

Supplementary Material and Methods

Real-time PCR analyses

S. typhi total RNA (500 ng input), isolated from different bacterial growth stages, was DNase-treated (Roche) and reverse transcribed using Transcriptor Reverse Transcriptase (Roche) and a gene-specific primer (MWG) at 55°C for 1 hr (Supplementary Table S1). Real-time PCR with 1:100 diluted cDNAs was performed using the LightCycler 480 (Roche) and SYBR Green I Master (Roche) in a 12.5- μ l reaction volume (at least in triplicates) under the following cycling conditions: 95°C, 5 min, followed by 45 cycles of 95°C for 20 s; 53°C for 40 s; and 68°C for 50 s. For relative quantification, 16S rRNA was used as reference control. The integrities of the PCR products were verified by gel electrophoresis on either 8% polyacrylamide (in 1x TBE buffer) or 2% agarose (in 1x TAE buffer) gels. In addition, a melting curve analysis was carried out for each reaction. The calculations of average Cp values, SDs, and resulting expression ratios for each candidate were performed using the Roche LightCycler 480 software.

Supplementary Results and Discussion

Interaction of *S. Typhi* Hfq protein with novel npcRNA candidates

Hfq protein is conserved in a wide variety of bacteria and is involved in many cellular functions, such as the stress response and regulation of gene expression. In Gram-negative bacteria this protein acts in pleotropic regulations, such as outer membrane protein biogenesis and the activation of *rpoS* during conditions of oxidative stress (1). Hfq is essential for the mobility of synechocystis species and for the virulence and pathogenicity of *Pseudomonas aeruginosa*, *Brucella abortus*, *Vibrio cholerae*, *Listeria monocytogens*, *Legionella pneumophila* and uropathogenic *E. coli* (2-8) and is required in *S. typhimurium* for invasion of and growth in epithelial cells and macrophages (9). Hfq is also essential for the translational repression or activation exerted many *trans*-acting npcRNAs. Therefore we randomly chose 2 to 4 candidates from each class of npcRNAs and tested their interaction with *S. typhi* Hfq protein, which we expressed in *E. coli* and purified by affinity chromatography (see Material and Methods)

We used *in vitro* binding assays to analyze whether selected npcRNA candidates were able to specifically interact and form stable RNP complexes with the *S. typhi* Hfq protein. The *in vitro* synthesized npcRNAs were radioactively labeled and incubated with increasing concentrations of recombinant *S. typhi* Hfq protein (from 25 nM to 400 nM). Complexes were formed in the presence of a vast excess of non-specific competitor (total yeast RNA in a molar ratio of 1:4100) and assayed on native gels (see Material and Methods) Out of 11 npcRNAs candidates examined (from the partially overlapping with ORF, antisense, and intergenic classes), six formed specific and stable complexes with recombinant Hfq protein with apparent K50s ranging from 25 to 200 nM (Supplementary Figure S4).

The StyR-296 npcRNA candidate is 293 nt long with a 71-nt overlap to the 5'- ORF region of the *rpoH* gene, which encodes the stress response transcription factor, sigma-32. The 5'-UTR region of *rpoH* mRNA regulates its translation in a temperature-dependent manner (10). Thus, the finding of a stable npcRNA transcript within this region might indicate that regulation of *rpoH* expression may be even more intricate than proposed, involving an additional specific StyR-296-Hfq RNP complex (Figure 6, Supplementary Figure S4). Moreover, during *in vitro* translation assays, increasing concentrations of recombinant Hfq protein positively regulated translation of an *rpoH* mRNA harboring the npcRNA in the 5'-UTR (data not shown). Furthermore, StyR-9 overlapped in the sense orientation with the ORF region of the *t4341* gene and also showed specific interaction with Hfq protein, binding with an apparent K50 of 100 nM (Figure 6, Supplementary Figure S4). These observations indicate that candidates from this class of stable small npcRNA molecules might recruit the Hfq protein into RNP complexes to exert their function.

The intergenically located StyR-10 and StyR-241 also formed specific npcRNP complexes with the Hfq protein with apparent K50s of 50 and 200 nM, respectively (Figure 2, Supplementary Figure S1, S4). Both putative npcRNAs belong to the subgroup of promoter-associated RNAs. Interesting, StyR-241 overlaps in an antisense orientation to a binding site for the Ntrc transcription factor (Supplementary Figure S1). Recently, it was suggested that promoter activity could be regulated by npcRNAs (11-14); hence, Hfq

protein might play a role as an RNA chaperone to stabilize npcRNAs during their functions.

Two repetitive npcRNA candidates (StyR-103 and StyR-215) did not interact with Hfq protein (Figure 5A, B, Supplementary Figure S4). StyR-103 was proposed to regulate *IS200* transposase gene expression in *cis*, whereby the Hfq RNP complex might not be required. StyR-215, derived from the externally transcribed spacer (*ETS*) of *S. typhi* pre-16S rRNA, might potentially be associated with rRNA biogenesis, whereby Hfq protein is likely not essential.

Although Hfq protein was shown to be required mainly for the function of *trans*-encoded regulatory small npcRNAs, we detected specific complex formations between Hfq and two *cis*-encoded antisense npcRNA candidates (StyR-151 and StyR-248) (Figure 4, Supplementary Figure S2). Sty-151 and StyR-248 Hfq complexes were both formed with apparent K50s of 75 nM (Supplementary Figure S4). These data suggest the possible existence of additional aspects of sense-antisense regulation as well as implicate the npcRNA candidates in other functions.

References

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Supplementary Figure legends

Supplementary Figure S1. Schematic representations of novel npcRNA candidates from intergenic regions of *S. typhi*. Coordinates of depicted genes are based on the completed genome of *S. typhi* Ty2 (AE014613). Locations of npcRNA candidates are depicted by red arrows. Light blue arrows represent ORFs (without UTRs) of flanking genes; protein products are indicated below. Black arrows indicate location and direction of predicted promoters. Drawings are not to scale. **(A)** Promoter-associated npcRNAs. Transcription factors that harbor binding sites within npcRNA coding regions are indicated by colored ovals. **(B)** Terminator-associated npcRNAs **(C)** Operon-associated npcRNAs **(D)** Putative independently transcribed npcRNA genes.

Supplementary Figure S2. Schematic representations of antisense *S. typhi* npcRNA candidates. Coordinates of depicted genes are based on the completed genome of *S. typhi* Ty2 (AE014613). Locations of npcRNA candidates are indicated by red arrows. Sense-encoded ORFs of protein-coding genes are indicated by light blue arrows. Drawings are not to scale. **(A)** npcRNA candidates antisense to the 5'-ends of ORFs. **(B)** npcRNA candidates antisense to the 3'-ends of ORFs. **(C)** npcRNA candidates antisense to both the 5'- and 3'-ends or to entire ORFs of protein-coding genes. Green arrow indicates *S. typhi* hypothetical protein-coding gene (annotated in this study). **(D)** *cis*-encoded antisense npcRNA candidate genes to ORFs of protein-coding genes.

Supplementary Figure S3. Expression analyses of antisense npcRNA candidates and *cis*-encoded mRNA pairs throughout the growth stages of *S. typhi*. Differential expression profiles of *cis*-encoded antisense npcRNA candidates and sense *S. typhi* protein-coding genes at bacterial growth stages as determined by real-time PCR. 16S rRNA was used for relative quantification. Expression ratios and growth stages are indicated on the Y- and X-axes, respectively. Expression profiles of antisense npcRNA and sense mRNA genes are indicated by red and black lines, respectively

Supplementary Figure S4. Interaction of Hfq protein with *S. typhi* novel npcRNA candidates *In vitro* transcribed, ³²P-labeled npcRNA candidates were incubated with increasing concentrations of recombinant *S. typhi* Hfq protein; from left to right 0; 25; 50; 75; 100; 200; 300; and 400 nM of Hfq protein were added, respectively, except for StyR-9 and StyR-280 whereby Hfq protein titration stops at 300 nM. The npcRNA candidates are depicted to the left of the blots and the K50 values to the right.

Supplementary Table legends

Supplementary Table 1: Compilation of oligonucleotides used for this study

ERNS: expressed RNA sequences

Supplementary Table 2. Compilation of 217 contigs of cDNA sequences derived from ORFs of the *S. typhi* protein-coding genes.

ERNS: expressed RNA sequences (StyR-); **cDNA (nt)**: length of cDNA (in nt), **cDNA sequence**: sequence of cDNAs contig, **ORF**: open reading frame of a hypothetical protein (HP) or a protein from which the corresponding cDNA is derived, **Comments**: those overlapping with ORFs are indicated.

Supplementary Table 3. Known npcRNAs in *E. coli* and/or other *Salmonella* strains.

These RNAs were not previously reported for *S. typhi*. **ERNS**: expressed RNA sequences of npcRNA candidate from *S. typhi*, **cDNA (nt)**: Length of cDNA clones in nt, **Coordinates in *S. Typhi* TY2 genome**: The npcRNA coordinates based on the completed *S. typhi* Ty2 genome annotation (AE014613). **N. blot**: Northern blot expression in *S. typhi*; NP, Northern not performed. **Known npcRNA in other enterobacteria**: Known npcRNA, as reported in a previous study, is indicated and follows the name of the organism in which they were previously identified. **Coordinates in *E. coli***: In the first line, coordinates of StyR- homologous sequences in *E. coli* are indicated, and in the second line, the coordinates for the annotated npcRNA in *E. coli*.

