |
| **149** | 3400834 | *SL1344_3187* | *yqjH* | promoter | -203 | | TTAGATATATCTAA |
| **150** | 3400834 | *SL1344_3188* | *yqjI* | promoter-5-UTR | -28 | -9 | TTAGATATATCTAA |

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|---|---|---|---|---|---|---|---|
| **151** | 3431481 | *SL1344_3215* | *tdcC* | Intra-CDS | 589 | | TGAGATCAACCTGA |
| **152** | 3511609 | *SL1344_3299* | *yhbL* | Intra-CDS | 73 | | TCAGAACGGCCTCA |
| **153** | 3564102 | *SL1344_3344* | *mreD* | Intra-CDS | 283 | | TTGGACGTGCCTGA |
| **154** | 3564754 | *SL1344_3345* | *mreC* | Intra-CDS | 117 | | TCGGATTTGACTGA |
| **155** | 3565116 | *SL1344_3345* | *mreC* | Intra-CDS | -245 | | TCGGAGATGTCTGA |
| **156** | 3601474 | *SL1344_3376* | *sapG* | Intra-CDS | 222 | | TCAGATGAAACTAA |
| **157** | 3606000 | *SL1344_3383* | *rpsD* | Intra-CDS | 418 | | TCGGACTAACCTGA |
| **158** | 3610551 | *SL1344_3392* | *rplF* | Intra-CDS | 332 | | TGAGAGAAACCTAA |
| **159** | 3611928 | *SL1344_3395* | *rplE* | Intra-CDS | 253 | | TCGGATAGCCCTGA |
| **160** | 3615850 | *SL1344_3404* | *rplB* | Intra-CDS | 256 | | TCGGATCGTACTCA |
| **161** | 3616673 | *SL1344_3406* | *rplD* | Intra-CDS | 355 | | TCAGACGATCCTGA |
| **162** | 3661230 | *SL1344_3452* | *damX* | Intra-CDS | 1273 | | TCAGATCGGCCTGA |
| **163** | 3676378 | *SL1344_3466* | *yhgE* | Intra-CDS | 1327 | | TCGGAGAGACCTTA |
| **164** | 3774367 | *SL1344_3550* | *yhhJ* | Intra-CDS | -86 | | TCGGACAGATCCAA |
| **165** | 3825707 | *SL1344_3586* | *yhjR* | Intra-CDS | 37 | | TTGGATCGGACTGA |
| **166** | 3826198 | *SL1344_3587* | *yhjS* | internalTSS | | -77 | TTAGATGAATCTCA |
| **167** | 3905765 | *SL1344_3656* | *sadA* | Intra-CDS | 3223 | | TCGGAACTGACTCA |
| **168** | 3936113 | *SL1344_3684* | *rfaI* | Intra-CDS | -270 | | TAGGAAATCCCTCA |
| **169** | 3941007 | *SL1344_3690* | *kdtA* | Intra-CDS | 356 | | TAAGATTGATCCTA |
| **170** | 3981014 | *SL1344_3726* | *slsA* | promoter | -138 | | TCAGAAAGAACTCA |
| **171** | 3984954 | *SL1344_3728* | *mgtB* | Intra-CDS | 628 | | TAAGAATTGACTGA |
| **172** | 4015302 | *SL1344_3759* | | Intra-CDS | 521 | | TAAGACATATCTAA |
| **173** | 4031827 | *SL1344_3776* | *hslT* | promoter | -185 | -85 | TGGGACAGCACTGA |
| **174** | 4042665 | *SL1344_3788* | *torA* | Intra-CDS | 2011 | | TGGGATGGCCCTGA |
| **175** | 4065494 | *SL1344_3805* | *dnaA* | Intra-CDS | 844 | | TGAGACGATCCTCA |
| **176** | 4114157 | *SL1344_3849* | *rbsA* | Intra-CDS | 761 | | TGAGATTCGCCTCA |
| **177** | 4143757 | *SL1344_3873* | *gppA* | Intra-CDS | 1096 | | TCAGACCGATCTCA |
| **178** | 4157613 | *SL1344_3886* | | Intra-CDS | 27 | | TCGGATATCCCTCA |
| **179** | 4168727 | *SL1344_3894* | *ascyaA* | internalTSS | | 1 | TGGGAATATCCTAA |
| **180** | 4170703 | *SL1344_3895* | | Intra-CDS | 138 | | TGGGATGCATCTTA |
| **181** | 4202443 | *SL1344_3928* | *tatB* | Intra-CDS | 137 | | TCAGAATGAACTGA |

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|---|---|---|---|---|---|---|---|
| **182** | 4226826 | *SL1344_3946* | *yihG* | Intra-CDS | 355 | | TAAGAAAGTACTTA |
| **183** | 4271020 | *SL1344_3987* | | internalTSS | | -108 | TGGGATCAAACTCA |
| **184** | 4272372 | *SL1344_3988* | *yiiG* | Intra-CDS | 614 | | TCAGACATTACTGA |
| **185** | 4283664 | *SL1344_3999* | *rhaT* | promoter | -293 | | TGGGAATAGTCTGA |
| **186** | 4283664 | *SL1344_4000* | | promoter | -325 | | TGGGAATAGTCTGA |
| **187** | 4285459 | *SL1344_4001* | | Intra-CDS | 679 | | TGGGAATGGCCTCA |
| **188** | 4287005 | *SL1344_4003* | | Intra-CDS | 643 | | TGAGAGCGAACTCA |
| **189** | 4290444 | *SL1344_4007* | *cpxA* | Intra-CDS | 743 | | TGGGAGATGTCTGA |
| **190** | 4312947 | *SL1344_4031* | *yiiQ* | Intra-CDS | 232 | | TCAGATTCGCCTTA |
| **191** | 4328724 | *SL1344_4047* | | Intra-CDS | 1388 | | TTGGATGGCACTAA |
| **192** | 4335694 | *SL1344_4051* | | Intra-CDS | 25 | | TTGGAAATAACTCA |
| **193** | 4407649 | *SL1344_4109* | *hupA* | Intra-CDS | -664 | -287 | TTGGAAATGACTCA |
| **194** | 4424718 | *SL1344_4119* | *aceA* | Intra-CDS | -244 | | TGAGAAAACACTGA |
| **195** | 4434791 | *SL1344_4124* | *yjbB* | Intra-CDS | 1214 | | TGAGATGGCCCTGA |
| **196** | 4436504 | *SL1344_4127* | | Intra-CDS | 323 | | TCAGACGCAACTGA |
| **197** | 4440169 | *SL1344_4131* | | Intra-CDS | 233 | | TGGGAGTGATCTTA |
| **198** | 4514468 | *SL1344_4197* | *assiiE* | internalTSS | | -505 | TTGGATTGAACTCA |
| **199** | 4570252 | *SL1344_4239* | | promoter | -100 | -22 | TGGGATAATACTTA |
| **200** | 4584409 | *SL1344_4255* | *asphoN* | internalTSS | | -15 | TCGGATAATACTAA |
| **201** | 4658678 | *SL1344_4333* | *ytfF* | Intra-CDS | 1 | | TCAGATTCTCCTCA |
| **202** | 4663803 | *SL1344_4339* | *ytfK* | promoter | -165 | -50 | TTAGATAATTCTGA |
| **203** | 4711325 | *SL1344_4378* | | Intra-CDS | 1346 | | TGAGATTGCCCTCA |
| **204** | 4721508 | *SL1344_4387* | *mgtA* | Intra-CDS | 1238 | | TCAGACCGGTCTAA |
| **205** | 4750668 | *SL1344_4416* | *yjgB* | Intra-CDS | 703 | | TGAGATCGAACTGA |
| **206** | 4779046 | *SL1344_4434* | | Intra-CDS | 10 | | TTAGACCATACTCA |

| predicted target (Locus ID) | Gene | RNAseq (WT) * | RNAseq (M88A) * | RNAseq (L108A) * | strand | TSS | start_locus | end_locus |
|---|---|---|---|---|---|---|---|---|
| *SL1344_0012* | *dnaK* | -0.46 | 1.87 | 1.74 | + | | 11592 | 13509 |
| *SL1344_0017* | | | | | - | | 17042 | 17486 |
| *SL1344_0019* | | | | | + | | 20057 | 23054 |
| *SL1344_0028* | *bcfH* | | | | + | | 31273 | 32119 |
| *SL1344_0029* | | | | | + | | 32157 | 32445 |
| *SL1344_0040* | *nhaA* | | | | + | 45888 | 44311 | 46027 |
| *SL1344_0047* | *ileS* | | | | + | | 53854 | 56689 |
| *SL1344_0056* | | | | | - | | 64861 | 66637 |
| *SL1344_0074* | *caiA* | | | | - | | 85511 | 86654 |
| *SL1344_0088* | *folA* | | | | + | | 100841 | 101321 |
| *SL1344_0131* | *ftsQ* | | | | + | 153253 | 152613 | 153534 |
| *SL1344_0135* | *yacA* | | | | + | | 158106 | 158631 |
| *SL1344_0152* | *aceE* | | | | + | | 176243 | 178907 |
| *SL1344_0181* | *panD* | | | | - | 211519 | 211501 | 212356 |
| *SL1344_0227* | *lpxD* | | | | + | 266079 | 265400 | 266426 |
| *SL1344_0368* | *yaiU* | | | | + | | 424650 | 427587 |
| *SL1344_0379* | *psiF* | 1.46 | | | + | 437138 | 437202 | 437523 |
| *STnc4150* | | | | | - | 437082 | 436953 | 437082 |
| *SL1344_0513* | | | | | + | | 579625 | 580504 |
| *SL1344_0521* | *allD* | | | | - | | 589467 | 590517 |
| *SL1344_0536* | *fimA* | 1.42 | | | + | | 603602 | 604160 |
| *SL1344_0535* | *folD* | | | | - | 603340 | 602189 | 603056 |
| *SL1344_0574* | *fes* | 0.26 | -2.43 | | + | | 643489 | 644704 |
| *SL1344_0577* | *fepE* | -1.05 | | | + | 649040 | 649083 | 650220 |
| *SL1344_0609* | *citF* | | | | - | | 683316 | 684846 |