Table S1. Compilation of oligonucleotides used for this study

ERNS	Oligonucleotides (5'-3')
StyR-3	GGCAACAGCAATAAGCATAGTAATAA
StyR3rev	TGGGGTGGTCGTCAGCGGCTCCCGCA
StyR-9	AACATGAGCAAAAAACGAGCCAACATCC
StyR-9new	CGAGCCAACATCCGCAGATGTTTCGC
StyR-10	CGGCGCATTGATAATCAGTCCGGCCT
StyR-10new	TAGGCAAAACGTGCAAAACACTGCGG
StyR-27	TACTGTGCCGGATGGCGGCTGCGC
StyR-29	GTGTTCTATATGGACAATTCAAAGG
StyR-29new	ATAGCTGCGTATACTTTCTTGAT
StyR-44	TTCGATTCATCATCGTGTTCGC
StyR-51	ACAGGTTCTGCGTTTAGTTGCCGCGC
StyR-51new	AAGACAGGTTCTGCGTTTAGTTG
StyR-55	TTCGACGGAGGCTGGATAGGCCAGG
StyR-88	CAAGTCTGACATTCCTCCGAGTAAATTGGTC
StyR-88new	CTCAAACCTGCCCCCTGCCCGGGTT
StyR-90	CAGGTTGTGCGCACCATCGATTTCCAGC
StyR-99	CCATTACGTCCTGATGAGGTGCAA
StyR-103	TACAGGAACAGGGAGTTCTGGTGCA
StyR-103new	TTTACAGGAACAGGGAGTTCTGG
StyR-122	GACGGCGCGCTGTTGCCACGCTATG
EcoR-122	GACGGCACGCTACTGCCGCGCTATG
StyR-137	GTGATGCGCACTGACGGCACGGTGAC
StyR-151	CACATGCTGATCGAATACCCACC
StyR-161new	CGATTGTCCTTTCGAGTTCACG
StyR-161	TTCCACGTAACGTCCGTTAAGGTTCT
StyR-169	ACTCAGAATCCCTTCCGAG
StyR-173	AATAGCCAGCAGGCTCAGGATA
StyR-195new	TCGTTACCCCAGTCACATAGTGGCCTA
StyR-195	TCGTTACCCCAGTCACATAGT
StyR-196	CTGCGCGCCGCTACTGGAATTA
EcoR-196	CTGTGCGCCAGCGTACTGGAATTA
StyR-199	GGATCACCTGCCGGTGGTGCTCGA
StyR-207	CCCGCAACATTGCGCCTCACC
StyR-207new	TAGCCCCCGTCAGGTTGCCAGG
StyR-215	GATTGTCTGATAAATTGTTAAAGAGCAG
StyR-219	CTGGATCAATTTATCGAAGCAAGTT
StyR-219new	AAAGACCTGCGTACTGGGGTGGAAACC
StyR-234	CTCGTTCCTACTGGCTGTGCCGATGAT
EcoR-234	CTCGTTCCTGCTGGCGGTGCCGATGAT
StyR-241	CCTTGTGATCGCTTTCACGGAGC
StyR-243	TATGAGCAACTGGCAGAGGCCATCCG
EcoR-243	TATGAGCAGCTGGCAGAGGCCATCCG
StyR-243new	TGTAAGCGCGACGGCGTGGTTTATC
StyR-248	GCCACCATAACGTTTCGGTTGGGCAA
EcoR-248	GCCACTTTACGTTTTGGCTGGGCTAA
StyR-248new	CATCTACCCGGCTTAATTACGC
StyR-252	GGCGCGCCGCTAATCTGGTTTCC
EcoR-252	GGCGCGCCGTTAATCTGGTTTCC
StyR-254	TCCTCCCACGCGTTGGCGCACGCTC
EcoR-254	TCCTCCCACGCCCTGGCCATGCGC
StyR-254new	GTCTCCCACGCGTTGGCGCACGC
StyR-264	GCATCCCTGCCACTCTCTGCGCACCG
EcoR-264	CATCCGTCCGCCGTTTCGGCGCATCG
StyR-264new	TGATCCACAGCGCCACCATATT
StyR-280	CAGGGTCCATGTGCGCTCCGGTAAGT
EcoR-280	CAGGTTCCATATAACCTCCGGTAAGT
StyR-280new	ACACACCGGTAAGACAGCAGAG
StyR-288	GAAAACCGCCGATCCTGTCCACC
StyR-296	GTGATTTTATCCACAAGTTCAATG
StyR-306	AGACAACGGTTCTCGAGGTTCAAT
EcoR-306	AGACAACGTTATTCGAGGTTCAAT
StyR-327	CCGTGTCCAAACTGGCTGCGCCAATTA
StyR-329	CGGTAAGCGCAGCGCCACCGGGCAA
StyR-329new	TAATGCCGGATGGCGCTAACGC
StyR-333	ACAAGTCGGCGTCCGATTACATGG
StyR-383	CATCAGGCGTCTGTTGAGGGTGT
Hfqforvndel	GAGCCATATGGCTAAGGGGCAATCTTTACAAGATC

Hfqrevxhol	GAGCCTCGAGTTATTCAGTCTCTTCGCTGTCCTGT
RamRndeIF	GAGCCATATGGCTCGTCCGAAGAGTGAAGAC
RamRxholR	GAGCCTCGAGTTATTGCTCTCGCGAGTCAG
Sty9t7	GATTAATACGACTCACTATAACCTTTCAACTCTCACCGAGGCTTTG
Sty9rev	AACATGAGCAAAAACGAGCCAACATCC
Sty10t7	GATTAATACGACTCACTATAGTAAATACCTTTCAACTCAACCCGAGGC
Sty10rev	TAGGCAAAAACGTGCAAAACACTGCGG
Sty55t7	GATTAATACGACTCACTATAATTGGAGCCTGGCCTATCCAGGCCTCCGTCG
Sty55rev	GGTCTACGCAGGGGATTAAGCCTCTTGCGAGAC
StyR103T7	GATTAATACGACTCACTATACATTTTATCCTCTTCAAGCTGGTGCTTT
StyR103rev	TTTACAGGAACAGGGAGTTCTGGTGCAGAGGGTAC
Sty151t7	GATTAATACGACTCACTATAAAAATCAATAAAATTCGTTTCGCAGACGGCG
Sty151rev	TCATGTCCACATGTGATCGAATACCCACC
Sty215t7	GATTAATACGACTCACTATACTCGCGACGGTGAGCTGAAAGCCGCG
Sty215rev	TCAGATTGTCTGATAAAATGTAAAGAGCAGG
Sty234t7	GATTAATACGACTCACTATAATCATCGGCACAGCCAGTAAGAACGAGAAC
Sty234rev	TGCTGCGCCTGTGGCCGGGCTTCTCGCG
StyR241T7	GATTAATACGACTCACTATAAGTGCTTCAATGTGAACATTAAGCA
StyR241rev	TGGTCACAAACATCCTCCGCAAAACAAG
StyR248T7	GATTAATACGACTCACTATAATTCCCCTTCCAGCTTGAATTGCCATTG
StyR248rev	CATCTACCCGGCTTAATTACGCTGAACGCTT
StyR280T7	GATTAATACGACTCACTATAATTTACTTACCGGAGGCGACATGGACCCT
StyR280rev	ACACACCGGTAAGACAGCAGAGGCAGGCT
Sty296t7	GATTAATACGACTCACTATACTGCAATGGGCTTCCGTTTCGCAGGGAAAGAG
Sty296rev	CGCCCGGATATAAGATTCCAGGTTGCCAACAGGGGC
RamRF2ntM	GCGTATCTTTGCTTCTATAAatgagtgCTTAcactcatAATCAAGGGCTGCCGCATGA
RamRR2ntM	TCATGCGGCAGCCCTTGATTatgagtgTAAGcactcatTATAGAAAGCAAAGATACGC
RamRF9ntM	GCGTATCTTTGCTTCTATATACTcactcatAATCAAGGGCTGCCGCATGA
RamRR9ntM	TCATGCGGCAGCCCTTGATTatgagtgAGTATATAGAAAGCAAAGATACGC
RamRF2	GCGTATCTTTGCTTCTATAAatgagtgCTTAcactcatAATCAAGGGCTGCCGCATGA
RamRR2	TCATGCGGCAGCCCTTGATTatgagtgAGTAAAGcactcatTATAGAAAGCAAAGATACGC

Oligonucleotides used for Real-time PCR analyses

ST173_F	CTGAGCCTGCTGGCTATTATG
ST173_R	GAAAATTAACGCCGAAAAGA
ST222_F	ATCGCCATTGCATCAGAC
ST222_R	ACGGGTTACAGTGGTTGAC
ST234_F	GCACAGCCAGTAAGAACGAGA
ST234_R	GTTCCGGAGCGACCATT
ST243_F	GCCTCTGCCAGTTGCTCAT
ST243_R	GACGGCGTGGTTATCTGC
ST315_F	CGGCTCGCTGCGAATAAT
ST315_R	CTGTCCGGAAAGTCAACAACG
ST322_F	CGTTCGGGCAGTTCCAAA
ST322_R	GGCCGTCAACTGTGTTATCAA
ST336_F	TCATCTGCGCCGACATTC
ST336_R	AGTATGCGCCGGTGTGGA
ST16S_F	GTTGTGGTTAATAACCGCAGCA
ST16S_R	CCAGTTTCGAATGCAGTTCCC

Table S2. Compilation of 217 contigs of cDNA sequences derived from ORFs of *S. typhi* protein-coding genes.

ERNS	cDNA (nt)	cDNA sequence	ORF	Comments
1. StyR-16	84	ATACGAACCGTCAGATCCATGCGTTGCGTG ATAACGTTGGGTTGGCGAAAGCGGAAGTG ATGGCCGAACGGATTCCGGCAAATTA	Conserved hypothetical protein	
2. StyR-17	178	ATGAATAAAATCGCCGAACCTCAAACGCGC CAAACGCCTGGCGCTCTCACTGTTGCTGAT AGCCGCCGCGACGTTTGTGACCACGCTTTT CCTGCCGCCAGTTTTTGGGTGCTGAGCGT AAAAGCTATTGCCGAAGCGGCGATGGTTG GCGCGCTGGCGGACTGGTTTCCGTGGTGG	Putative membrane protein	
3. StyR-18	103	ATTCCGCAAATCTCCACTGGCGATATGCTG CGCGCCGAGTAAAATCAGGCTCCGAGTT GGGCAAACAGGCGAAAGATaTCATGGACG CCGGTAAACTGGTGA	Adenylate kinase	
4. StyR-21	353	ATATATGAAACCGATGGTACTGGCGGATAT CGCCCAGGCCGTCGAGATGCACGAATCCA CTATATCCCGCTGACCACGCAGAAGTATT TGCACAGCCCAGCGGGTATTTTTGAACTCA AATATTCTTTTTCCAGCCACGTCAATACCG AAGGCGGAGGCGAAGCCTCTTCCACCGCG ATTCGCGCTGGTGAAGAAGTTAATTGCG GCGGAAAACCCGCGAAAACACTGAGCGA CAGCAAAGTTAACCTCTCTGTGTCAGAAC AGGTATCATGGTGGCACGCCGACTGTTGC GAAGTACCGAGAGTCTTTATCCATTCCGCC GTCAAACCAACGGAAAACAGCTGGTTT	RNA polymerase sigma-54 factor (sigma-N)	
5. StyR-28	321	GCTACATGGAGATTAACCTAATCTAGAGG GTATTAATAATGAATCGTACTAAACTGGTA CTGGGCGCGTAATCCTGGGTTCTACTCTG CTGGCTGGTGTCTCCAGCAACGCTAAAAATC GATCAGCTGTCTTCTGACGTTCCAGACTCTG AACGCTAAAGTTGACCAGCTGAGCAACGA CGTGAACGCAATGCGTTCCGACGTTCCAGGC TGCTAAAGACGACGCAGCTCGCGCTAACCC AGCGTCTGGACAACCAGGCTACTAAATAC CGTAAGTAATAGTACCTGCGTAATAAAAAAT GGCGCACATCGTGCGCCATTTTTTTT	Major outer membrane lipoprotein	
6. StyR-31	94	CCCAAATCAGCAAAGTGCGCACGGGTCGT GCTTCTCCAGCCTGCTGGATGGTATTGTC GTAGAATACTATGGCACTCCGACCCCGCTG CGCCA	Ribosome recycling factor	
7. StyR-32	96	GTATTCGTCCGTTACATGATCGTGTGATCG TCAAACGTAAGAAAGTTGAGTCCAAATCT GCTGGCGGCATCGTACTGACCGGTTCCGCA GCGGGTA	GroES protein	
8. StyR-33	113	ATTATCAGAAATGACGATTTACGCATTAAG AAATCAACGAGTTATTACCTCCGGTCGCGC TGCTGGAAAAGTTTCCCGCCACGGAAAAT GCAGCAAATACCGTTGCTCACGCA	Phospho-2-dehydro-3-deoxyheptonate aldolase	
9. StyR-34	49	ATTCGAACCTCCGTTGATCACGGCACCGCG CTTGAACCTGGCGGGCCGAG	Pyridoxal phosphate biosynthetic protein PdxA	
10. StyR-36	175	CCATGCGCTTGCCTAAGAGACGTCAGGTA TCTATGGAGGAACAAGTTATGGATACAAA CGAACTTGGCTTAGTTAAGGCGCGTGTGA ACTGATCACCGCTATGCTCAAATGCGCAAC CGCGTTTGTGGCTTAGTTGGTGGGTTTA CGCCGTTCTTAACATGGCCCTCAACT	Hypothetical protein (Specific for <i>S. typhi</i>)	Overlap entire ORF
11. StyR-37	228	ATTTTTGAACTTTAACGAAAGTGCAAGAGG GCAGCATGGAACCAAAGATCTGATCGTG ATAGGCGGGGCATTAACGGTGCAGGCAT CGCGGCTGATGCCGCCGACGCGGTTTGTG CGTACTCATGCTGGAAGCGCAGGATTTGGC CTGCGCAACCTCTTCCGCCAGTTCGAAACT TATCCACGGCGGCTTACGCTACCTTGAACA	Aerobic glycerol-3-phosphate dehydrogenase	