|  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|
| *SL1344_0618* | *ccrB* |  |  |  | - |  | 692669 | 693053 |
| *SL1344_0621* | *lipA* |  |  |  | - |  | 694349 | 695315 |
| *SL1344_0622* | *ybeF* | 1.16 | -0.96 |  | - | 695730 | 695520 | 696474 |
| *SL1344_0718* | *sucA* | -0.26 |  | 1.13 | + |  | 801155 | 803957 |
| *SL1344_0758* | *modA* | -2.22 |  | 1.67 | + | 844835 | 844928 | 845702 |
| *SL1344_0776* | *slrP* | 0.45 |  |  | + | 866177 | 866199 | 866496 |
| *SL1344_0779* | *moaB* |  |  |  | + |  | 869892 | 870882 |
| *SL1344_0825* | *yliB* |  |  |  | + |  | 919265 | 920804 |
| *SL1344_0834* |  |  |  |  | + |  | 929592 | 931278 |
| *SL1344_0839* | *dacC* | 0.70 |  |  | + | 934578 | 934757 | 935960 |
| *SL1344_0838* | *yliJ* |  |  |  | - | 934563 | 933887 | 934514 |
| *SL1344_0844* |  |  |  |  | - |  | 939853 | 941065 |
| *SL1344_0864* | *artM* |  |  |  | - |  | 958830 | 959547 |
| *SL1344_0880* | *ybjY* |  |  |  | - | 974644 | 974051 | 975020 |
| *SL1344_0908* |  |  |  |  | - |  | 1010170 | 1010497 |
| *SL1344_0952* |  |  |  |  | + |  | 1062810 | 1063794 |
| *SL1344_1026* | *pipA* |  |  |  | - |  | 1132771 | 1133647 |
| *SL1344_1107* | *mviN* |  |  |  | + |  | 1211143 | 1212679 |
| *SL1344_1109* | *flgM* | -2.93 | -1.38 | -2.28 | - | 1213566 | 1213573 | 1214232 |
| *SL1344_1126* | *maf-a* |  |  |  | - | 1231246 | 1230632 | 1231217 |
| *SL1344_1127* | *yceD* |  |  |  | + | 1231413 | 1231414 | 1231936 |
| *SL1344_1137* | *tmK* |  |  |  | + | 1239531 | 1238753 | 1239776 |
| *SL1344_1149* | *ycfJ* | 3.35 | -1.50 |  | + | 1252055 | 1252078 | 1252618 |
| *SL1344_1177* |  |  |  |  | + | 1282751 | 1282935 | 1284060 |
| *STnc150* |  |  |  |  | - |  | 1282521 | 1282677 |
| *SL1344_1212* |  |  |  |  | + | 1310955 | 1310991 | 1311303 |
| *SL1344_1235* |  | -3.35 | 1.43 | 2.97 | + | 1337044 | 1337070 | 1337346 |
| *SL1344_1234* | *gdhA* |  |  |  | - | 1336897 | 1335488 | 1336832 |
| *STnc1640* |  |  |  |  | + | 1345883 | 1345883 | 1345970 |
| *SL1344_1256* | *ydjM* |  |  |  | - |  | 1358455 | 1359055 |
| *STnc3570* | *STnc3570* |  |  |  | - | 1359183 | 1359017 | 1359183 |

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|---|---|---|---|---|---|---|---|---|
| *rprA* | *rprA* | | | | - | | 1401682 | 1401790 |
| *SL1344_1311* | *lpp* | | | | - | 1416505 | 1416230 | 1416467 |
| *SL1344_1311* | *lpp* | | | | - | 1416505 | 1416230 | 1416467 |
| *SL1344_1371* | *ydhF* | | | | + | 1471902 | 1471635 | 1471875 |
| *SL1344_1373* | *asSL1373* | | | | - | 4778995 | 1473398 | 1475438 |
| *SL1344_1379* | *mliC* | 1.81 | | | + | 1479085 | 1477958 | 1479080 |
| *SL1344_1449* | *marA* | | | | - | | 1553946 | 1554381 |
| *SL1344_1493* | *osmC* | 2.67 | | | - | 1601743 | 1601089 | 1601521 |
| *SL1344_1494* | *yddX* | 2.96 | | | + | 1601773 | 1602033 | 1602249 |
| *SL1344_1496* | *sfcA* | | | | + | 1602588 | 1602663 | 1604361 |
| *SL1344_1509* | *narY* | | | | + | | 1621276 | 1622821 |
| *SL1344_1518* | *yncD* | 2.26 | | | + | | 1630762 | 1632883 |
| *SL1344_1546* | | | | | + | | 1662322 | 1662760 |
| *SL1344_1563* | *PBPb* | 1.26 | | | + | 1680392 | 1680743 | 1681505 |
| *SL1344_1562* | | | | | - | | 1679492 | 1679837 |
| *SL1344_1565* | | | | | + | | 1682183 | 1682915 |
| *SL1344_1582* | *ynaF* | | | | + | | 1702983 | 1703418 |
| *SL1344_1607* | | | | | - | 1727733 | 1726800 | 1727706 |
| *SL1344_1608* | | | | | + | | 1727824 | 1728754 |
| *SL1344_1637* | *osmB* | 5.12 | -2.47 | | + | 1756633 | 1756775 | 1756994 |
| *SL1344_1640* | *yciM* | | | | - | | 1758367 | 1759537 |
| *SL1344_1644A* | *ymiA* | -1.10 | | | - | 1765037 | 1764838 | 1765000 |
| *SL1344_1654* | *trpE* | | | | + | | 1775402 | 1776965 |
| *SL1344_1659* | *yciG* | 3.01 | | | + | 1782355 | 1782410 | 1782593 |
| *SL1344_1792* | | | | | - | | 1916256 | 1916457 |
| *SL1344_1793* | *pagO* | | | | + | 1917054 | 1917074 | 1917989 |
| *SL1344_1792* | | | | | - | | 1916256 | 1916457 |
| *SL1344_1793* | *pagO* | | | | + | 1917054 | 1917074 | 1917989 |
| *SL1344_1836* | *aspS* | | | | - | | 1952677 | 1954450 |
| *SL1344_1857* | *motB* | -3.24 | | 2.25 | - | 1977502 | 1976764 | 1977694 |
| *SL1344_1860* | *flhD* | -1.87 | | | - | 1979837 | 1979283 | 1979634 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| *SL1344_1860* | *flhD* | -1.87 | | | - | 1979837 | 1979283 | 1979634 |
| *SL1344_1863* | *otsB* | | -1.33 | | - | 1983117 | 1982263 | 1983066 |
| *SL1344_1889* | *fliD* | -2.94 | | 1.99 | + | | 2006969 | 2008373 |
| *SL1344_1911* | *rcsA* | 1.72 | | | + | | 2024994 | 2025618 |
| *DsrA* | *DsrA* | | | | - | | 2026216 | 2026302 |
| *SL1344_1937* | | | | | - | | 2047581 | 2048922 |
| *SL1344_1969* | | | | | + | | 2074182 | 2075010 |
| *SL1344_1983* | | | | | + | | 2084635 | 2086330 |
| *SL1344_2057* | *udg* | | | | - | | 2155672 | 2156839 |
| *SL1344_2057* | *udg* | 0.98 | | | - | 2156959 | 2155672 | 2156839 |
| *SL1344_2078* | *wcaK* | 2.91 | | | - | | 2181675 | 2183154 |
| *SL1344_2093* | *wzc* | 4.43 | | | - | | 2196615 | 2198775 |
| *SL1344_2103* | | | | | + | | 2211999 | 2213241 |
| *SL1344_2125* | *rcnB* | 0.75 | | | + | 2239870 | 2239970 | 2240285 |
| *SL1344_2124* | *thiM* | | | | - | 2239713 | 2238763 | 2239561 |
| *SL1344_2144* | *bglX* | | | | - | | 2258888 | 2261186 |
| *SL1344_2208* | *oafA* | -1.23 | | | + | | 2329845 | 2331675 |
| *SL1344_2229* | *asnapA* | | | | - | 2355822 | 2354133 | 2356620 |
| *SL1344_2335* | *accD* | | | | - | | 2476405 | 2477320 |
| *SL1344_2353* | *aroC* | | | | - | 2493498 | 2493377 | 2494310 |
| *SL1344_2368* | | | | | - | 2511814 | 2511512 | 2511755 |
| *SL1344_2374* | | | | | + | | 2519935 | 2520934 |
| *SL1344_2416* | | | | | + | | 2560298 | 2561576 |
| *SL1344_2435* | *maeB* | | | | - | | 2577694 | 2579974 |
| *RS27105* | | | | | - | | 2586885 | 2587084 |
| *SL1344_2459* | *yfgE* | | | | - | | 2607575 | 2608301 |
| *SL1344_2462* | *purM* | | | | + | | 2610788 | 2611826 |
| *SL1344_2474* | *shdA* | | | | - | | 2625305 | 2631458 |
| *SL1344_2486* | *yfgA* | | | | - | 2656287 | 2656412 | 2657579 |
| *SL1344_2494* | | | | | - | | 2665478 | 2670413 |
| *SL1344_2520* | *cadB* | | | | + | 2696182 | 2696252 | 2697584 |

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|---|---|---|---|---|---|---|
| *SL1344_2538* | *yfhL* | | + | 2719376 | 2719406 | 2719667 |
| *SL1344_2546* | *gogB* | | + | | 2726692 | 2728186 |
| *SL1344_2584* | | | - | | 2763221 | 2763455 |
| *SL1344_2632* | | | - | | 2816455 | 2816794 |
| *SL1344_2693* | | | + | | 2873444 | 2874278 |
| *SL1344_2700* | | | - | 2881126 | 2880884 | 2881073 |
| *SL1344_2731* | | -1.67 | + | | 2908637 | 2909921 |
| *SL1344_2746* | | | - | | 2926179 | 2927463 |
| *SL1344_2752* | | | - | | 2930995 | 2932978 |
| *SL1344_2780* | | | - | 2968491 | 2968275 | 2968434 |
| *SL1344_2780* | | 2.68 | - | 2968491 | 2968275 | 2968434 |
| *SL1344_2797* | | | + | | 2982015 | 2983200 |
| *SL1344_2806* | *csrA* | | - | 2993839 | 2993946 | 2996577 |
| *SL1344_2850* | *orgA* | -1.41 | - | | 3037572 | 3038330 |
| *SL1344_2855* | *hilD* | -0.66 | + | | 3040411 | 3041341 |
| *SL1344_2904* | *nlpD* | 1.39 | - | | 3089109 | 3090243 |
| *SL1344_2933* | *mazG* | | - | 3122960 | 3122072 | 3122873 |
| *SL1344_2934* | *SteA* | | + | | 3123478 | 3123622 |
| *SL1344_2941* | *gudD* | | - | | 3132001 | 3133342 |
| *SL1344_2944* | | | - | 3137017 | 3137006 | 3137789 |
| *ST4-CrsA* | *CsrA* | | - | | 3138522 | 3138160 |
| *SL1344_2966* | | | + | | 3159365 | 3160253 |
| *SL1344_3002* | *yohM* | | + | | 3205638 | 3206475 |
| *SL1344_3008* | *stdA* | | - | | 3212551 | 3213262 |
| *SL1344_3020* | *xerD* | | - | | 3225144 | 3226041 |
| *SL1344_3043* | *yggB* | 1.24 | - | 3250061 | 3249143 | 3250004 |
| *STnc3030* | *STnc3030* | | + | | 3250106 | 3250210 |
| *SL1344_3142* | *ygiR* | | - | | 3349641 | 3351813 |
| *SL1344_3175* | *ygiF* | | - | | 3387705 | 3389007 |
| *SL1344_3187* | *yqjH* | | - | | 3399863 | 3400631 |
| *SL1344_3188* | *yqjI* | | + | 3400843 | 3400862 | 3401510 |

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|---|---|---|---|---|---|---|---|---|
| *SL1344_3215* | *tdcC* | -1.58 | | 2.05 | - | | 3430738 | 3432070 |
| *SL1344_3299* | *yhbL* | | | | - | | 3511028 | 3511682 |
| *SL1344_3344* | *mreD* | | | | - | | 3563818 | 3564871 |
| *SL1344_3345* | *mreC* | | | | - | | 3563818 | 3564871 |
| *SL1344_3345* | *mreC* | | | | - | | 3564935 | 3565979 |
| *SL1344_3376* | *sapG* | | | | + | | 3601252 | 3602629 |
| *SL1344_3383* | *rpsD* | | | | - | | 3605797 | 3606418 |
| *SL1344_3392* | *rplF* | | | | - | | 3610349 | 3610883 |
| *SL1344_3395* | *rplE* | | | | - | | 3611641 | 3612181 |
| *SL1344_3404* | *rplB* | | | | - | | 3615284 | 3616106 |
| *SL1344_3406* | *rplD* | | | | - | | 3616422 | 3617028 |
| *SL1344_3452* | *damX* | | | | - | | 3661225 | 3662503 |
| *SL1344_3466* | *yhgE* | | | | - | | 3675995 | 3677705 |
| *SL1344_3550* | *yhhJ* | | | | - | | 3774279 | 3777021 |
| *SL1344_3586* | *yhjR* | | | | - | | 3825540 | 3825744 |
| *SL1344_3587* | *yhjS* | | | | + | 3826276 | 3825988 | 3827560 |
| *SL1344_3656* | *sadA* | | | | + | | 3902542 | 3906928 |
| *SL1344_3684* | *rfaI* | -0.55 | | | - | | 3935847 | 3936927 |
| *SL1344_3690* | *kdtA* | | | | + | | 3940651 | 3941929 |
| *SL1344_3726* | *slsA* | | | | + | | 3981152 | 3981833 |
| *SL1344_3728* | *mgtB* | | | | - | | 3982855 | 3985582 |
| *SL1344_3759* | | | | | - | | 4014902 | 4015823 |
| *SL1344_3776* | *hslT* | | 1.85 | 1.73 | - | 4031742 | 4031228 | 4031642 |
| *SL1344_3788* | *torA* | | | | - | | 4042123 | 4044676 |
| *SL1344_3805* | *dnaA* | | | | - | | 4064937 | 4066338 |
| *SL1344_3849* | *rbsA* | | | 2.23 | + | | 4113396 | 4114902 |
| *SL1344_3873* | *gppA* | | | | - | | 4143371 | 4144853 |
| *SL1344_3886* | | | | | + | | 4157586 | 4158666 |
| *SL1344_3894* | *ascyaA* | | | | + | 4168729 | 4167911 | 4170458 |
| *SL1344_3895* | | | | | + | | 4170565 | 4170919 |
| *SL1344_3928* | *tatB* | | | | + | | 4202306 | 4202855 |

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|---|---|---|---|---|---|---|---|---|
| *SL1344_3946* | *yihG* | | | | - | | 4226272 | 4227181 |
| *SL1344_3987* | | | -1.43 | | + | 4271128 | 4271128 | |
| *SL1344_3988* | *yiiG* | | | | + | | 4271758 | 4272859 |
| *SL1344_3999* | *rhaT* | | | | - | | 4282336 | 4283371 |
| *SL1344_4000* | | | | | + | | 4283989 | 4284673 |
| *SL1344_4001* | | | | | - | | 4284830 | 4286138 |
| *SL1344_4003* | | | | | - | | 4286664 | 4287648 |
| *SL1344_4007* | *cpxA* | | | | - | | 4289813 | 4291187 |
| *SL1344_4031* | *yiiQ* | | | | - | | 4312582 | 4313179 |
| *SL1344_4047* | | | | | - | | 4328321 | 4330112 |
| *SL1344_4051* | | | | | - | | 4334999 | 4335719 |
| *SL1344_4109* | *hupA* | | | | + | 4407936 | 4407262 | 4407853 |
| *SL1344_4119* | *aceA* | | | | + | | 4423327 | 4424929 |
| *SL1344_4124* | *yjbB* | | | | + | | 4433577 | 4435209 |
| *SL1344_4127* | | | | | + | | 4436181 | 4436721 |
| *SL1344_4131* | | | | | - | | 4440131 | 4440422 |
| *SL1344_4197* | *assiiE* | | | | + | 4514974 | 4503765 | 4520445 |
| *SL1344_4239* | | | | | - | 4570230 | 4569885 | 4570152 |
| *SL1344_4255* | *asphoN* | | | | - | 4584425 | 4584168 | 4584921 |
| *SL1344_4333* | *ytfF* | | | | - | | 4657713 | 4658679 |
| *SL1344_4339* | *ytfK* | 1.72 | | | + | 4663853 | 4663082 | 4663639 |
| *SL1344_4378* | | | | | + | | 4709979 | 4711953 |
| *SL1344_4387* | *mgtA* | | | | + | | 4720270 | 4722979 |
| *SL1344_4416* | *yjgB* | 3.23 | | | - | | 4750351 | 4751371 |
| *SL1344_4434* | | | | | + | | 4779036 | 4779948 |

| **predicted target (Locus ID)** | **Gene** | **description** |
|---|---|---|
| *SL1344_0012* | *dnaK* | Chaperone protein dnaK |
| *SL1344_0017* | | hypothetical membrane protein |
| *SL1344_0019* | | hypothetical chitinase |
| *SL1344_0028* | *bcfH* | hypothetical exported protein |
| *SL1344_0029* | | hypothetical membrane protein |
| *SL1344_0040* | *nhaA* | Na(+)/H(+) antiporter 1 |
| *SL1344_0047* | *ileS* | isoleucyl-tRNA synthetase |
| *SL1344_0056* | | oxaloacetate decarboxylase alpha chain |
| *SL1344_0074* | *caiA* | probable carnitine operon oxidoreductase CaiA |
| *SL1344_0088* | *folA* | dihydrofolate reductase type I |
| *SL1344_0131* | *ftsQ* | cell division protein FtsQ |
| *SL1344_0135* | *yacA* | conserved hypothetical protein |
| *SL1344_0152* | *aceE* | pyruvate dehydrogenase E1 component |
| *SL1344_0181* | *panD* | aspartate 1-decarboxylase |
| *SL1344_0227* | *lpxD* | UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase |
| *SL1344_0368* | *yaiU* | puative autotransporter/virulence factor |
| *SL1344_0379* | *psiF* | phosphate starvation-inducible protein |
| *STnc4150* | | |
| *SL1344_0513* | | probable metabolite transport protein |
| *SL1344_0521* | *allD* | ureidoglycolate dehydrogenase |
| *SL1344_0536* | *fimA* | type-1 fimbrial protein, a chain precursor |
| *SL1344_0535* | *folD* | bifunctional methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase |
| *SL1344_0574* | *fes* | enterochelin esterase |
| *SL1344_0577* | *fepE* | Ferric enterobactin transfer protein |
| *SL1344_0609* | *citF* | citrate lyase alpha chain |

| | | |
|---|---|---|
| *SL1344_0618* | *ccrB* | hypothetical membrane protein |
| *SL1344_0621* | *lipA* | lipoic acid synthetase |
| *SL1344_0622* | *ybeF* | lysR-family transcriptional regulator |
| *SL1344_0718* | *sucA* | 2-oxoglutarate dehydrogenase E1 component |
| *SL1344_0758* | *modA* | molybdate-binding periplasmic protein precursor |
| *SL1344_0776* | *slrP* | Type III secretion system effector protein, leucine rich repeat-Acts as a ubiquitin ligase for thioredoxin |
| *SL1344_0779* | *moaB* | molybdenum cofactor biosynthesis protein B |
| *SL1344_0825* | *yliB* | hypothetical ABC transporter periplasmic binding protein |
| *SL1344_0834* | | hypothetical flavoprotein |
| *SL1344_0839* | *dacC* | D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 6 precursor) |
| *SL1344_0838* | *yliJ* | glutathione s-transferase family protein |
| *SL1344_0844* | | hypothetical membrane protein |
| *SL1344_0864* | *artM* | arginine transport system permease protein ArtQ |
| *SL1344_0880* | *ybjY* | hypothetical exported protein |
| *SL1344_0908* | | hypothetical conserved hypothetical protein |
| *SL1344_0952* | | Gifsy-2 replication Protein O |
| *SL1344_1026* | *pipA* | Type III secretion system effector protein, homologous to pipA |
| *SL1344_1107* | *mviN* | virulence factor MviN |
| *SL1344_1109* | *flgM* | negative regulator of flagellin synthesis (anti-sigma factor) |
| *SL1344_1126* | *maf-a* | septum formation inhibitor Maf |
| *SL1344_1127* | *yceD* | conserved hypothetical protein |
| *SL1344_1137* | *tmK* | Thymidylate kinase |
| *SL1344_1149* | *ycfJ* | hypothetical secreted protein |
| *SL1344_1177* | | predicted bacteriophage protein |
| *STnc150* | | |
| *SL1344_1212* | | annotation |
| *SL1344_1235* | | hypotheticalñ exported protein |
| *SL1344_1234* | *gdhA* | glutamate dehydrogenase |
| *STnc1640* | | ncRNA |
| *SL1344_1256* | *ydjM* | membrane protein |
| *STnc3570* | *STnc3570* | |

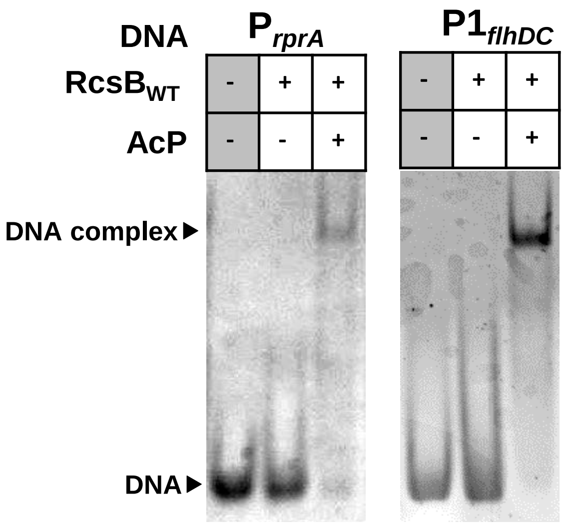
| | | |
|---|---|---|
| *rprA* | *rprA* | antisense sRNA RprA |
| *SL1344_1311* | *lpp* | major outer membrane lipoprotein |
| *SL1344_1311* | *lpp* | major outer membrane lipoprotein |
| *SL1344_1371* | *ydhF* | hypothetical oxidoreductase |
| *SL1344_1373* | *asSL1373* | hypothetical membrane protein |
| *SL1344_1379* | *mliC* | lipoprotein |
| *SL1344_1449* | *marA* | multiple antibiotic resistance protein MarA |
| *SL1344_1493* | *osmC* | osmotically inducible protein C |
| *SL1344_1494* | *yddX* | conserved hypothetical protein |
| *SL1344_1496* | *sfcA* | NAD-linked malic enzyme; malate oxidoreductase |
| *SL1344_1509* | *narY* | respiratory nitrate reductase 2 beta chain |
| *SL1344_1518* | *yncD* | probable TonB-dependent receptor YncD precursor |
| *SL1344_1546* | | hypothetical phosphotransferase enzyme |
| *SL1344_1563* | *PBPb* | hypothetical periplasmic amino acid-binding protein |
| *SL1344_1562* | | hypothetical membrane protein |
| *SL1344_1565* | | ABC transporter ATP-binding subunit |
| *SL1344_1582* | *ynaF* | conserved hypothetical protein |
| *SL1344_1607* | | LysR family transcriptional regulator |
| *SL1344_1608* | | aromatic alcohol reductase |
| *SL1344_1637* | *osmB* | osmotically inducible lipoprotein B precursor |
| *SL1344_1640* | *yciM* | conserved hypothetical protein |
| *SL1344_1644A* | *ymiA* | YmiA family putative membrane protein |
| *SL1344_1654* | *trpE* | anthranilate synthase component I |
| *SL1344_1659* | *yciG* | conserved hypothetical protein |
| *SL1344_1792* | | hypothetical protein |
| *SL1344_1793* | *pagO* | inner membrane protein (PagO) |
| *SL1344_1792* | | hypothetical protein |
| *SL1344_1793* | *pagO* | inner memebrane protein |
| *SL1344_1836* | *aspS* | Aspartyl-tRNA synthetase |
| *SL1344_1857* | *motB* | motility protein B |
| *SL1344_1860* | *flhD* | Transcriptional activator flhD. |