12.	StyR-38	136	CTACGAGTTCCGTCTGGTCA TTACGGCGGATCGCTGACTTATGCAATCGG CGAAGGCTTCTGTGCGGTGGCGCTATCAC CACGTCTAAACGTAAGTCCGATCAGAACA ACACCGCTAACGCTCGCCTGTATGGTAACG GCGATCGCGCCACGGAA	Outer membrane protein C	
13.	StyR-39	144	TTTTTTGTGCGCCCGACTGGCTTGCCGAA CATATTGATGATCCGGAAATACAGATTCTT GACGCCGTATGGCGCCACCAGGACAGGA ACATCGTGATATGGCGGGCGAATATCGCG CCGGACATATTCCCGGCGCGCTGTTT	Putative thiosulfate sulfurtransferase	
14.	StyR-40	133	ATCAGCCGCGAAGTAAATTCCTTACTGC GCTTTCCGATCTGGAATTAAGAAAGATTAG AGAAAGAGGTCAACTGGAATCCTTAAGGC ATGAACTAAGAACTCAAGGCATGACTTGC AAGGAAAACGTGTG	Hypothetical protein	
15.	StyR-41	122	TACGGCAGCGCAATTTGCGAAAGGCGTGC AGTTGCATAATGAAAAAGATCTCACTAAA CCCCTACGCTGGAGGTGATAACACCTGTG CAGGTCCTGCTGACCATCAGCGAAGGCCGT TATA	Ribosomal small subunit pseudouridine synthase	
16.	StyR-42	122	ATGTAAATACTCACTCACCTGGAGAAA ATGTGCGAAAGATAACACTACGGAACATCT GCGCGCTGAGTTGAAATCCCTGACCGATAC GCTCGAAGAAGTGCTGAGCTTTCGGGCG AAAA	Conserved hypothetical protein	Overlap putative 5'- UTR- 30 nt
17.	StyR-43	115	CTTTAGGAACGCAATCGCAGTAATGAAGC AACTTTGGTTTGCCATGTCCCTTGTTGGCGG CTAGCCTGTTCTTCTCAGTAAACGCTCGG CCGACCCTGCGTCCGGGGCGTTATT	Sigma-E factor negative regulatory protein, rseA Sigma-E factor regulatory protein RseB precursor, rseB SufI protein	
18.	StyR-45	156	CATTTTTTCAGGCACAACCTCTTAGCCTGTT TTACATGGAGCTTATATGTCATTACAGTCGG CGTCAGTTTCTTCAGGCATCGGGAATCGCA CTATGTGCAGGCGGATTCCCCTCAGGGCG AATGCTGCCGTCAGCAACAGCCGTTGCCT GTTCC		Overlap putative 5'UTR- 46 nt
19.	StyR-46	136	ATAACGCATTGCTGGAGCTAGAATTAATG TCATATATCGTTTCGTTTCACTGGGCTACTA CTACTCAACGCATTTATTGTGCGCGGTAGA CCGGTGGGCGGCATTCAACATTAAGTCAGC TCGAAGTCAAACAAAA	leu operon leader peptide	
20.	StyR-48	93	TTTTGGCGGCGCGCTGGACATGCTGGAAGA GAACCCGCTACCGGGCGGTGGCGGTGGTGA TCCCAAGCTGGACTTTCAAAGTACCGCCT CGCT	cell division protein	
21.	StyR-49	90	ACAAAAATGACAGCCCTTCTACGAGTGATT AGCCTGGTCGTGATTAGCGTGGTGGTGATT ATTATCCACCGTGCGGGGCTGCACTTGGGA	ilvGMEDA operon attenuator peptide	
22.	StyR-52	194	TATCGAACTATGCGCCAGGCGGACGCG AATACCCACAGCTTGACGGTATTTTTTGCA CCAACGATGACCTGGCGGTGGGGGCGGCM TTCGAATGCCAGCGCCTGGGGCTAAAAATC CCGGACGACATGGCGATCGCCGGGTCCA CGGTCATGACATCGGCCAGGTGATGGAAC CGCGTCTGGCAAGCGTCC	gluconate utilization operon repressor	
23.	StyR-57	232	ATGATGAGTACTGAAATCAAACTCAGGT CGTGGTACTTGGGGCGGGCCCGCAGGCT ATTCTGCGCTTTCCGTTGCGCTGATTTAG GTCTGGAAACCGTAATTGTAGAACGCTACA ACACCCTTGGCGGTGTTGTCTGAACGTCG GCTGTATCCCTYCTAAAGCGCTGCTGCACG TAGCAAAAAGTTATCGAAGAAGCCAAAGCG CTGGCTGAACACGGTATCGTCTTCG	dihydroliipoamide dehydrogenase	
24.	StyR-60	113	ACTTGCTTTATTTCTGCTCTCTTTAAGGAAA TCTCATGCTCAAATCGACTCTGGCGGCTGT CRCAGCTGTTTTGCTCTTTCTGCTCTTTCT CCCGTAGCGTTGGCAGCAAAA	peptidyl-prolyl cis-trans isomerase	
25.	StyR-61	75	CTATAAAGTCTCCGGTGGTCTGCACGGGGT GGGCGTCTCGGTAGTCAACGCTCTGTCGCA	DNA gyrase subunit B	

26.	StyR-62	201	AAAACCTGGAGCTGGT ATATTTCTAACCATAAACCCTACGTTACCT CATTCAGACATGGGATAATCGGAGCGATA AGCCCGGCTTTTGGCATGAATTTAGAAAAA ATCMACGAGTTAACCGCGCAAGATATGGC GGGTGTCAATGCGACAATCCTTGAACAGCT TAATTCGACGTTCAACTGATTAATCAGCT AGGATATTACATTATTAGCGGCG	Octaprenyl-diphosphate synthase	
27.	StyR-63	142	CTTCCTTTAAATCCACACGTATCCAGCACG AAATAATATGCAAAAAGTTTGATACCAGGA CCTTCCAGGGCTTGATCCTGACCTTACAGG ATTACTGGGCTCGCCAGGGCTGTACCATTG TTCAACCATTGGACATGGAAGTC	glycine-tRNA synthetase, alpha subunit	
28.	StyR-65	160	CTTTTATTAACATAAAGGAGTACATAATGCG CGTAGCGAAAAATCGGGGTGATCGCCCTTTT CCTGCTGATGGCTATTGGCGGGATCGGCGG CGTGATGCTGGCAGGTTACAGTTTTATTT GCGTGCCGGGTAAGCGCGCGCTCAGCCTT TCAAACAGGC	Hypothetical protein	
29.	StyR-67	36	TTACATGGAAATTTATGCCGCGATGGACCG CCTCCG	Putative exported protein	
30.	StyR-73	153	ATTCCTTACGTGCGAAAGTTTCTACCGGC ACGCCGCAAAGCCCCTACGGCAAAAAGTAA ATTGATGGTAGAACAGATCCTCACCAGTCT GCAAAAAGCCCAGCCGAGTGGAGTATTG CGCTGCTGCGTTATTTCAATCCGGTCGGCG CGCAC	UDP-glucose 4- epimerase	
31.	StyR-75	132	ATAGATCAATAGCGGAATCTCATGTACTCA TGAACACTGAAAAACCGTCGGTAGCTCAC AACGTTGACCATAATGAAATCGCCAAATTC GAAGCCGTCGCGTCCGCGTGGTGGGATCTG AAGGGCGAATTCA	3-demethylubiquinone-9 3-methyltransferase	Overlap putative 5'- UTR-28 nt
32.	StyR-79	91	TTAAATGAGCGANAAACGTTGATGTCGAA TTCTTATGACTCCTCCAGTATCAAAGTCCT GAAAGGGCTGGATGNGGTGCGTAAGCGCC CGG	DNA gyrase subunit B	Overlap putative 5'UTR-21 nt
33.	StyR-80	121	ATTGCAATATCAGACACAGCGGCTGGAATT TGATTATTATGCCCTGTGTGTTTCGTCATCCC GTTCCCTTTACCCGGcTAAAAATATCGCTTC GTACCACTTATCCTCAGGCGTGGGTAACG ATGTA AAAACAGCCGAACTCTGCGCCGC GCTACGAAAAGTCAAGGCAGACAAAAAATG ACTCAGCATACTCAAACCTTCAATGCCT TCTCCGCTCTGGCAATACTGGCGCGGTCTT TCCGGCTGGAAC	Cell-division regulatory protein	
34.	StyR-81	130	TTTCTCAAGCGTGTGGGTTACGTAAACC GCGTATCGCCGTGGCAGGCGTGAATCCTCA TGCGGGCGGAGAATGGTCTGTTGGCGATGA AGAGACgCGTATCCTGACGCCAGCCATTAC CGATGCCCGCGCAAA	Putative membrane protein	5' and 3' overlap of two putative ORFs, respectively
35.	StyR-82	135	GGCTTATATCCTCAAAAACAACGGTGGTCC GACATATAGAGGGcCACCTTCT	PdxA-like protein	
36.	StyR-83	52	GGCTTATATCCTCAAAAACAACGGTGGTCC GACATATAGAGGGcCACCTTCT	Penicillin-binding protein 3 precursor	
37.	StyR-84	77	ATTCGAAATCACATATATCCTGTGTGTTTT AAAGTAAAAATCATTGGCAGCTTGAAAAA GAAGGTTACATGTCAAA	Aspartate ammonia- lyase and Hypothetical protein	
38.	StyR-85	72	TTTGCTGTGTAATGGAAATCTCACTATGGT CATTAAAGGCGCANAGCCCCGGGTTTCGC GGAAGAGTATAT	Fatty acid-fatty acyl responsive DNA- binding protein	
39.	StyR-86	87	AAAATCGGTCACGTTAGCGGAAAAAGAAA ACGTTTATTTCCCGACGCCATCACCGAAC GAGGGCAAAAACATCTTCGGGAGTTGAT	Sugar fermentation stimulation protein	
40.	StyR-87	59	ACGGAAGCGGTGCGCCTGCTGGAAGCGTG TCCGCTCTTCAATGCGGGTATCGGCGCGGT	Putative L-asparaginase	