| | | |
|---|---|---|
| *SL1344_1860* | *flhD* | Transcriptional activator flhD. |
| *SL1344_1863* | *otsB* | trehalose phosphatase |
| *SL1344_1889* | *fliD* | flagellar hook associated protein (FliD) |
| *SL1344_1911* | *rcsA* | colanic acid capsullar biosynthesis activation protein A |
| *DsrA* | *DsrA* | |
| *SL1344_1937* | | predicted bacteriophage protein |
| *SL1344_1969* | | predicted bacteriophage protein |
| *SL1344_1983* | | hypothetical exported protein |
| *SL1344_2057* | *udg* | UDP-glucose 6-dehydrogenase |
| *SL1344_2057* | *udg* | UDP-glucose 6-dehydrogenase |
| *SL1344_2078* | *wcaK* | colanic acid biosynthesis protein |
| *SL1344_2093* | *wzc* | tyrosine-protein kinase |
| *SL1344_2103* | | hypothetical efflux system protein |
| *SL1344_2125* | *rcnB* | nickel/cobalt homeostasis protein RcnB |
| *SL1344_2124* | *thiM* | Hydroxyethylthiazole kinase |
| *SL1344_2144* | *bglX* | periplasmic beta-glucosidase precursor |
| *SL1344_2208* | *oafA* | hypothetical lipopolysaccharide modification acyltransferase |
| *SL1344_2229* | *asnapA* | probable nitrate reductase |
| *SL1344_2335* | *accD* | acetyl-CoA carboxylase beta subunit |
| *SL1344_2353* | *aroC* | Chorismate synthase |
| *SL1344_2368* | | conserved hypothetical protein |
| *SL1344_2374* | | hypothetical ion-channel protein |
| *SL1344_2416* | | conserved hypothetical protein |
| *SL1344_2435* | *maeB* | NADP-dependent malate dehydrogenase (decarboxylating) |
| *RS27105* | | hypothetical protein |
| *SL1344_2459* | *yfgE* | conserved hypothetical protein |
| *SL1344_2462* | *purM* | Phosphoribosylformylglycinamidine cyclo-ligase |
| *SL1344_2474* | *shdA* | host colonisation factor (ShdA) |
| *SL1344_2486* | *yfgA* | conserved hypothetical protein |
| *SL1344_2494* | | hypothetical lipoprotein |
| *SL1344_2520* | *cadB* | probable cadaverine/lysine antiporter |

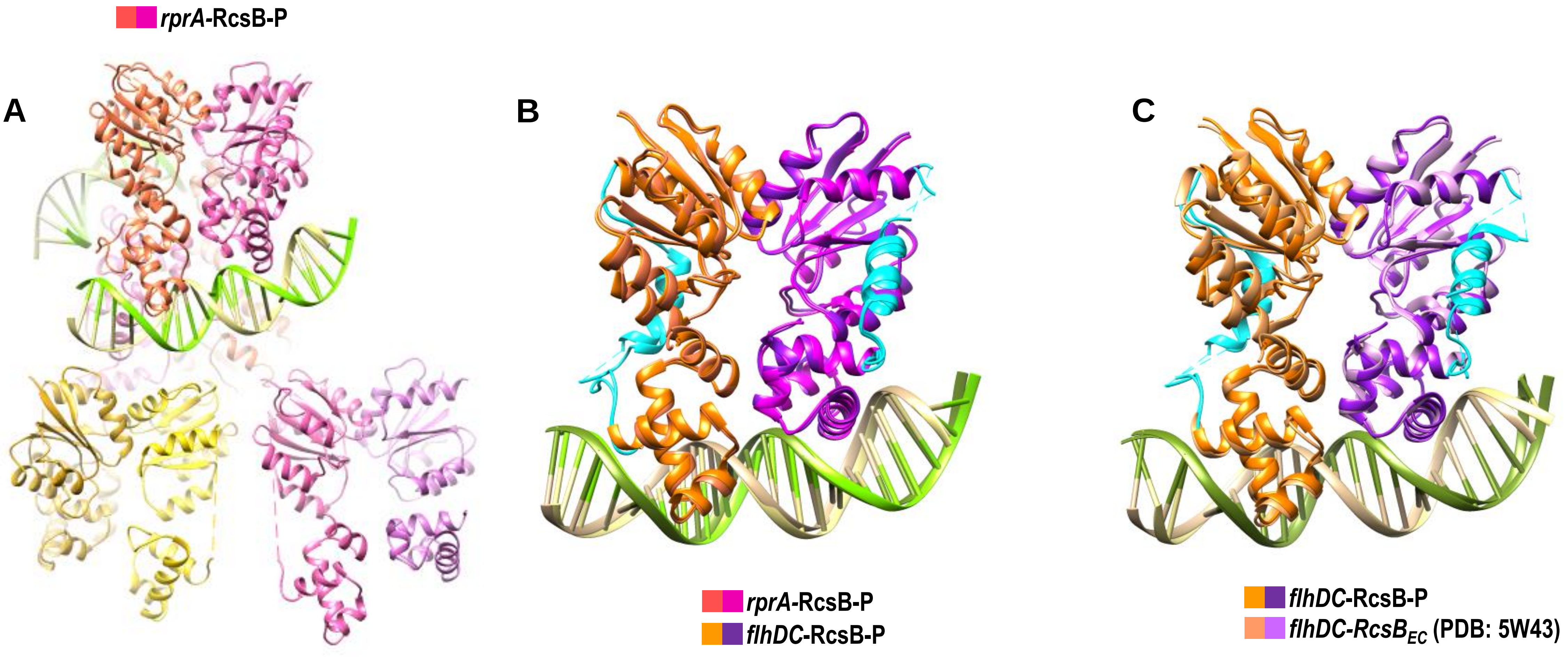
| | | |
|---|---|---|
| *SL1344_2538* | *yfhL* | hypothetical ferredoxin |
| *SL1344_2546* | *gogB* | Type III secretion system effector protein |
| *SL1344_2584* | | hypothetical damage-inducible protein |
| *SL1344_2632* | | hypothetical exported protein |
| *SL1344_2693* | | phage capsid protein |
| *SL1344_2700* | | predicted bacteriophage protein |
| *SL1344_2731* | | conserved hypothetical protein |
| *SL1344_2746* | | hypothetical inner membrane protein |
| *SL1344_2752* | | probable terminase subunit |
| *SL1344_2780* | | YqaE/Pmp3 family membrane protein |
| *SL1344_2780* | | YqaE/Pmp3 family membrane protein |
| *SL1344_2797* | | hypothetical transmembrane transport protein |
| *SL1344_2806* | *csrA* | carbon storage regulator |
| *SL1344_2850* | *orgA* | type III secretion system apparatus |
| *SL1344_2855* | *hilD* | AraC-family transcriptional regulator |
| *SL1344_2904* | *nlpD* | lipoprotein NlpD precursor |
| *SL1344_2933* | *mazG* | nucleoside triphosphate pyrophosphohydrolase |
| *SL1344_2934* | *SteA* | fimbrial protein SteA |
| *SL1344_2941* | *gudD* | probable glucarate dehydratase 1 |
| *SL1344_2944* | | conserved hypothetical protein |
| *ST4-CrsA* | *CsrA* | |
| *SL1344_2966* | | EamA family transporter RarD |
| *SL1344_3002* | *yohM* | hypothetical High affinity Nickel transport protein |
| *SL1344_3008* | *stdA* | fimbrial protein StdA |
| *SL1344_3020* | *xerD* | Tyrosine recombinase xerD. |
| *SL1344_3043* | *yggB* | mechanosensitive ion channel protein MscS |
| *STnc3030* | *STnc3030* | |
| *SL1344_3142* | *ygiR* | conserved hypothetical protein |
| *SL1344_3175* | *ygiF* | conserved hypothetical protein |
| *SL1344_3187* | *yqjH* | siderophore-interacting protein |
| *SL1344_3188* | *yqjI* | PadR family transcriptional regulator |

| | | |
|---|---|---|
| *SL1344_3215* | *tdcC* | threonine/serine transporter |
| *SL1344_3299* | *yhbL* | conserved hypothetical protein |
| *SL1344_3344* | *mreD* | rod shape-determining protein |
| *SL1344_3345* | *mreC* | rod shape-determining protein |
| *SL1344_3345* | *mreC* | rod shape-determining protein |
| *SL1344_3376* | *sapG* | potassium transport protein |
| *SL1344_3383* | *rpsD* | 30S ribosomal subunit protein S4 |
| *SL1344_3392* | *rplF* | 50S ribosomal subunit protein L6 |
| *SL1344_3395* | *rplE* | 50S ribosomal subunit protein L5 |
| *SL1344_3404* | *rplB* | 50S ribosomal subunit protein L2 |
| *SL1344_3406* | *rplD* | 50S ribosomal subunit protein L4 |
| *SL1344_3452* | *damX* | cytoplasmic membrane protein with SPOR domain |
| *SL1344_3466* | *yhgE* | hypothetical membrane protein |
| *SL1344_3550* | *yhhJ* | hypothetical ABC-2 type superfamily transport protein |
| *SL1344_3586* | *yhjR* | conserved hypothetical protein |
| *SL1344_3587* | *yhjS* | conserved hypothetical protein |
| *SL1344_3656* | *sadA* | autotransporter |
| *SL1344_3684* | *rfaI* | lipopolysaccharide, 3-galactosyltransferase |
| *SL1344_3690* | *kdtA* | 3-deoxy-D-manno-octulosonic-acid transferase |
| *SL1344_3726* | *slsA* | hydrolase |
| *SL1344_3728* | *mgtB* | Magnesium transport ATPase, P-type 2 |
| *SL1344_3759* | | hypothetical carbohydrate kinase |
| *SL1344_3776* | *hslT* | heat-shock protein IbpA |
| *SL1344_3788* | *torA* | trimethylamine-N-oxide reductase precursor |
| *SL1344_3805* | *dnaA* | chromosomal replication initiator protein |
| *SL1344_3849* | *rbsA* | high affinity ribose transport protein |
| *SL1344_3873* | *gppA* | guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase (guanosine pentaphosphatase) |
| *SL1344_3886* | | conserved hypothetical protein |
| *SL1344_3894* | *ascyaA* | adenylate cyclase |
| *SL1344_3895* | | hypothetical inner membrane protein |
| *SL1344_3928* | *tatB* | sec-independent protein translocase protein |

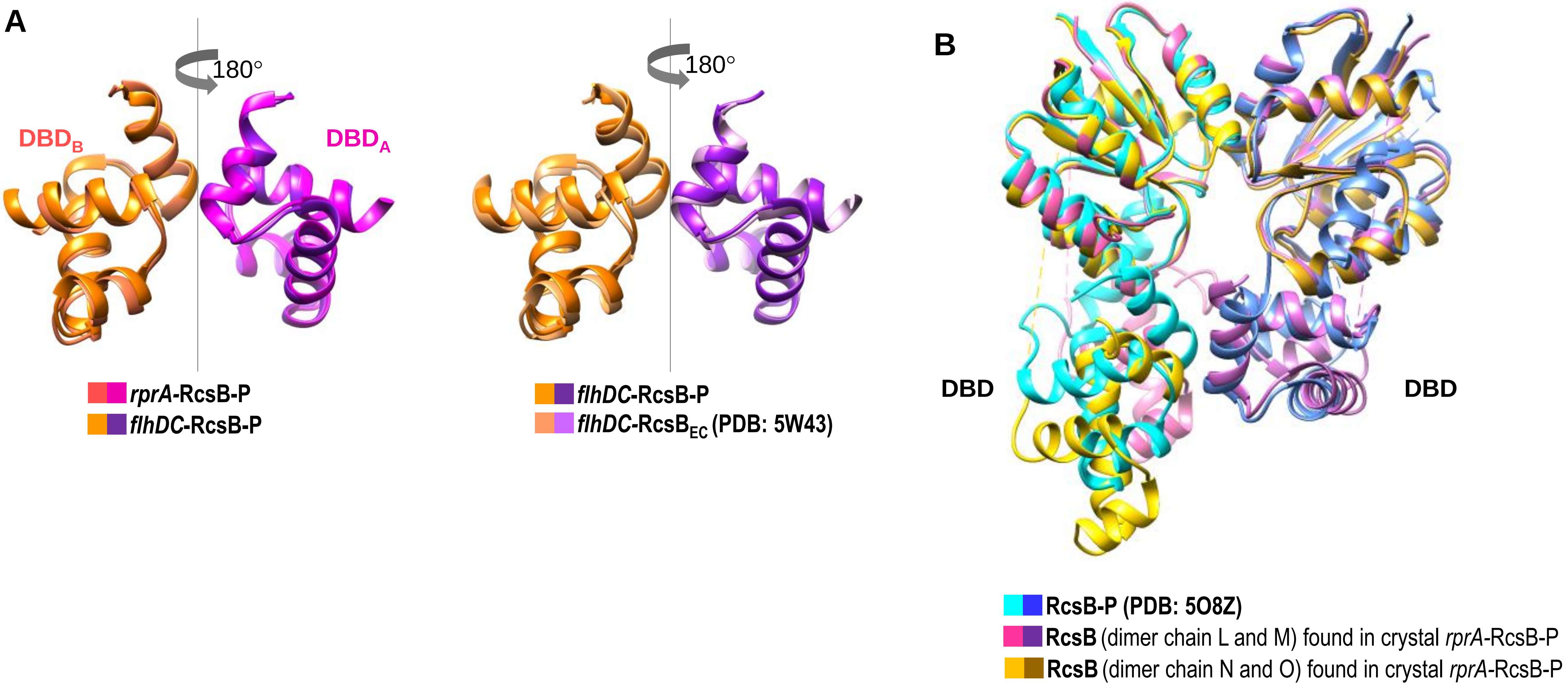
| | | |
|---|---|---|
| *SL1344_3946* | *yihG* | hypothetical acyltransferase |
| *SL1344_3987* | | hypothetical lipoprotein |
| *SL1344_3988* | *yiiG* | hypothetical lipoprotein |
| *SL1344_3999* | *rhaT* | L rhamnose-proton symporter |
| *SL1344_4000* | | conserved hypothetical protein |
| *SL1344_4001* | | hypothetical membrane transport protein |
| *SL1344_4003* | | trap dicarboxylate transporter, dctp subunit |
| *SL1344_4007* | *cpxA* | two-component sensor kinase protein |
| *SL1344_4031* | *yiiQ* | conserved hypothetical protein |
| *SL1344_4047* | | hypothetical arylsulfate sulfotransferase |
| *SL1344_4051* | | inner membrane protein |
| *SL1344_4109* | *hupA* | histone like DNA-binding protein HU-alpha (NS2) (HU-2) |
| *SL1344_4119* | *aceA* | isocitrate lyase |
| *SL1344_4124* | *yjbB* | hypothetical membrane protein |
| *SL1344_4127* | | conserved hypothetical protein |
| *SL1344_4131* | | hypothetical protein |
| *SL1344_4197* | *assiiE* | large repetitive protein |
| *SL1344_4239* | | hypothetical protein |
| *SL1344_4255* | *asphoN* | nonspecific acid phosphatase precursor |
| *SL1344_4333* | *ytfF* | hypothetical membrane protein |
| *SL1344_4339* | *ytfK* | conserved hypothetical protein |
| *SL1344_4378* | | hypothetical BglB-family transcriptional antiterminator |
| *SL1344_4387* | *mgtA* | Mg(2+) transport ATPase, P-type |
| *SL1344_4416* | *yjgB* | hypothetical alcohol dehydrogenase |
| *SL1344_4434* | | |



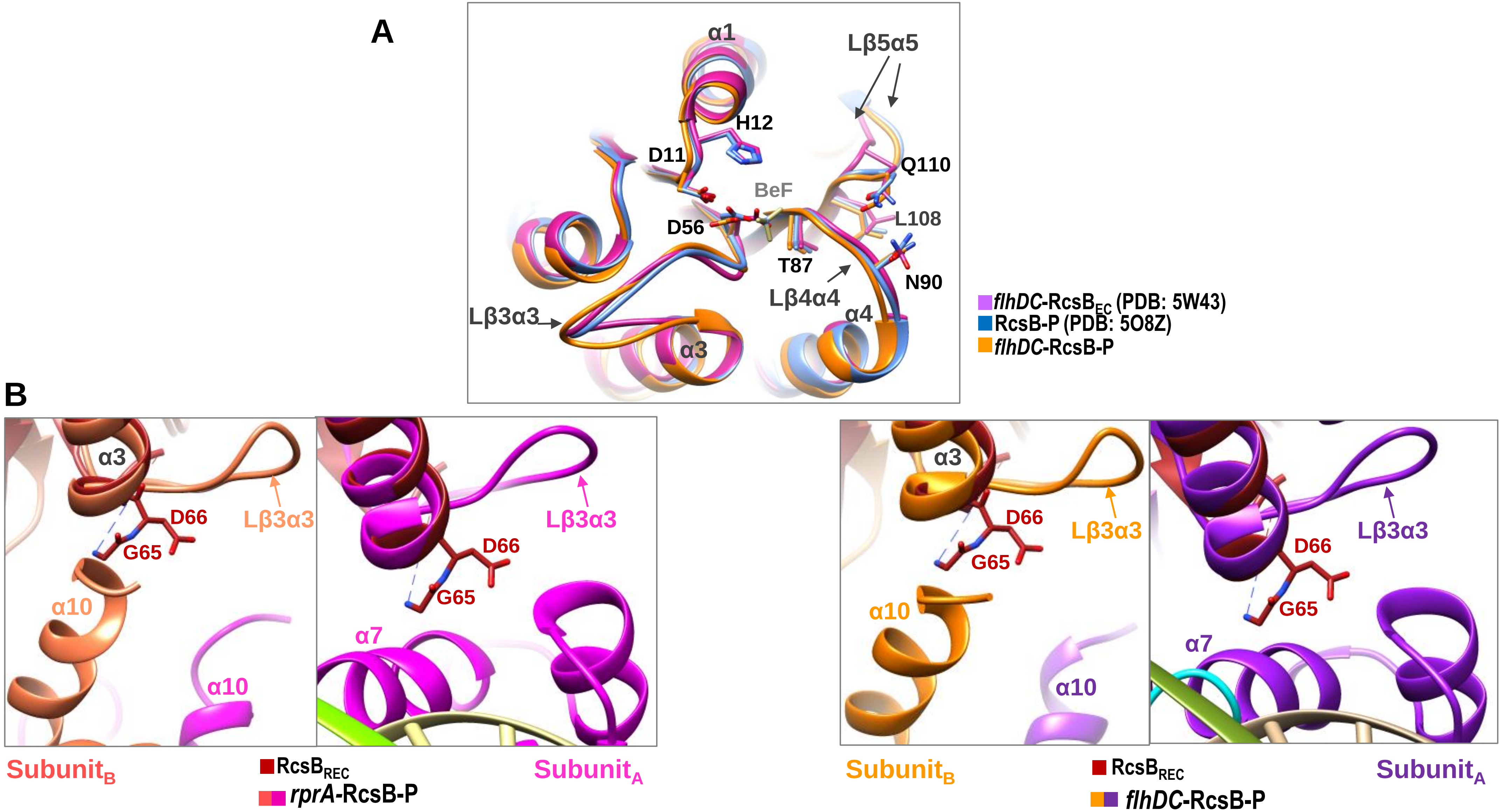
**Supplementary Figure S1.** EMSA experiments performed with RcsB wild-type to test binding to $P_{rprA}$ and $P1_{flhDC}$ of 23-mer in the absence and presence of phosphodonor acetyl phosphate (AcP).