41.	StyR-89	141	CTTATGGTATCAACGACGTCCAGGATATCG TTTACAATCCCAGCTACGACACCCTTTATC AGGAAGAACTTAATCCTGGTCTGGAAGGC TATGAGCGTGGCGTGTAACTAACCTGGGC GCTGTTGCCGTTGATACCGGTA	Phosphoenolpyruvate carboxykinase	
42.	StyR-91	196	ATTACTAAAGCCGCTAACGACGACCTGCTG AATTCCTTCTGGCTGCTGGACAGCGAAAAA GGCGAAGCGCGCTGCATCGTTGCAAAATC CGGCTTGGCTGAAGATGAAGTTGTGGCTGT CAGCAAACCTGGGCGAGATTGAATACCGTG AAATCCGATGGAAGTTAAACCGGAAGTA CGCGTTGAAGCGGTCAGC	Conserved hypothetical protein	
43.	StyR-92	125	CTGCTGACCTGCCTTTTGCACAGTCGCGTT TTTGGCGCGGGAAGGCCTGAGCAACGTT ATTACGCTTTCACCTCTGCGTAATAACGAG TTTCTAAAAAACTACGGCGTCGAAATCGTT GACGGC	Thiol peroxidase	
44.	StyR-93	260	ATTTATTACATTCGCGTTCCTAATACAAAT ATTTTGTCCAGTGTCTTAACCAACTTGAT ATAGCGGAGCCGAAATACATTTCCATAAA AGAACGTTATTAAGCGTGGCGACGCTTGGT ATGTTGGCTGTTTCAGTCGACTGATGGTA GTTTGGGTACGAAACAGTAACCATAGTTCT ATTAATACTAATGAATTTTTATGTACGACN AGAACGGTAACGACGATAACNGCCTAAAGA TATCCATGCCGATGGCAGTCTT	hypothetical protein possible transmembrane regulator	
45.	StyR-95	129	AAAAGCATGGATTTCGCGGCGAAGATATGT TGATTTGTTCAAAGCGTGAAATCAGCGACT ATATGCTGCAACTACTCGTTAAGAAAATA AGTTTAAGGAATCAAAGTAATGACAGCAA ATAACCTGCGT	putative dehydratase RfbH CDP-glucose 4,6- dehydratase	5' and 3' overlap of two ORFs, respectively
46.	StyR-96	125	ATACGGAATCACCGTTGGTCTCGATAGATT TTAACCACGACCCGCACAGCGCCATTGTTG ATGGCACGCAAACCCGGGTCAGTGGCGCC CACCTGATCAAGACGCTGGTCTGGTGCAT AATGAA	D-erythrose 4- phosphate dehydrogenase	
47.	StyR-98	51	ATCTACTCAAAGCAAACTCGCTCACATCGCC AGTACCTGGGAGCTGGCGGAA	Putative dimethyl sulphoxide reductase subunit	
48.	StyR-100	156	GTTGAATCGCGACAGAAAAGATTTTGGGA GCAAGCGATGCGCAAAGTTACGCTGCTGT TATGGCCTCAACGCTGGCATTTCAGTTTTTT AAGCCACGCAGCTGAAGTTGTACAAGCG ATAACTGGCACCCCGGTGACGGGGCCACG CAGCGTAGC	extracytoplasmic stress protein for protein- mediated toxicities	Overlap putative 5'- UTR- 36 nt
49.	StyR-102	178	ATTAATTGAAAAAATGCAGGCCGGACGCA TTCGCGGACTGGTGGTGATTCCGGTGGATT TCGCGCAGCAAATGGCGCGCGACGGTGAC AGCGCGCCGATTTCAGGTGATTACCGACGG CAGCGAGCCAAAATACCGCAACTTCGTTCA GGGCTATGTTGAAGGCATCTGGCAAATCTG G	putative inner membrane protein	
50.	StyR-104	181	CTTCGCAAAAAGAGTTGACGCTGCAGCCGTT CAATCACTGGGCGTTTCATTCCTGTCAACTT AATCCTTGAAGGGGTAAGTCTGCTGTCCAA ACCGGTTTCTCTCGTCTGCGACTGTTCGG CAACATGTATGCCGGTGAGCTGATTTTCAT TCTGATTGCTGGTCTGTTGCCGTGGTGGTC A	ATP synthase A chain	
51.	StyR-105	100	CTTCATCGAATCGCTGTTAGCGCCGTGGCG CGAAGGGCCATTTCAGCAAGCACTTCAACT GGCAGAAAATTGAAGCGCTCAAGCCTTTC GGCGGTATTCGC	proline dipeptidase	
52.	StyR-106	120	TTAATTACATCTGTCATAAGAGAGTACTA ATGGATCGTATCATTACATCATCGCGTGAT CGTAGCTCGCTACTGAGTACGCACAAAGTA CTGCGCAACACCTATTTCTGTTGAGCCTG	putative membrane protein	
53.	StyR-107	137	ATTCCTCGATATGATCACGCCGAATATCT	phospho-2-dehydro-3-	

			GGCCGATCTGATGAGCTGGGGCGCCATTG GCGCACGGACTACTGAATCCCAGGTTTCATC GCGAACTGGCGTCTGGCCTCTCTTGTCCGG TCGGTTTTAAAAATGGTA	deoxyheptonate aldolase	
54.	StyR-108	126	ATTTTTTGGCAGACAAGGAGAGACGCGTG AGGCGATTGCCGGGGATTTTATTGCTCACT GGAGCCGCGCTCATCGTCATTGCAGCGCTG CTGGTTAGCGGGCTGCGCCTGGCGTTGCCT CATCTTG	possible exported protein	Overlap of putative 5'- UTR- 27 nt
55.	StyR-109	131	ACGACGCCGTGAACGACAGCGGTAAACGC GCCGCGATGTTTGGTTCCGTGGCGGTGATC CGCGAGTCCGGCGTTCACAGTCTGCGCGTT GGCGATATCTATTACGTCGGACATCTGCCG TGGTTTGAGCGG	putative polysaccharide biosynth protein subunit B	
56.	StyR-110	79	GTTTGAACCTATGGAATAACCAACGACGC GGTGATTACAGTCATCGGCGTCGGTGGTGG CGGCGGTAACGCTGTTGAA	cell division protein FtsZ	
57.	StyR-112	46	AGTTATGCGTCGGTTTGCTCCATTGATAGC AGCGCTGTTATTAAGC	putative exported protein	
58.	StyR-113	69	AGCTAACCTGAACGATCAAATCTCCCGTAT GACGGGCGTAGGCGGGGCGCATCGCCGA ACGACCTGCT	flagellar hook- associated protein 1	
59.	StyR-114	87	CTTATTGGACATACTCAACCGCGTCGTCTG GCGGCGCGCACCGTCGCTAACCGCATTGCC GAAGAGTTGCAAACGGAGCCTGGCGGC	ATP-dependent helicase HrpA	
60.	StyR-115	70	ATGTCTCAATTGATGCAATTAAGGACGTC GCCGAGACACCCGCTGGGGCCGCTTTCC GGCGAAGTAA	vitamin B12 ABC transport ATP-binding protein putative glutathione peroxidase/vitamin B12 transport per...	
61.	StyR-116	26	TCGGTTGAATGCCATCGTTGCCTGGA	ferredoxin-type protein NapF	
62.	StyR-117	119	CTCTATCTTTACGGCCACTGCGCTGAAGGC GACTGCCCGAAGACGAGCACGCGCACGA TGACGCGACTAAATAAGTGTAATCTTTTCG AAGAGCCAACCGCCCGTTGGCTTTTTTAT	ferric uptake regulation protein	Overlap of putative 3'- UTR- 44 nt
63.	StyR-118	78	AAAAAATGCCTCCTTCCGAACCGGGCGCAA GAAGAGGAAGAAAAGCGGGCCGCTGAACCT CTCCACGCCCTGGCCCATCA	putative exported protein	
64.	StyR-120	175	AAGTGTATCCTGGCTTTTATGAAGAGAGAA ACTGGTGGACGAACTGACAGCGCAGGCAT TGAAAGCCTTACGACGCTTACTGCGACG CGTGGCAAGAAAAACACGGTAGCTGGCCG TTGAGCGAAGAACTGTATGGCGTACCTTCT CCGTGCATTATTTCTCAACCCGCGAT	syd protein	Overlap of putative 5'- UTR- 35 nt
65.	StyR-121	71	GCTAAAGACCAGGCTGGCATCGACAAAAAT CATGATCGACCTGGACGGTACTGAAAACA AATCTAACTTCGG	enolase	
66.	StyR-123	24	CTATCTGCTCATTGCCGGAACCTA	putative membrane protein	
67.	StyR-124	35	CTTCTCTGACGACAAAGGCAGCGACGGCG ACCAGA	outer membrane protein C	
68.	StyR-125	38	GTTGGGCATCGCCGAAAAAAGCCTTTTAGG TTCGGCGT	sigma-E factor regulatory protein RseC	
69.	StyR-127	48	ATGAGAACCCGCGTAACGTAGGGTCGTTTG ACAACAACGACGATAACG	NifU-like protein	
70.	StyR-129	27	ATTTGAAAAATGCTCTGAAAATCCCGG	conserved hypothetical protein	
71.	StyR-130	79	ATTCTCATTAACGCCTGCCGCGCCCGGTG GTGGATAACGCCGATTGTGGCGCGACTC AATGCCGGGCAGCCGCTGA	erythronate-4-phosphate dehydrogenase	
72.	StyR-131	49	ATTATTGTCGTCGCTGTTTAAAGTGAGCA GCTATCATCAGGCTAAGGC	putative membrane protein	

73.	StyR-132	162	TTATCGACGATCCGGTTGCCGGGACGCCG TGGTGGTACCGCTGGGGCGCGATAGTCG CCCACACAGATGACAAAAGCCGGATATCGC TATCCGGCTTTTCGGGTAAATCAGACTAAC CGTTCACTATCGCCAGCGGTTTTCCATT TACGCGAGACCAT	ferric enterobactin transport ATP-binding protein FepC	
74.	StyR-133	67	ATCGAAGACGAGGTAGCGACTATACTTGCT GGTTTCGGTCAGGGAGAANGGCACGTCTTT AACCTTG	uroporphyrinogen decarboxylase	
75.	StyR-135	70	ATTCATCCGCTGATTGACGCGCTGGACGAT GCGAAACTGGCGCCGATTGCGGCCAAAGC GCTGTCTACA	aconitate hydratase 2	
76.	StyR-138	42	CTTTGCCGATATTCCGGGAGTGATCACGCC GTATCACTGTA	hypothetical protein	
77.	StyR-139	138	CTATCATCGCGACGGCGCTAATCGATACCG GTTCCAAGATGGACGAAGTTATCTACGAA GAGTTTAAAGGCACCGGTAACATGGAGCT GCATCTCTCGCGTAAGATCGCTGAAAAACG TGTCTCCCGGCTATCGACT	transcription termination factor	
78.	StyR-140	125	TTTTGAACTCATCATCGACTATGTATCGC TGGAGAAAAGAATTGGCAGTAAAAATTGG AGTACGTGAGCCGCGCTATCTGTTATTGCC GGATTCACTTTACTGTAATGCGGTAA TTTTTA	Vi polysaccharide biosynthesis protein	
79.	StyR-144	77	GTAATCTGACGTAAGTACTGACCGTTTCTACC GTAACTCTCAGGATCAGGTAACCCAAAA ACCCCTGCGTGACTCGGT	Fis DNA-binding protein	
80.	StyR-146	173	ATTACACCGGATCTGATTGAGATCCTGCTG AGCATTCTCAAAGCGGTGGTATTCTGCTG GTGGTCGTCACCTGCGGGGCTTCATGAGC TTTGGCGAACGTCGTCGCTGGGTCTGTTC CAGAACCCTTATGGACCAAACCGCGTTGG CTGGGGCGGCTCGCTCCAGCTGGT	NADH dehydrogenase I chain H	
81.	StyR-147	203	TTGCACAGCGTTTGATCGTCCAGGATAAAG CATCTGCGATGTTCCCGCTCGGTATCAACG AAGAGATGGCAAACACACTGGGCGCGTTG ACCCTGCCGACAGATGGTCAAACCTGGCGGA GACGAACCAGTTAGTTTGTCAATTTCCGGTT TGACGATCATCAGACGATCACCCGTTTGAC TCANGATTGCGCGCTCGATGACTTA	flagellar transcriptional activator FlhD	
82.	StyR-148	96	ATCGTGCTGCTGGTGGCGTCTATTTACTTC GGCGGCGTAAATGCCACGACCCGTAAGTGG GGCCCGGCGCTGACCTTTAAAGACACCACC ATTACC	probable carbon starvation protein	
83.	StyR-152	81	CTAAACCAGAAACCGTAAAACGCGACTGG TATGTTGTTGACGCGACCGGTAACACTCTG GGCCGTCTGGCTACTGAACTGG	50S ribosomal subunit protein L13	
84.	StyR-153	88	GATCATCAAGTTTGTGATCAGCTGAAAAA AGCGGGGACGGTAACACTACGACGCGCTGG GCGCGGTATGTACACCCTGCTCAGCGTA	putative inner membrane protein	
85.	StyR-154	26	CTCTGGGAACCTCTGTACGCTGCTA	phosphoenolpyruvate carboxylase	
86.	StyR-155	66	CTCTCCGAAAAATCTCATCTGATAGCGCCG CCGTGCGACAGGGTATGCTACCCTGTCGCG CAAATT	putative hydrolase putative membrane protein	5' and 3' overlap with two putative ORFs, respectively
87.	StyR-156	78	ATTAACGATAACATTGACCTGTAGACCTGA TTATCATGGACAAATTTGACGCTAATCGCC GCAAGCTGCTGGCGCTTG	putative exported protein	Overlap of putative 5'- UTR- 35 nt
88.	StyR-157	50	ATCCGCGCGCTGGACGGCGATATGCAGGG ACGCTGCTGGCGGCCATGA	putative glycerol metabolic protein	
89.	StyR-158	122	ACATCAGGCGATTGTGCGTAAAGTGGCTGG AAGCGCGCAACCTTGAAGAAGTCCGAACC AGCGAACTTTTCGACGTTTGGTGGGACTAA TAAGTACAGGGTCGGCAAATGCCGGCCCC CTTTG	conserved hypothetical protein	Overlap of putative 3'- UTR- 34 nt
90.	StyR-159	116	TTTTTGAAACGCATGCGTCGCCGGGGCGGC GAATTTATTATCGATACCGTGGAGGCCGTT	L-isoaspartyl protein carboxyl	Overlap of putative 3'- UTR- 19 nt

		CGCTTCGTCCCGTTAGTCAAGGGAGAGCTG GCCTAGTTTGCCTGCAAAACAGCCA	methyltransferase type II		
91.	StyR-160	37	ATTATAACAATGGCAACTTATCTCATCGGC GACGTTTC	bis(5'-nucleosyl)- tetraphosphatase	
92.	StyR-162	130	ACGCAGATAAAGACAGCGGCCAAAGCGTA CCGCTGGACACCAAGTCCCGCGACAAGCCA GGATACGACGCCAGCGCAAACGGCTCCGG CTCCTGCGACGCCGGTTGATTGACGCGCGG CAACGCAAAATAC	putative DNA-binding protein	
93.	StyR-163	130	CCGCCGCTTTATGAAAGAGCCGAGGAAG TGCGCATTCAAGTCCAGCGTGACTACCCGTC CTGACATCAGCCAGAGCTACTGGACTGTCT GGGGTATGCGTAAAAACGAAGCACTGGTG CGTTTCCTGGAA	ATP-dependent RNA helicase (dead-box protein)	
94.	StyR-164	290	ATTGAAGCCGCTGAGAGCAGCCGCATGTG CGATGATGTGGCCGGTTGGGCCACTGCGCT ACAGTTGATCGCCCTCTCCGCGCGCCAGAA CCATACCTCTGCGCATCACTCCGCCCGCCG TCTTGCCGGGATTAATGCCAGCCACCTTTC TGATTATCTGGTGGACGAAGTACTGGATAA CGTGGATGTCAGCACCCGACATTTCTTACT TAAAAGCGCGATCTTACGCTCAATGAATGA CGCGTTGATCGTGCGCGTGACCGGCGAAG AAAACGGCCAGATGCGGCTGGAAA	MalT regulatory protein	
95.	StyR-166	117	CACTTCTCACGTTGAATACGATACCCCGAC CCGCCACTACGCACACGTAAGACTGCCCGG GGCAGCCGACTATGTTAAAAACATGATC ACCGGTGCTGCTCAGATGGACGGCGCGAT TTGTTTTAGTCAACGGAGTATTACATGTCC AGAAGGCTTCGACAGAACCAAAATCGTTAC CACGTTAGGCCCGGCAACTGACCGCGATA A	elongation factor Tu	
96.	StyR-167	89	CTTACTCGATCCTGCGCGTGCGGGGGCTAC AGGAGTGAT	pyruvate kinase A	Overlap of putative 5'- UTR- 25 nt
97.	StyR-168	39	AAAAACTGGCGAAAGACGACGCGGAAAAA TACCAACCTTCTGGAAACAGTTCGGTCTG GTGTTGAAA	putative RNA methyltransferase	
98.	StyR-170	68	TTTCTCTCACGTTACGGCGATGCAATGCC CGCGTCCGCCACCGCAT	heat shock protein HtpG	
99.	StyR-171	49	ATCACTCAATAGCGGGATAAAACAATGAA CGACAGTGAATTTATCGCTGGCTGACG TAATGAACCCCTTCCATGCTGAACGCGACCC TACTAACAACTGCGCCATCTCGCGCAGTGG T	coproporphyrinogen III oxidase	
100.	StyR-174	58	TCTTTATGACGTGAAAAATGAAATCCAGCG CGCGCTGGAGCGTAAAGTTGAACTCAAGT CTGGCGGTTATCTGATTA	CyaY protein	Overlap of putative 5'- UTR- 11 nt
101.	StyR-176	61	CTCCTAAAAACTCTCACATCGCGCCGCCAG GTACTCAAAACAGGTCTGGCGGCCCTGAC GC	ilvBN operon attenuator peptide	
102.	StyR-177	77	AATTTGAAAGACAAATAACAGGAGTCATT GTGGTAATTGGACCTTTTATTAACGCTGGC GCAATTTTATTCGGCGGCGTTATTGGCGC ATCTGGCGCAAAATGCAGAAAAAGCATCT GGCGTTTGATGAACTCTTTGACGTGCGCGC CGTGCGTATCGTTCGTAACGCTCTG	ribonuclease G	
103.	StyR-179	61	ATCGATAACAAAAACGCAAGTCTGACATAA ATGACCGATATGAGCACTGCAATTACACG ACAGATTGCTCCTCGATAACCGAAACCACCG TATGAACCAGATAGGCGCGCACTATGAAG GTCACAAGATTATTGA	probable N- acetylmuramoyl-L- alanine amidase	
104.	StyR-180	88	ATCTGGCGCAAAATGCAGAAAAAGCATCT GGCGTTTGATGAACTCTTTGACGTGCGCGC CGTGCGTATCGTTCGTAACGCTCTG	putative membrane protein	Overlap of putative 5'- UTR- 19 nt
105.	StyR-181	84	ATCATAAAGTTACAGAGGTAGTCAATGATTA GAAAAATCGGTGTGTTGACAAGCGGCGGTG ATGCGCCGGCATGAACGCGGNAATCCGC GGCGTTGTGCGCGCAGCGTTGACGGAAGG GCTGGAAGTCATGGGCATTTATGACGGCTA TCTGGGCCTGTATGAAGATCGTATGGTTCA GCTTGACCGTTACAGCGTATCTGACATGAT CAACCGTGGCGGTACTTCTCCTCGGTTCCGC	GTP pyrophosphokinase	
106.	StyR-182	133	ATCATAAAGTTACAGAGGTAGTCAATGATTA GAAAAATCGGTGTGTTGACAAGCGGCGGTG ATGCGCCGGCATGAACGCGGNAATCCGC GGCGTTGTGCGCGCAGCGTTGACGGAAGG GCTGGAAGTCATGGGCATTTATGACGGCTA TCTGGGCCTGTATGAAGATCGTATGGTTCA GCTTGACCGTTACAGCGTATCTGACATGAT CAACCGTGGCGGTACTTCTCCTCGGTTCCGC	DNA polymerase III epsilon subunit	Overlap of putative 5'- UTR- 38 nt
107.	StyR-185	243	ATCATAAAGTTACAGAGGTAGTCAATGATTA GAAAAATCGGTGTGTTGACAAGCGGCGGTG ATGCGCCGGCATGAACGCGGNAATCCGC GGCGTTGTGCGCGCAGCGTTGACGGAAGG GCTGGAAGTCATGGGCATTTATGACGGCTA TCTGGGCCTGTATGAAGATCGTATGGTTCA GCTTGACCGTTACAGCGTATCTGACATGAT CAACCGTGGCGGTACTTCTCCTCGGTTCCGC	6-phosphofructokinase	Overlap of putative 5'- UTR- 12 nt

108. StyR-186	224	CCGTTT CCTGCCCGCTCACTCCTTCAGGTAGCCGCT CATGAGTAAACCGTTCAAACCTGAATTCCGC TTTTAAACCTTCTGGCGATCAGCCGGACGC TATACGTCGTCTGGAAGAGGGGCTGGAGG ACGGGCTGGCGCATCAGACGTTATTGGGC GTGACCGGCTCCGGGAAGACATTACCATC GCCAACGTCATTGCGGACTTGCAGCGGCCA ACGATGGTGCTT	excision nuclease ABC subunit B	Overlap of putative 5'- UTR- 31 nt
109. StyR-188	51	ATTCATCAGGAACACAATATGGCATTACAG TCCGCTGCTGGGTGTCCTCTT	ribonuclease I precursor	Overlap of putative 5'- UTR- 7 nt
110. StyR-189	161	ATTAACCTCAACGCGTGATTCACATGTTGA AGCCGAAGCAAAGATTGACGACGCTAAAG TGCACCTTTTGACTGTAATCCCGTCTTTGCC CTATTACGCTTCACTGGGACTGGCTTATTC AGCAGAGCTCCCGCAATGGACGATTTGA AAGCCGAAGCC	conserved hypothetical protein	
111. StyR-190	53	CTTCACCGGTCTGGGCGCGCCGACTGGGA TCCGTATGCCCGCGGCCATT	glycerol kinase	
112. StyR-191	127	ACAATACAGGCTAAAGTTGAGCCGCCAGG CTAGACTTAGTTCCACAACACTAAACCTA TAAGTTGGGAAATACAATGTTCCAGCAA GAAGTTACCATTACCGTCCGAACGGTCTG CACACCCGC	phosphocarrier protein HPr	
113. StyR-193	61	CTCATCAACGGCCCGCTGCCGCTGCGCCAG ATTTATTTTGGCAGCGCCAGCGGCCAGCG C	putative AraC-family transcriptional regulator	
114. StyR-194	81	CTTCCTCTCTACGCCTTTATCAATACCAACT CCACGCTGGACGTTAGCGTTCACGATATGC GCATGGCGCTGTGGTTTTTT	lysine decarboxylase	
115. StyR-197	53	ACAGCTGCGATTCCTGCGCAAGAGAAGA AATTTACGTTGCGGGCTGGCCCT	conserved hypothetical protein	
116. StyR-200	63	CTTGAAGCGAAGCGCCGTAATAACCCCA GGGCGACGATCTGGCGCCGGGCGTGCTGA AGATC	DNA-directed RNA polymerase, beta- subunit	
117. StyR-201	105	CAGCATGTGGGCGTTATTCATGATAAGAAA TGTGAAAAACAAGACCTGTCAATCTGG ATCTACAAACGATTTCGGTCCCCATCACAG CGATAGCGTCCATTCT	succinate dehydrogenase cytochrome b556 subunit	
118. StyR-203	172	CTAACGACGCCTATCCGACAGGCTTCCGTG TAGCGGTTACGCCTCTATCGTCAAACCTGA TCGATGCCATCAACCAGTTGCGTGAAGGTT TCGAACGTAAGCGGTTGAATTCCAGGAC ATCCTGAAAAATGGGTGCTACCCAGTTGCAG GACGCCGTACCGATGACGCTTGG	aspartate ammonia- lyase	
119. StyR-204	52	CTGCGCGGCTGGGTTATGTGCTGGAGCGC GGCGATGAAGTGGGTTAAGCCG	putative two-component system sensor kinase transcriptional regulator	
120. StyR-205	143	TTTGGCGCGCTGCTGCTTCCGATATGCG GCGGCTGGCTTGGCGTTGCTTTGCTTAAAG GCAAAGCGCTATTCGCCAGTTTAGCGGAT GATTATGATGTGAATAATTCGCGCTGGT TTTTAAAACGGCGCTACTTTTT	putative membrane protein	Overlap of putative 3'- UTR- 51 nt
121. StyR-206	181	ATACCGCAAAAGCCTTTAACGAAGCGCTG CCGTTAACCGGTGTGGTGCTGACCAAAGTT GATGGTGATGCGCGTGGCGGTGCGGCGCT CTCTATTCGTCAATCACCGGCAAGCCGAT TAAATTCTCGGTGTCGGCGAGAAAACCG ACGCGCTGGAGCCGTTCCACCCGGATCGTA TCG	signal recognition particle protein	
122. StyR-208	69	CTTTCGGCACCGTTTCCAGCCCTGCATCG ATACCAGCCAGGTGCCAGGCCAGGCGAC GCTGCCAAGC	serine protease	
123. StyR-209	113	ATCCTGGCTGATATCGCGTATTCGACAAA GTCGCGTTCACCGCGCTGGTTGAAAAAGCG AAAGCAGCTCTGGCATAAGCCAGTGAAAA GAGGGAGCCTGGCTCCCTCTCTTT	50S ribosomal subunit protein L20	Overlap of putative 3'- UTR- 35 nt
124. StyR-210	61	ATTAATCCCGTGTGCTGTTAGGTCGTAGT CTGATTATGGGATTTAGTAGCGGCGCGTTG	ferredoxin-type protein NapH	