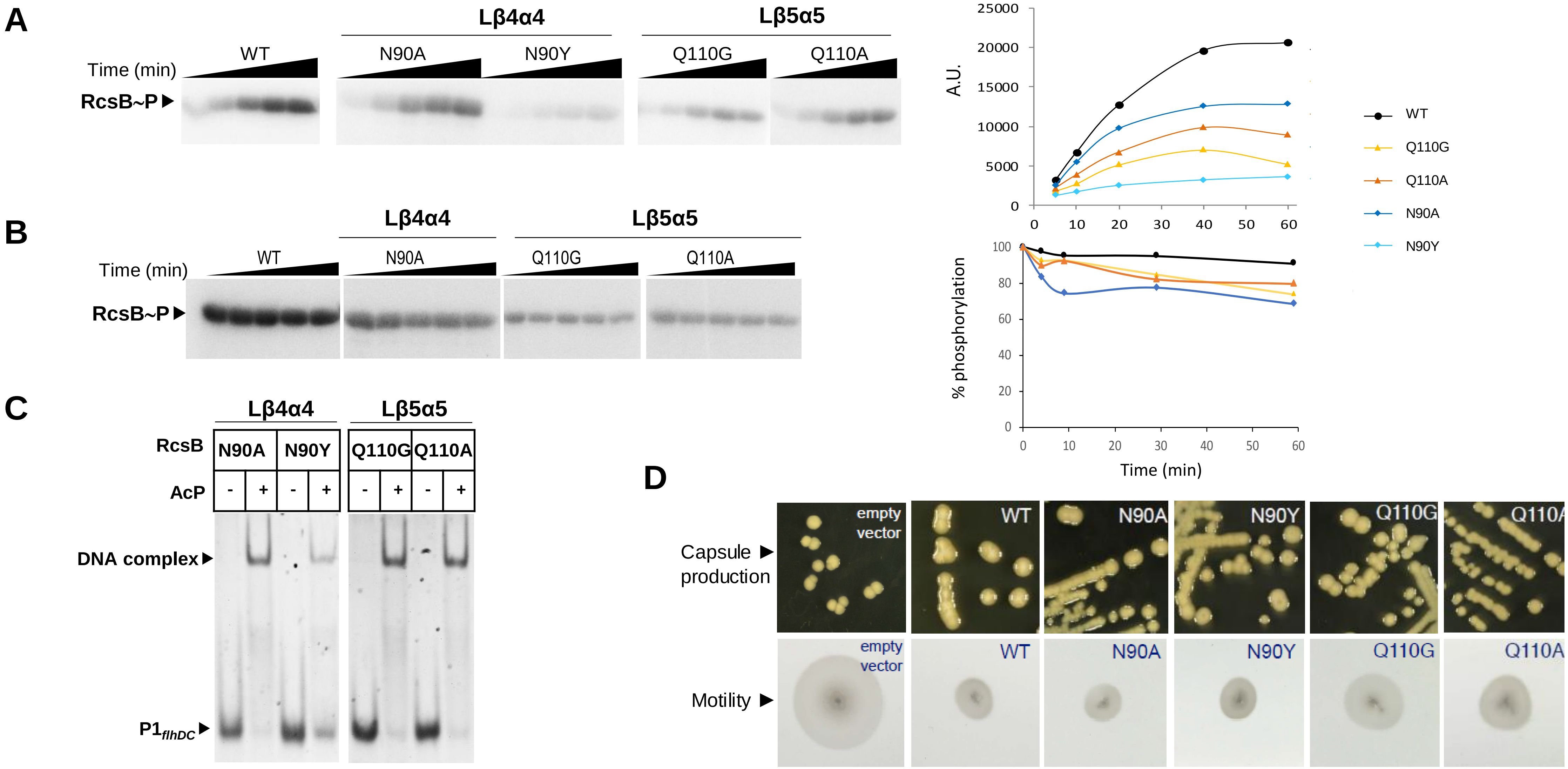
**Supplementary Figure S2.** (A) Asymmetric unit for the crystal having RcsB and P$_{rprA}$ promoter which is formed by two complexes of *rprA*-RcsB-P and two dimers of RcsB. (B) Superposition of the *rprA*-RcsB-P complex with f*lhDC*-RcsB-P complex. (C) Superposition of f*lhDC*-RcsB-P complex with unphosphorylated *flhDC*-RcsB$_{EC}$ (PDB: 5W43).



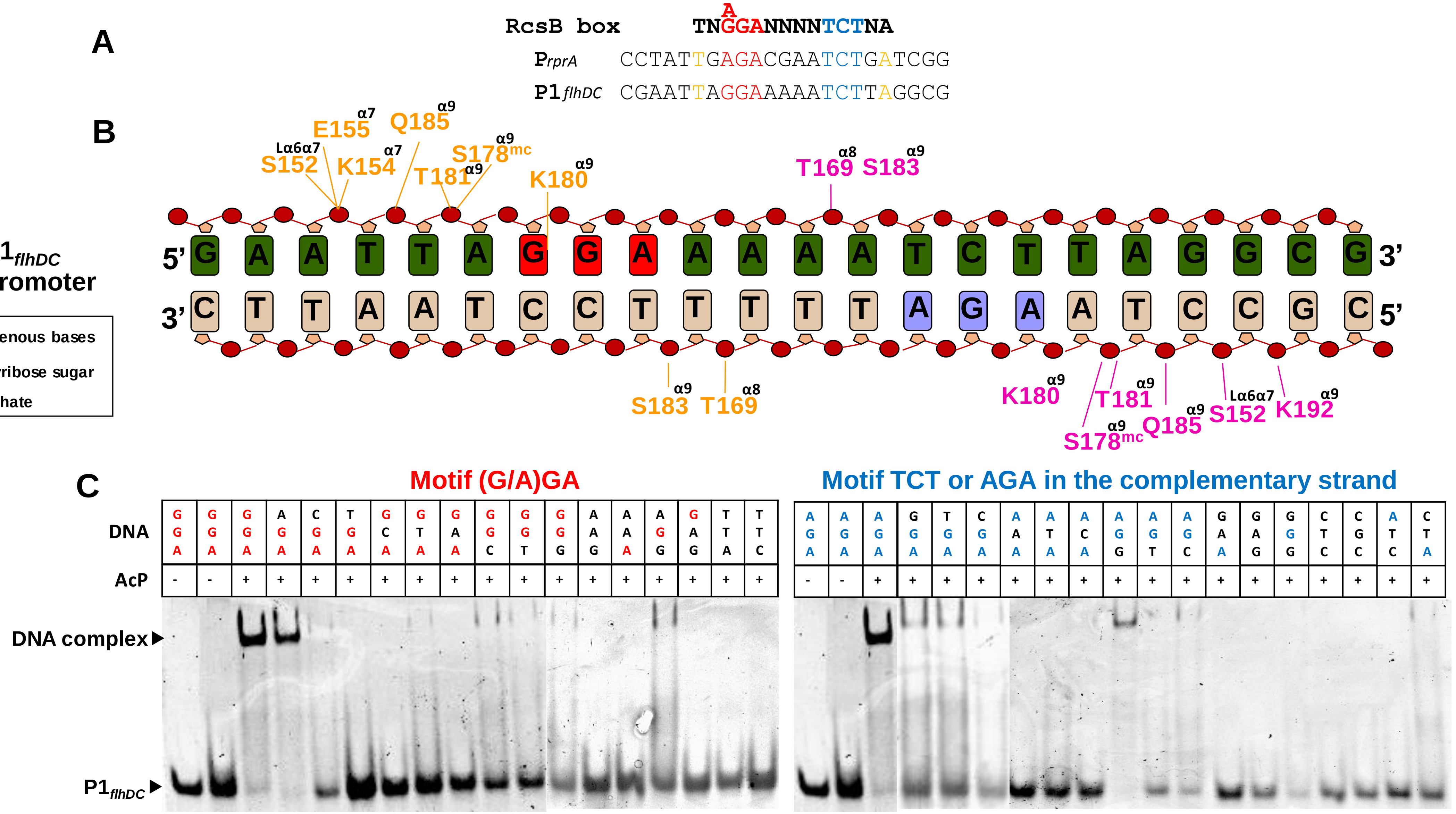
**Supplementary Figure S3.** (A) Superposition of DBD domains found in the dimer of the *rprA*-RcsB-P complex and the *flhDC*-RcsB-P complex (left panel); Superposition of DBDs in the dimer of the *flhDC*-RcsB-P complex and the unphosphorylated *flhDC*-$\text{RcsB}_{\text{EC}}$ complex (PDB: 5W43). (B) Superposition of the RcsB-P dimers found at PDB: 5O8Z and in the crystal containing $\text{P}_{rprA}$ and RcsB-P.



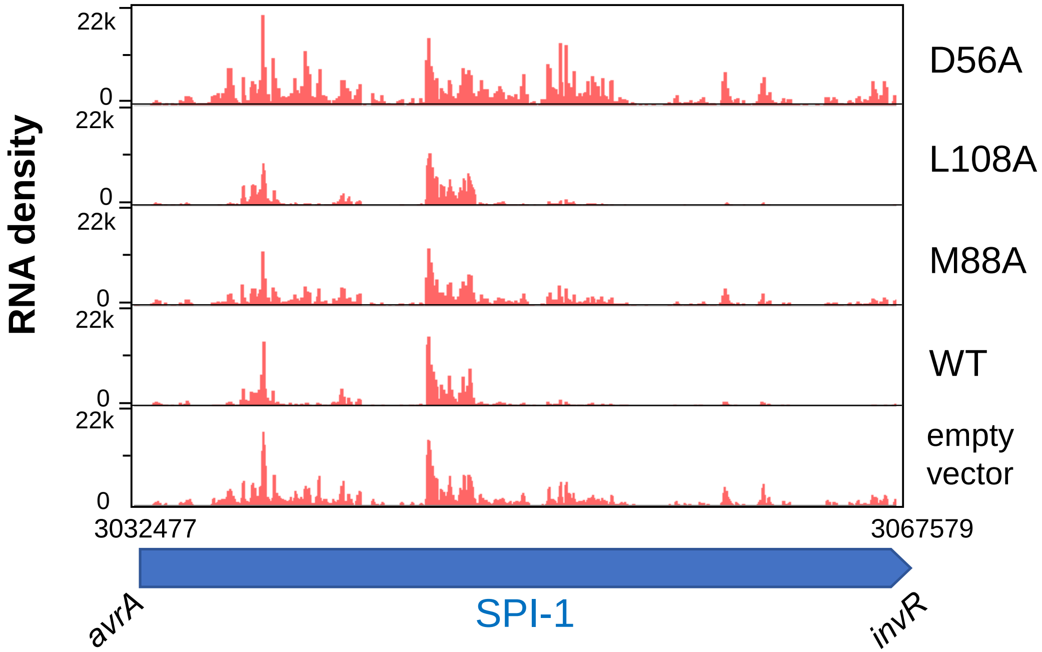
**Supplementary Figure S4.** (A) Zoom of the active site for the REC domain in superposed structure RcsB-P (in blue; PDB: 5O8Z), *flhDC*-RcsB-P complex (in orange) and unphosphorylated *flhDC*-RcsB$_{EC}$ (in magenta, (PDB: 5W43)). (B) Superposition of isolated REC domain in apo form (in red) with *rprA*-RcsB-P complex (in pink and magenta) *flhDC*-RcsB-P complex (in orange and purple). Residues at the end of Lβ3α3 are shown as sticks in the apo form.