125. StyR-211	95	C TCCTGGCGCCGCTGCTGTACCTCCTGCACG CCATTTGACTGGTATCAGCCTGTCGTCG CGACGTTGCTGGGTATCCATGCGGGCTTCT C	pts system, N- acetylglucosamine- specific IIABC component	
126. StyR-212	36	GGTTATCAATATTCCAGGTTGTCCGCAAAA CCC	hydrogenase-2 small chain protein	
127. StyR-213	205	ATAACCATTCTTTTAATGTGCATGTTAACA AAAGAGGTTTAAATGAGAATAAACGTA ACTACTAACCAGTCTGTTAGTAGCTGGACC GGCACTGGCAGGAGAAGCTCACGTTTGTA AATCACAGACGGTAGCGAACTCTGCAGCG AATGCCGAGTTGACGGATAACACGGTATTT AAATGCGGCGAAAGCATTTCCGGA CTTATTCTGTGGAGTTATATATGAGCGAT AAAATTATTCACCTGACTGACGACAGTTTT GACACGGATGTACTCAAAGCGGACGGGGC TATCCTCGTTGATTTCTGGGCAGAGTGGTG CGGGCCGTGTAATAATGATCGCTCCGATTCT GGATGAAATCGCTGA	hypothetical protein	Overlap of putative 5'- UTR- 42 nt
128. StyR-214	164	ATATTTAGAAAACGCAAATTGCGTTCTTTTC ACTCCCGCAAGGGATTTCAAACAGTGGCAT ACATATGAAAAAACTTTACTCGCAGTCAG CGCAGCGCTGGCGCTCACCTCATCTTTAC TGCTAACGCAGCAGAAAATGATCAGCCGC AGTATTGTCCGACTGGTGGCACCAGAGCG TAAACGTGGTAGGCAGCTACCATA	thioredoxin	Overlap of putative 5'- UTR- 9 nt
129. StyR-217	203	TTTTACGACTGGCCGCTGTTCTGCGCTTTT CCGCAGGTA CTGTTACCGGTGGTTACGCTCAGAGCGACG CGCAGGG	nucleoside-specific channel-forming protein tsx precursor	
130. StyR-218	100	CTTCATCAACAGCACCATCCGCGGGCATGA GTGCTGACAGGAA	outer membrane protein X precursor	
131. StyR-220	43	CGTCTGTCTCTTATACCGACACGCAAATC AGTCGCTGGGGGGCCAACTTCCACGA AATTCCGATTAACCGCCCTACCTGCCCTA CCATAACTTCCAGCGTGACGGTATGCACCG GATGGATATCGACACCAATCCGGCGAACT ATGAACCAAATCCATTAATGACA ACTGGC CACGCGAAACGCCAGCCGCAAAAACGC GGCGGCTTCGAA	site-specific integrase/recombinase	Overlap of putative 3'- UTR- 13 nt
132. StyR-221	219	CCAAACCGAAGCGATGACGACGGTAGATA TCAATACCGCGCGTTTTGTCGGACACNGTA ATCTCGACGACACCATTTTAATACCAATA TTGAAGCGACGAGGCCATTGCCCGCCAG CTACGCCTGCGTAATCTGG	catalase HP11	
133. StyR-223	137	ACAGAGAATATCAATGAAGAAAATCGTCA CGCTGGTCGCCCTGAGCATATAATGACAG GGTGTGTGA	ribonuclease G	
134. StyR-225	68	ATTTTGAAGAAAGTCAAACGTCATGACG CGCATGAAATATCTGGTGGCAGCAGCCAC GTTGAGCCTGTTTCTGGCGGGTTGCTCGGG TTCAAAGGAAGAGGTGCCCGATAATCCGC CGAATGAAATCTACGCGACTGCTCAGCAA AAGCTGCAGGACGGTAACTGGAA	heat shock protein,	Overlap of putative 5'- UTR- 3 nt
135. StyR-226	169	CTTAACGAGAAGCTTAGCTGATGACGCTAT AATTAGCGCATAAACACCTGGCGCTGTTGC AGGTGAGGAGGAACAATGAAAATTA CTGT ACTGGGATGCGGAGCCTTAGGACA ACTTTG GCTTTGCGCACTGTGCAAAATGACATGA CGTACAGGGCTGGCTACGGGTGCCACAAC CTTAT	putative lipoprotein	Overlap of putative 5'- UTR- 8 nt
136. StyR-227	183	CGCTAAACGAGACAAAAGAAAACGGCATT CGCCTGACCGAACGTAAAGAGACGTTAGG CGATGTGA	4-methyl-5(b- hydroxyethyl)-thiazole monophosphate biosynthesis protein	Overlap of putative 5'- UTR- 75 nt
137. StyR-230	66	ATTCCATGGTAAAAGTCGGCGTTTACCAG AAGTGAACCGCTGGCGACCGTTTTATTGG TGCTGTCTCTGGTAATGGTCATTGCCAGCC	signal peptidase I	
138. StyR-231	135		spermidine/putrescine transport system permease protein PotC	

139. StyR-233	226	AGTTATTGCTCGTGATAAAACCAAGGGCC GATAAGGCCCGTAAT CTATCGTGTGATGTATATCGCATCATCAAT TTAAAGTCAGGTGGGATGCCTGTCTGTAA CGCCCCTTTGGGATTGGGGGTTCTGCTGA GCATCTATGAAGCTGAATAAACTTATATA AATATCAGAGATAAATGGTGGGACTACC GCTCATTCTCCCTTCGATTTACTACCTGTT TTAAGTAGCGCAAATACTTATGCGCTTACC AGCACTGGAAATGTGG	putative membrane protein	
140. StyR-235	95	TTCCCTTCCCTAAATCTCCATTATGATTATT GAAAAAAGGTTAAAACTATACCGTCTTT GTCAAAAAAGACGGTGAAAAATATATT	lipopolysaccharide core biosynthesis protein,	
141. StyR-236	112	TTTTTAACGCTTACAGGACGATGAAAAAGAA AAGACCCGTACTTCAGGATGTAGCCGACC GCGTGGCGTGACCAAAATGACGGTCAGC CGCTTTTTGCGTAAACCCGGA	gluconate utilization operon repressor	Overlap 5'-UTR- 10 nt
142. StyR-237	213	TTTGCTATGGTCAAAATCGTCGCCATCGTG GCGTTGATGTGGTTGGGTTGGTGTGATT GCGATGCACTTTAAATCGCCGACCGGCGTT GAAGCGTCTTTCGCGCATCTGTGGAATGAC GGCGGCTGGTCCCGAAAGGTATTAGCGG GTTCTTGCCGGTTCCAGATTGCGGTGTTT GCCTTCGTGGGCATTGAGCTGGTCCGGTACT ACC	D-serine/D- alanine/glycine transporter	
143. StyR-238	144	ATGTAATTGTGCGGAGAACGAAAAATGAAC TTTGGAGAGCGTTTACAAAGAGTGCTTAA GAGACTGGGATCACCAATCTGAGTTAGGT CGTAGAGTCGCGCTACCTCTCAATCAGTT AATGGTTGGTGTCAAGTCCGGCATTTC	putative DNA-binding protein,	Overlap of putative 5'- UTR- 23 nt
144. StyR-240	92	ATGCACGAGAATCAACAACCACAAACCGA GGCTTTTGTAGCTGAGTGGCGCAGAGCGTG AAGCGATAGAGCACGAGAAGCACCCTAC GAAGA	NADH dehydrogenase I chain E,	
145. StyR-242	123	CTGTAAAGATGAGCAGGGCCGTTACGTGT CGGCGCGGGCGTCCGGCGCAGGCGGGCA ACGAAGAGCGCGTTGACGCGCTGGTGGCG GCAGGCGTTGACGTCTGTGATCGACTCT TCTCA	inosine-5'- monophosphate dehydrogenase	
146. StyR-244	237	CTAAACCGCTGACGGAGTCATCAATCCCGT CGGAAGCACTGGCAGCGGTTCCCTCATGAG CTTCCGGTAGCGACGGCCGATGAAGAAAG CCAACAGTTGCTGTTAAGCGGCATGAGCTG CGCCAGTTGTGTACCCGCGTACAACATGC GCTACAAAGCGTACCGGGCGTACGCAGG CACGGGTAAACCTGGCGGAACGCACTGCG CTGGTGTGAGGCGAGCGCTCCGCCGCTGA	copper-transporting ATPase	
147. StyR-245	236	CTCCGATTCAACGTAGAAAATCGACACGTA TTTACGTTGGGAATGTGCCGATTGGCGATG GCGCCCCTATCGCCGTCCAGTCGATGACTA ACACGCGTACCACTGACGTGGAAGCGACG GTTAATCAGATCAAAGCGCTGGAGCGCGTT GGCGCAGATATGTTCTGTGTTCTGTACCG ACCATGGACGCCCGCAAGCGTTCAAGCTT ATCAAACAGCAGGTTAGCGTCCCCTG	GcpE protein	
148. StyR-246	144	ACACTCCTTCGGTAAAAGAGGAGCGTTTTTC GCGCGTTTCTCGGTGTGCCGATCATTACAG GTCCGCAACTTCTCGGCGTGTGGTCTGTC AGCAGCGCAATTGCGCCAGTACGATGAA AGCGAAGAGTCTTTCCTCGTACCGC	phosphoenolpyruvate- protein phosphotransferase	
149. StyR-247	154	CATACTTCCAGCGTCATGACTTTATCGCCA ATGGCGGAAAACCTCAAGCCGCAGGAAAAC CCGAACGCGCAAGCGATTACAGACGAACT CAAAGAGATCGACTCGGAATAAACGGCAG TAAATAAAAAGGTGAGCGCAATGCTCACC TTTTTGAT	VacJ lipoprotein precursor	Overlap of putative 3'- UTR- 44 nt
150. StyR-249	291	TTAATTAAGGCTCCGTCATATGGAGCCTTTT TACTCGGTCAGAGGACCGTATGAAACGA ATTTTCCTTACCTGCGCGGCGTTGTTGTTCA GCAGTCAGGCGTTGGCCGATGAGTGTGCC	putative secreted protein	Overlap of putative 5'- UTR- 50 nt