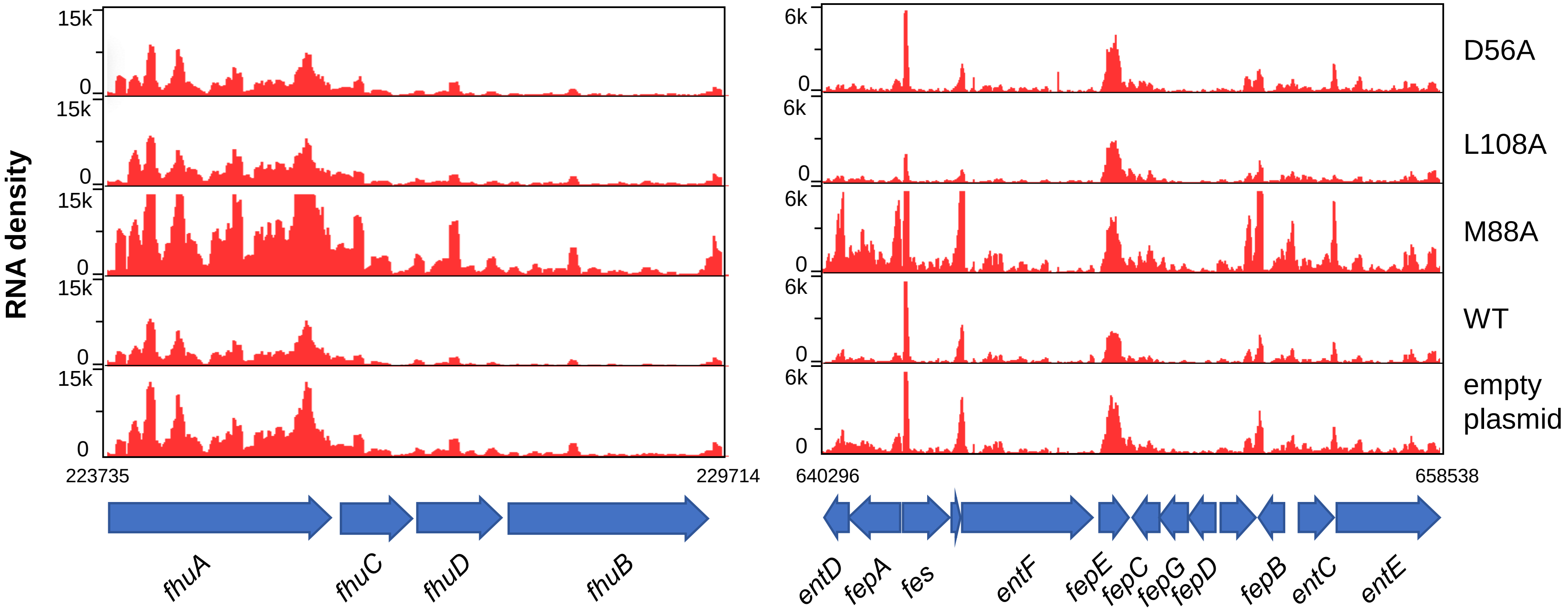
**Supplementary Figure S5**. (A) Phosphorylation of RcsB WT and mutant variants N90A, N90Y, Q110G and Q110A using radioactive phosphodonor AcP at room temperature. Phosphorylation intensity in arbitrary units (A.U.) was obtained with Multi Gauge MFC Application Software (Fujifilm). (B) Dephosphorylation of RcsB at room temperature. Mutant N90Y was not included in the experiment due to its low phosphorylation. Phosphorylation intensity was obtained with Multi Gauge MFC Application Software (Fujifilm) and the percentage of phosphorylation for each sample was calculated with respect to time 0. (C) EMSA experiments performed with RcsB wild-type and mutant variants N90A, N90Y, Q110G and Q110A in order to test binding to $P1_{flhDC}$ in the absence and presence of phosphodonor AcP. (D) Effect of RcsB mutations N90A, N90Y, Q110G and Q110A in capsule formation and motility. Overexpression of RcsB mutants in the *S*. Typhimurium strain MD4821 (*igaA1 ΔrcsB*) to monitor effect on colanic capsule production and motility in vivo. Expression of the WT and empty vector (as control).



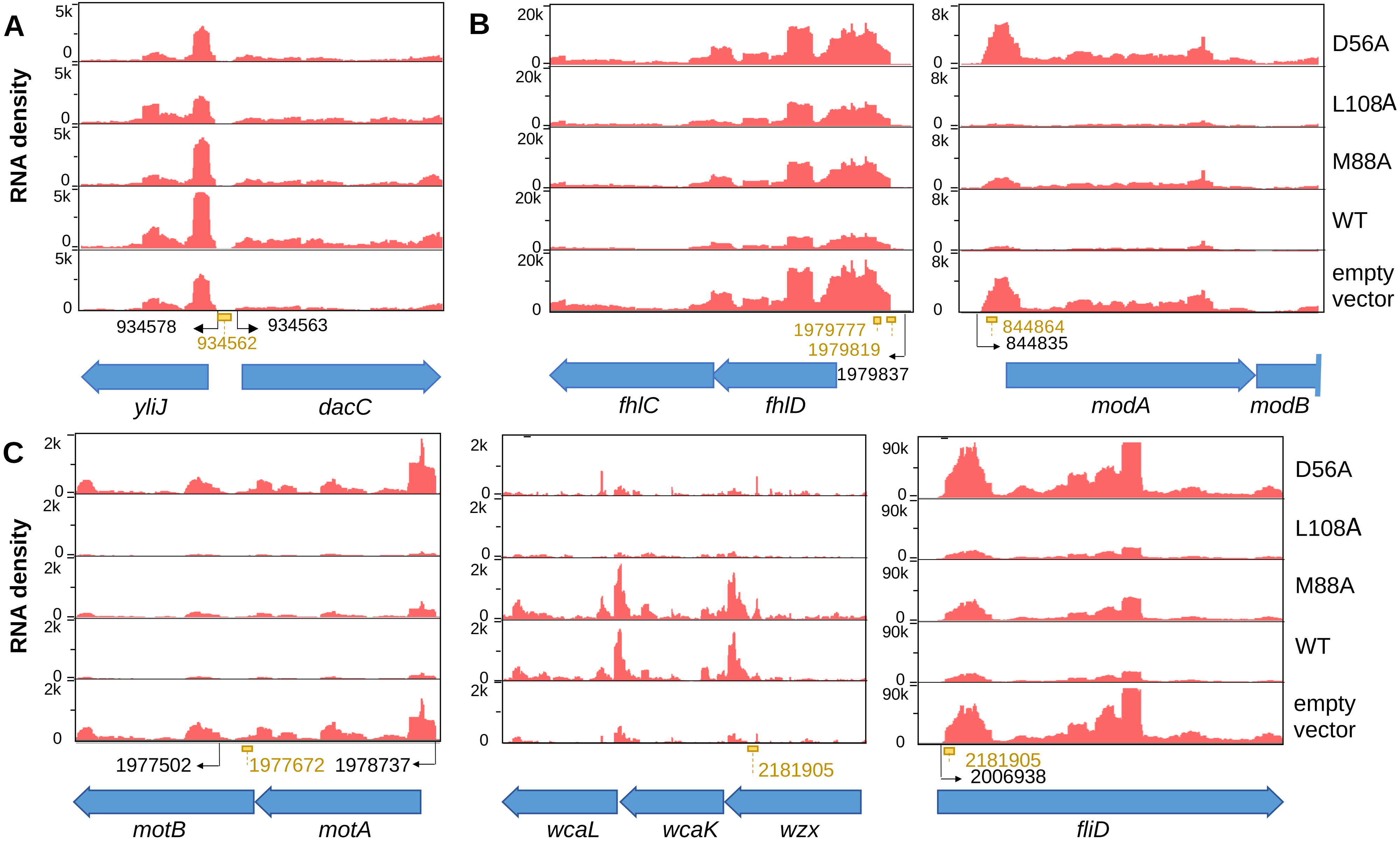
**Supplementary Figure S6.** (A) Sequence comparison of promoter $P_{rprA}$ and $P1_{flhDC}$ highlighting nucleotides in color that form the pseudopalindromic RcsB box. (B) Detail interaction of each DBD domain of the RcsB dimer (in orange and purple) with the $P1_{flhDC}$ promoter indicating the residues involved in the binding with the nucleotides at each strand of the promoter (in dark green and grey). (C) EMSA experiments with $RcsB_{ST}$ and the $P1_{flhDC}$ sequence shown in A, including mutations of nucleotides at motif (G/A)GA shown in red or motif TCT, which is AGA in the complementary strand, shown in blue. Assays were performed in absence and presence of phosphodonor AcP. Mutated residues are colored in black.



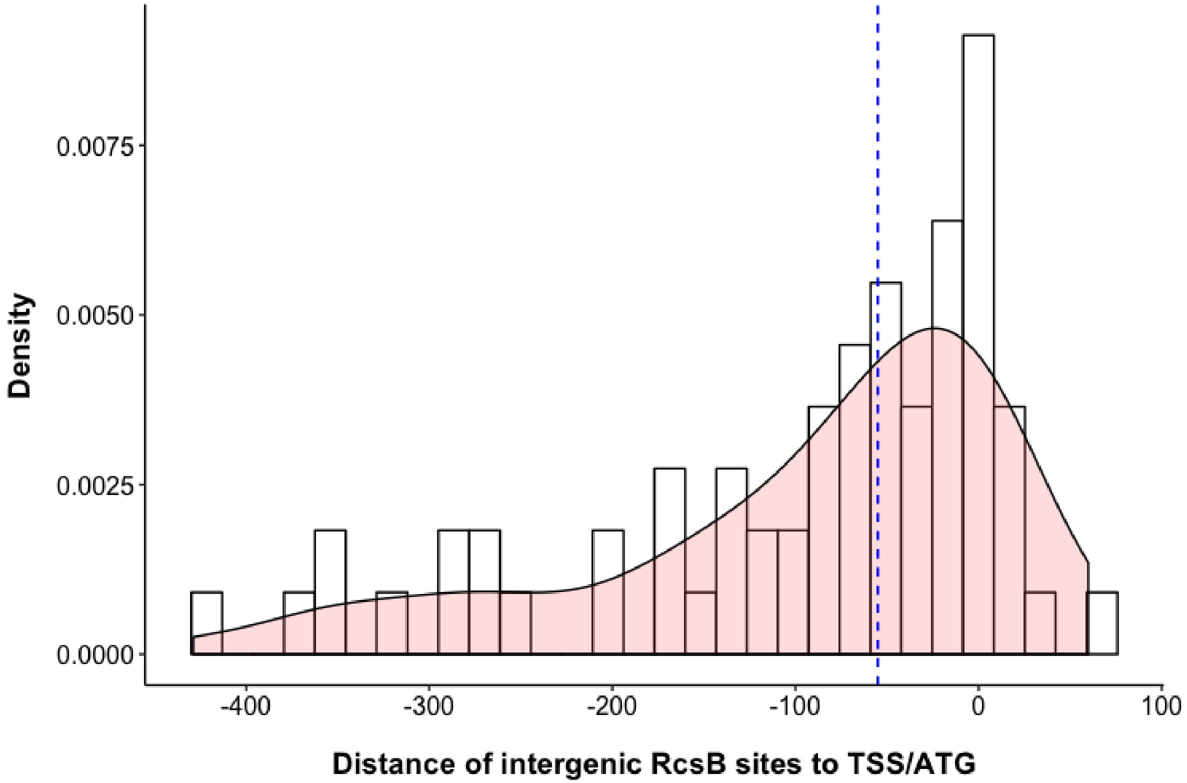
**Supplementary Figure S7**. Read coverage of the genomic region encompassing the *Salmonella* pathogenicity island 1 (SPI-1) in S. Typhimurium strains expressing distinct RcsB variants. The region depicted in the image encompasses from gene *avrA* to *invR*. Values in the X-axis indicate genome coordinates. Values in the Y-axis indicate RNAseq read density profiles.