151. StyR-251	133	AGCGCCAGTACGCAGCTGGAAATGAATCG CTGCGCCGCCGCAATACCAGGCGGCAG ATAAAAAGCTGAACGAAACCTATCAAAGC GCGATTAAGCGTGCGCAACCGCCGAGCG TGAGCTATTGCAAAAAGCGCAGGTGGCAT GGATTGCCCTGCGCGACGCCGATTGCG CCTGGCGCCGCTGGCTAAAGTTATCAACGA CAACTTCGGCATCATCGAAGGTCTGATGAC TACTGTTCACGCGACTACCGCAACCCAGAA AACCGTTACGGCCCGTCTCACAAGACTG GCGCGCGGCCGC	glyceraldehyde 3- phosphate dehydrogenase A	
152. StyR-253	173	ATTAAGCAAACAAGCGCGTGAAAACC GACGGATTCTGGTCGCTTTCTTTGCCAG AGAAACGAACTCTACGTACCTAAGATGC TGGCATTGAGTGAAATTCTAAAAACAGC AAACGCTACGGCGTACGTCTGCCAACAA AGATGAAAGCCGAGCGCTGGCACGAGT CCTCTTTGCTCCTGCTATGCTTGAAGAGTG ACGGGTATAACAGGAGCGGAGTCATGCAA TACAACACGTTAGGAAAATACCGATCTTCGG GTGTCCCGCCTTTGTCTGGGCTGTATGACA TTCGGCGAGCCGAGTCGCGGCAATCACGC CTGGACGCTTCCCGAAGAGAGCAG	membrane-bound lytic murein transglycosylase d precursor	
153. StyR-257	172	AAAATGGCAGCTGCTGTACGACGCGCTGTC GCCAATAGCGACAAAACCTGCGACATGATCA TCATGCCCGCCTGTTTCGGGCTGGCGAACG ATACGCTGTGGCGCTGGCTAACGAACGTC TGCCCTGCGCGCTCACGCTGCTGCCGACG CTTGGCCGCGGCCTGGTGGCGTAAAACG ATCTGGTTTTTTTTGATAACGGTCCGAAA TGCCATTAGTCATCAGCATGATACCGGATG ATATTACCTTTACCGGGATTGCTACTCGC ATCGGGTATTTATCGCGCTGAATGAAAAGC CTAATGCCACAGCGATTCTGTGCGGCGGCA CCT	putative oxidoreductase	Overlap of putative 5'- UTR- 57 nt
154. StyR-258	150	GTCATGCAGGCCAGAAACATTCTTATGTG AAAATCACCGCCAGCCGCTACGAAAAGG AATGTTGAAAGCGGTACG	anaerobic glycerol-3- phosphate dehydrogenase subunit B	
155. StyR-260	186	TAATTGCGCTGTTACAGCCCTGGAAAGGGT TTGCTGTATTACAGTGAACGTATCGTCGCC GT	putative DeoR-family transcriptional regulator	
156. StyR-261	79	TTTTTCCACCCGAAAAGGCAACGAATACCA TGGAATACGCGTTTTTCGCCAGGAAGATT TCGAAGAGGTGATTACCCTCTGGGAGCGTT GCGACCTGCTGCGTCCATGGAACGATCCTG AAATGGATATTGAACGCAAGGTGAATCAC GATGT	tRNA hydroxylase	
157. StyR-263	62	ATGCCCCGATCCCGACGTACCGGAAGCGC GTGTGATCTTGCCAAAACCTGGTAAAAGCGC GCGAAGCGCAAGGTCA	putative exported protein	
158. StyR-265	154	CTTAACCCGGCGGATGCGAAGTTGGGC GTCAATGCCGGGACTCGCGTCTTCTTTAGC	putative acetyltransferase,	Overlap of putative 5'- UTR- 29 nt
159. StyR-266	75	ATCATGGACCTCGCCCGTTTTCCGACGCT CTCGACGCAGGAAACCGGACGCTTTA CTTCTCGTCAGATATCGAACTGAAGGCGG TCTGGTTACCTGGCGCTGGCGTTAACCC ATCGCATCTGAAAATTGTGAGCCCGGTGGT GATGGGCTCCGTGCGCGCCCGTCTGGACCG ACTGGA	biosynthetic arginine decarboxylase	
160. StyR-267	60	ATTGAACGCGGCTGATCAAAGAAGTCGA TCAGCAGGCCTTACCGGAGGCCCGCG CTA	NADH dehydrogenase I chain G	
161. StyR-268	56	ATGGTGTGGGCGCTGGTCATTATTCACGGT AGCGCGTTGGCGCCGCATCTGAAAATTGTC AGTTACGTGTTGACGGGGATCGTGGCATT CTGATGTGATCCAGGCAAAGCAGCTATTG CTTCTTTTGTTCGGGAACATTTATCGGCG CCTGCGCGACA	alpha-amylase	
162. StyR-269	126	ATTGAAACGAATATCGTTGGTACTTACACC	2-oxoglutarate dehydrogenase E1 component	
163. StyR-270	62	ATGGTGTGGGCGCTGGTCATTATTCACGGT AGCGCGTTGGCGCCGCATCTGAAAATTGTC AGTTACGTGTTGACGGGGATCGTGGCATT CTGATGTGATCCAGGCAAAGCAGCTATTG CTTCTTTTGTTCGGGAACATTTATCGGCG CCTGCGCGACA	N-acetylglucosamine repressor	
164. StyR-271	162	ATTGAAACGAATATCGTTGGTACTTACACC	putative membrane protein	
165. StyR-274	95		UDP-N-	

		TTGCTGGAAGCCGCTCGCGCTTACTGGTCC GCGCTTGACGCGGACGCTAAAGCGGCGTT CCGCTT	acetylglucosamine epimerase (UDP- GlcNAc-2-epimerase)	
166. StyR-276	26	CTCCCAAACCTCTGTCGTTGCCGCGTC	menaquinone biosynthesis protein	
167. StyR-278	142	GTTTTCCCGTTCTTTAACATCCAGTGAGAG AGACCGATGCATCCGATGCTGACCATCGCC GTGCGCGCAGCGCGCAAGGCGGGTAATGT AATTGCCAAAACTATGAAACTCCGGACG CTGCAGAAGCGAGCCAAAAAGG	extragenic suppressor protein SuhB	
168. StyR-279	85	ATAGCGATGTGGTGGCGGAGGCGTTAAC GCATATAACGCGACCAAATGACGCAGAAC CCGGCGCAGGTTAGCCTGCGCCCAAAT	mannitol operon repressor (mannitol repressor protein)	5' and 3' overlap with two putative ORFs, respectively
169. StyR-283	103	ATATTCGTAAAGATCGTTCGTAACGAGGAA GTGGGTGACACCGGGCGTTATAACTTCGGT CAGAAATGCGTATTCTGGGCGGCGATTATC TTCTGGTGCTGCT	mannitol-1-phosphate dehydrogenase formate dehydrogenase- O gamma subunit	
170. StyR-284	186	ATCTTAAACCCATTGTCTGGGAACTGGTCA TCAACCCTGACCAGAACGAAATGGCGCGC GACTGGCAGCTTATGTTATTAGCGTGCCA GTTATCTTATTGATTGAGATGCTATTTGCG ACATGGAGTTGGCAAAAGCTGCGCAGTCT CACGCGCCGCCCATTTGCAAGGCCGCT TGCGGC	putative sulphatase	
171. StyR-286	63	GTCAGACTCACGGTTAAGTATGCCAACCAG ATGGCCTGGTGATGGCGGGATCGTTGTATA TTT	conserved hypothetical protein,	Overlap of putative 3'- UTR- 21 nt
172. StyR-289	26	TCACGAACCCCGCGGTTGCAGTTG	DNA polymerase III subunits gamma and tau	
173. StyR-294	73	TTAACAGCGATAAAGCCTACTGGAACAAC TTAAAGACCCCTTTTAAAGCTCGAATTTAC CATCAGGGGATGTA	periplasmic glucans biosynthesis protein MdoG precursor	
174. StyR-297	55	TTTGCAGACTCAACTGGAGGCGCTGCCTTT TCATCCTCAGCCTGACCTGACTTA	para-aminobenzoate synthase component I	
175. StyR-298	160	ATATTACGCTGGAGAAAGGCGAATCGCTT AACTTCCAGCTTCACGGGCGCGCCTAT TTGCAGTCGATTCACGGTACGTTCCACGCG ATGACGCACAACGAAGAACGCGAGGCGTT AACCTGCGGAGATGGCGCATTTATTCGTGA TGAACCTAACAT	conserved hypothetical protein	
176. StyR-299	73	TTTATGGACCGCGTGGTAGGCTATATGGTC TCGCCGTGCTGTGGAAAAAGATCGCCCGT GGTTTGTGCGGACG	DNA topoisomerase I, omega protein I	
177. StyR-300	82	TTACGAAGCGGAACTCAAATACTTGGTGG ATCACGAATGGGTGCGCCGACTGAAGAC GCTATCTGGCGTTCGACCAAAGAA	aerobic glycerol-3- phosphate dehydrogenase	
178. StyR-301	79	ATGACTGAACTGCGTAAAGCAGGTCGTGA AGCTGGCGTATACATGCGTGTGTTTCGTAA CACCTGCTGCGCCGCGTCCG	50S ribosomal subunit protein L10	
179. StyR-303	48	ACTGCAAAAATGGTGTCTCAAAGAGCAGCGT TTTCACTCGATCATGGACA	guanosine-3',5'- bis(diphosphate) 3'- pyrophosphohydrolase	
180. StyR-304	45	ACCATGGTACGTGATTGGCAGTACCGACG ATAATCCGGACATCAC	detergent-resistant phospholipase A	
181. StyR-307	132	ATTTCCGCCACTGATAGGTAACCGTATTTA CGGCTGCGATGACTGCCAGCTTATCTGTCC GTGGAATCGTTACTCTCAGTTGACCGACGA AGCAGATTTAGCCACGCAAGGCGCTGC ATAACCCAGATTT	putative 4Fe-4S binding protein	
182. StyR-308	175	ATGCATAACGATAAAGATCTCTCTACGTGG	probable transport ATP-	