**Supplementary Figure S8**. Read coverage of the genomic region encompassing iron related genes affected in *S. Typhimurium* strains expressing distinct RcsB variants. Values in the X-axis indicate genome coordinates. Values in the Y-axis indicate RNAseq read density profiles.



**Supplementary Figure S9.** Read coverage of potential RcsB target genes in (A) bidirectional promoter region in intergenic region (*yliJ, dacC*). (B) RcsB motif sites located at 5'-UTR region of target genes. (C) RcsB intragenic motif sites (intra-CDS sites) located close to internal TSS (*motB*), controlling downstream gene (*wcaK*) and intragenic site proximal to ATG codon (*fliD*). Coloured arrows represent gene positions, black arrows indicate TSS, yellow box represent RcsB motif sites. Values in the X-axis indicate genome coordinates. Values in the Y-axis indicate RNAseq read density profiles.

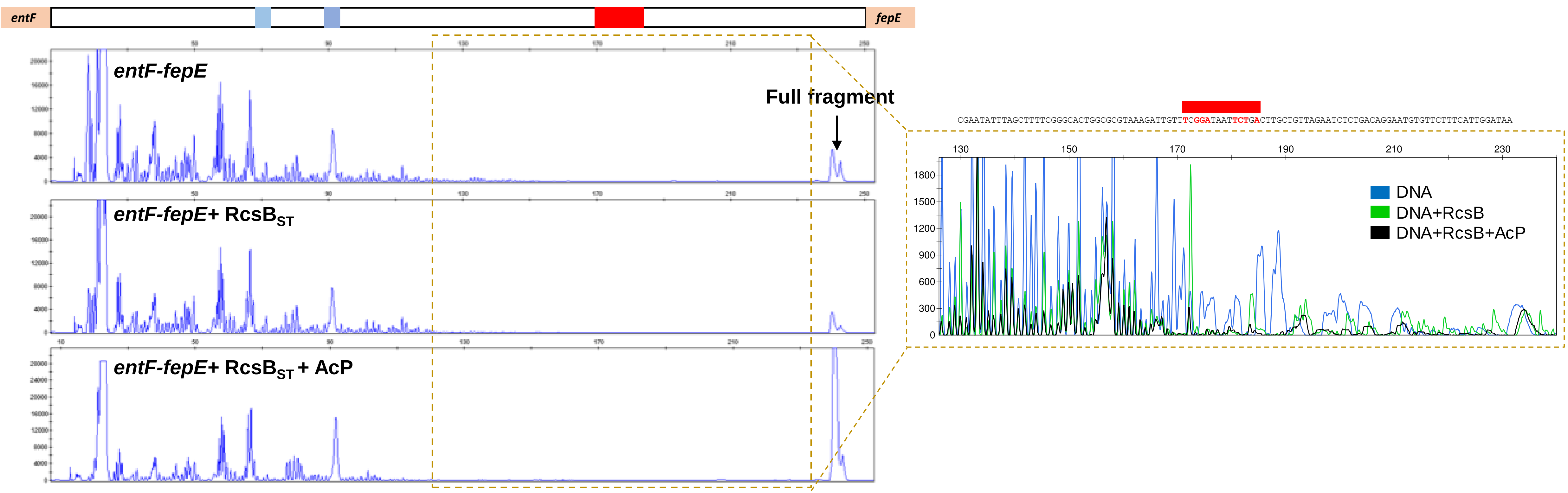


**Supplementary Figure S10. Distance of intergenic RcsB motif sites to either TSS or initial ATG codon**. Bar plot and density plot of intergenic RcsB motif sites respect to either TSS or initial ATG codon. Median value is indicated as a blue dashed line.

-35 predicted -10 predicted

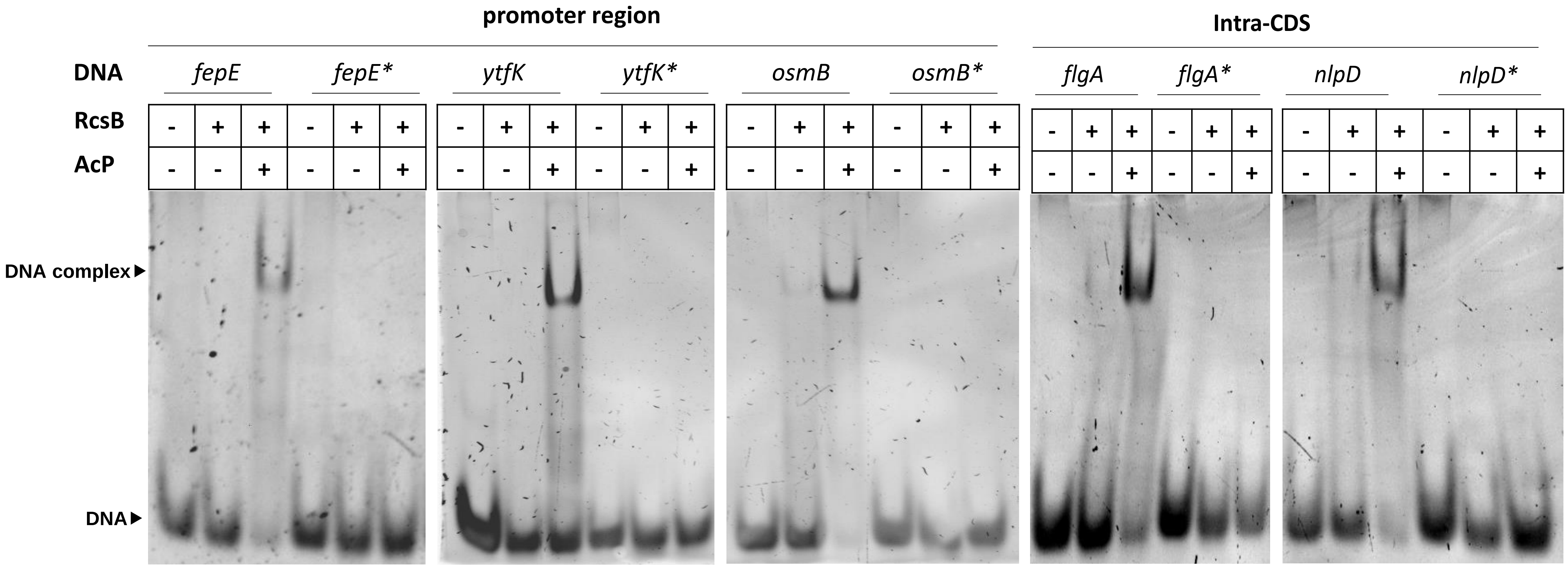
*entF* CGGGCGTTGTTTCTGCCTTTAACAAATTAAATCCTGAAACCCATAATAATTACTAATTATTATGGGTTT**TTTATT**GCAACTATTAATTC**TTTTAACAT**
AAGTGATACATGCTACAGGCAAGTTTAATTCCGAATATTTAGCTTTTCGGGCACTGGCGCGTAAAGATTGTT**T**C**GGA**TAAT**TCT**G**A**CTTGCTGTTAGA
ATCTCTGACAGGAATGTGTTCTTTCATTGGATAAATTTTTCAGGTCATACGGC *fepE*

RcsB box

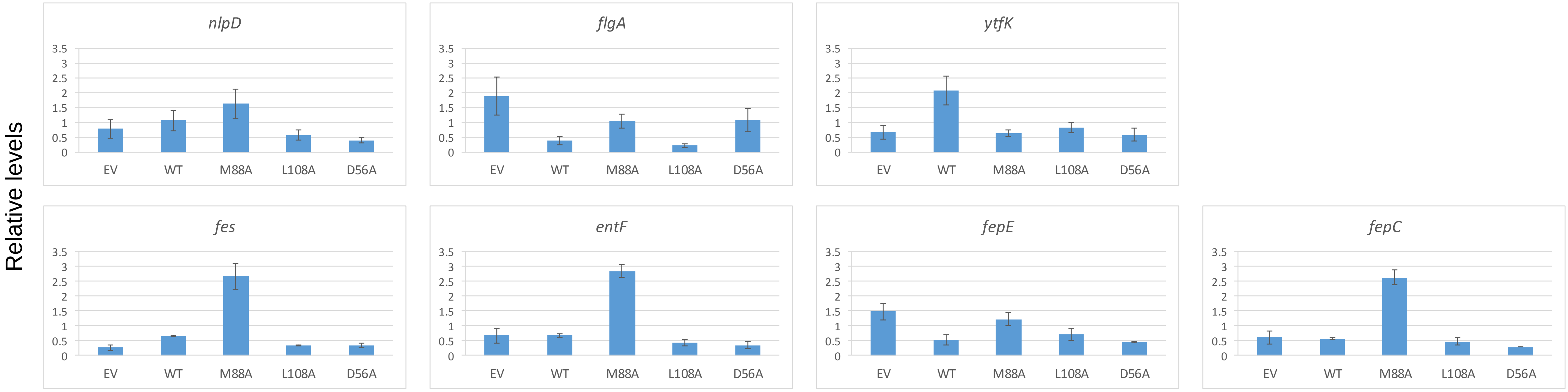


**Supplementary Figure S11.** Nuclease protection assay for the intergenic region between *entF-fepE.* The y-axes are in relative fluorescence units and the x-axes indicate DNA fragment size. Overlay of electropherograms of DNase I-digested DNA which comprises the upstream regulatory region of *fepE* that overlaps with 3’ region of the upstream gene *entF* (sequence from -1 to -249, shown above) in the absence of RcsB (top panel), in the presence of RcsB (middle panel) and in the presence of RcsB with AcP (low panel). The non fragmented PCR product is on the right indicated as full fragment. The regions that are boxed show protection for fragmentation. In the figure, blue colored squares indicate the predicted -35 and -10 sites and a red colored square indicate the RcsB box.

| | | | |
|---|---|---|---|
| ***fepE*** | TTGTTTCGGATAATTCTGACTTG | ***flgA*** | GTTAATAAGAATATTCCCATCAG |
| ***fepE**** | TTGTTTCGTATAATTATGACTTG | ***flgA**** | GTTAATAATAATATTACCATCAG |
| ***ytfK*** | GATGTTTAGATAATTCTGAATAA | ***nlpD*** | ACCTTTCGGAATATTCCCATACT |
| ***ytfK**** | GATGTTTATATAATTATGAATAA | ***nlpD**** | ACCTTTCGTAATATTACCATACT |
| ***osmB*** | CTCTCTAAGACTTTTCTGACATC | | |
| ***osmB**** | CTCTCTAATACTTTTATGACATC | | |



**Supplementary Figure S12.** EMSA experiments with RcsB and several DNA sequences (*fepE, ytfK, osmB, flgA and nlpD*). Nucleotide substitution at each sequence is highlighted in yellow and located at the same position in the central base of the (G/A)GA or TC(T/C) motif. Assays were performed in the absence and presence of phosphodonor AcP.



**Supplementary Figure S13**. RNA relative levels for the newly identified genes *nlpD, flgA, ytfK, fes, entF, fepE* and *fepC* regulated by RcsB in the strain MD4821 (*igaA1 ΔrcsB*) expressing RcsB variants empty vector (EV), WT, M88A, L108A and D56A.