		CAGACCTTCCGCCACTGTGGCCAACCATA GCGCCTTTTAAAGCAGGCTCGATCGTGGCG GGCATAGCGTTAATTCTCAACGCAGCCAGC GATACCTTCATGCTATCGCTCCTCAAGCCA TACTGGATGATGGTTTCGGTAAAA ATATTGAGGCAAGTCACCATCCCCGTTAATT CAGAGTAAAAGTATGTTTTGTGTGATCTAT AGAAGTAGCAAGCGCGATCAAACCTATTT GTAT	binding protein MsbA	
183. StyR-310	93		conserved hypothetical protein	Overlap of putative 5'-UTR- 3 nt
184. StyR-311	105	ATCTCAACTTCCGCCGGTTCGCGCCCGGCT GGTGTGTTAGCCGCCCCACCTGGTCAAAC TGGTGAAACGCTTTTTCAACGCGAAAGCT TTGCCGCACCGAAG	putative glutathione transferase	
185. StyR-313	111	GTATTACCGAGCCTATCGAGTTCTCCTTCA TGTTCTGGCGCCGATCCTGTACATTATTC ACGCGATTCTGGCAGGTCTGGCATTCCCGA TCTGTATCCTGCTGGGGATGC	PTS system, glucose-specific IIBC component	
186. StyR-318	82	ATGATCATGTGGCGCTGGCGGGATGCGAT AACAAACGATAAAACCGCCCCGACGACTAA AAGCGAAGCGCCAGCCGTAGCGT	putative lipoprotein	
187. StyR-319	80	ATGAAGATTGCCGGCTTGCTGACGCTGGTC GCCGGCATCGTATTGATCAAATCAGGGAC GCGTAAACCGGCAAACCGGT	putative conserved membrane protein	
188. StyR-320	59	ACCGAAGCCTGGCGACCGTGTAGAGCCGG ATATGATGCCTGCCGCAACGCAGGCGCTG CTACGGCACGCTGATTAGCGAACTCAAAG CCCGTAAAGGTGATTGTCAGCGTCGCCCGG A	DedD protein	
189. StyR-321	60	CTACGGCACGCTGATTAGCGAACTCAAAG CCCGTAAAGGTGATTGTCAGCGTCGCCCGG A	glycine dehydrogenase (decarboxylating)	
190. StyR-324	26	TCAATCTGCTCACGGCGCATGACGG	glycogen operon protein	
191. StyR-325	52	AGTCTCATACCCGATCAAACGCCTGAAC TTCTGGTTTTACCTGTTACTCA	periplasmic divalent cation tolerance protein CutA	
192. StyR-326	49	TGCATGAACCACGTACGCCGAGGATAAA GACACCATGTTGCCTTCTC	NADH dehydrogenase I chain G	
193. StyR-332	85	TGATGGCTATCATGTCCAAGTATTGCCA TAAATACTACCCTGGCCGTTGGCGACTACG CCTCCAGTGAACATGATGGCCCAAG	putative fimbrial protein	
194. StyR-334	95	ATCAACGACTCANGATGAGGGTCAGGATC GCCAGGAGGCGAAGACACAGGATTGTCAG GAAGACAAACGTCGGGAGACGTTAGTAAA AGGAAATG	hypothetical protein	
195. StyR-337	175	CCAATCTTTTGTATGTCTGATCGTTTCCATT TGAGTATCCTGAAAACGGGCTTTTCAGCAT GGTACGTACATATTAATAGTAGGAGTGC ATAGTGGCCCGTATAGCAGGCATTAACATT CCTGATCAGAAAACGCCGTGATCGCGTTA ACTTCGATCTACGGTGTGCGCAAGA	30S ribosomal subunit protein S13	Overlap of putative 5'-UTR- 93 nt
196. StyR-338	59	CTTGCAACCCAGCAATCTCACATTCCCGCT AAGGCGGTTGAAGACGCGGTAAGAGAT TTCAGATTGCCGAATATTTTCGTACGCCGT TGCC	integration host factor beta-subunit (IHF-beta)	
197. StyR-339	34		motility protein B	
198. StyR-340	203	ATTGAAACCAACGTAGACGCCACCAGCAC GCTGTTGAGCGAGGACCATCCGCGCAGG AAAAACTCAAAGAAGTACGTGAAGATGAC GATGATGCGGAGATGACCCACTCGGTAGC GGTAAATATTTATCCTGCCACGACGCGGAT GCCGCAGTTAACCATCGTGGTGGTTCGATAC CATTCCGATAGAGCTAAAACGCTCCTA ATCAGCGACGGTACGGTACTGGCCAGCCAG GTACGAACGACGCGGTTGCCGAAAGTAA CGCACGCGAAATTAATCTCGCGCCGGTCAA TAAACTGATCGACGACATCGTACAGGCTA ACGCGGGTAAATCCTGAGGTGCGTGTGATG CAACAGCAAAAACCGCTGGAAGGCGCGCA G	sensor protein PhoQ, regulator of virulence determinants	
199. StyR-342	177		multidrug resistance protein A multidrug resistance protein B	
200. StyR-343	122	CTGCGTAAGCTGAACATGGGGCCAGAGTT CTTGTCGGCGTTTACCGTAGGCGACCAGTT	aspartate-semialdehyde dehydrogenase	Overlap of putative 3'-

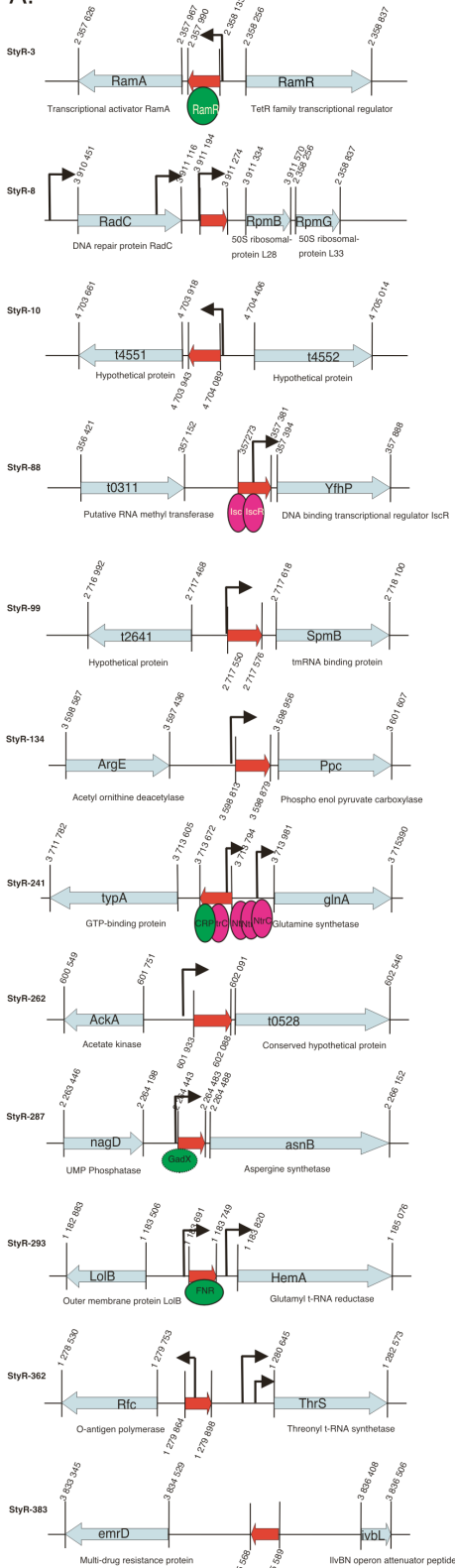
		GTTATGGGGCGCCGCCGAGCCGCTGCGTCA AATGCTGCGCCAGTTGGCGTAGTGGCTATT GCA		UTR- 11 nt
201. StyR-344	122	ATTAGCCCCGGCAATACAGAAGGCCGATA GCTGCTGCTGCGAAGAACATTGCGCGTCCA GCGCGCCTGTTTCTACTGCCGTGGCAGGCA CGCGCTATACCTGAAAAATCTCCGGCATGG ACT	heavy metal- transporting ATPase	
202. StyR-345	191	CCTCCGAAAACCTACACCAGCCCGCGCGTG ATGCAGGCCGAGGGGTCTCAGCTGACCAA CAAATACGCTGAAGGATATCCGGGCAAGC GCTACTACGGCGGTTGCGAATACGTTGATG TCGTAGAGCAGCTGGCTATCGACCGCGCG AAAGAAGTTCGGCGCCGACTACGCTAA CGTGCAGCCGCACTCC	Serine hydroxymethyltransferase	
203. StyR-346	191	ATTATGCCAGGCATGAGGAGAATAGAATG AAGCAACAGACCAACCGAAATCGTCGTTG GGTTTTGGCTCGCGTCCCCACGGCGCGCC GCAGATGGATAACTTCCGCTCGAAGAAG ATGACGTCGCGACGCCCGGTGAAGGGCAG GTGCTATTGCGTACCGTTTTTTTATCACTCG ACCCTTATATGCGT	Putative NADP- dependent oxidoreductase	
204. StyR-347	138	TTATGAAAAAATTGTCAGGCGTTTTTCCTTC TGCTGTTGGTTGTGCTGGGTATTGCCACGG GCGTGGGGATGTGGAAAGTTCGCCATCTG GCGAACAGCACGTTACTTATTAACAAACGA GACTATCTTACGCTCAAGG	Putative secreted protein	Overlap of putative 5'- UTR- 2 nt
205. StyR-348	93	ATTTTCGGTTTGTAACTATTGTGCCATTTT TCTGGGCATGCTGGCGCTGCGCGCCTGGC ACTATGACGAGAATCATTACAGTGGCGCA ATA	Phosphatidate cytidyltransferase	
206. StyR-349	149	ATTAACAAACATGAGAACCATACGACGC CATGAGCGACGACAATTCACACAGTAGTG ACACAGTAAACAGTAAAAAGGGATTTTTTT CCCTGCTACTCAGCCAGCTTTTCCACGGTG AACCTAAAAACCGTGATGAGTTGCTG	Haemolysin-related protein,	Overlap of putative 5'- UTR- 12 nt
207. StyR-350	253	TTGATGGAACCAGAGGAAAGCATGATGGG TATGAAAAGAGACAGTTAGCAATATTGTGA CCAGCCAGGCAGAGAAAGGAGGCGTTAAA CACGTCTATTACGTGGCGTGCGGCGGTTCT TATGCGGCGTTCTATCCGGCGAAAGCATTT TTAGAAAAAGAAGCGAAAGCGTTGACTGT CGGTCTGTATAACAGCGGAGAATTTATTA CAACCCGCCGCTAGCGCTGGGAGAAAATG CCGTTGTGGTTGTGCGCT	Putative phosphosugar- binding protein	Overlap of putative 5'- UTR- 14 nt
208. StyR-351	184	AGTTGAAATCGTTGGTATCAAAGAGACTCA GAAGTCTACCTGTACTGGCGTTGAAATGTT CCGCAAACCTGCTGGACGAAGGCCGTGCCG GTGAGAACGTAGGTGTTCTGCTGCGTGGTA TCAAACGTGAAGAAATCGAACGTGGTCAG GTACTGGCTAAGCCGGGCACCATCAAGCC GCACAC	EF-Tu	
209. StyR-352	131	ATTTCTCAAGGAGAAGGGTTATCCATGCAA AATATCGTCATTATCGTAACGGCGCCGCC TACGGCAGCGAATCATTATTTAATAGCCTG CGTCTGGCCATTGCGCTTCGCGAGCAGGAA AGCCATCTCGA	conserved hypothetical protein	Overlap of putative 5'- UTR- 24 nt
210. StyR-353	386	CGGCTAAGTTACAAGATGCTACTCAGACCT CCGAAAAAGACATGATGAATCTGATGGAC GTGATCCAGAAAGGATTCTACGGGGGGT AGATTCAGGAAATATGCTGCAGGGTTTCTC AAAAATCAGCAGCGGATGAATATCATCA ATAAGAAGGGGTTGGAAGCGGTCAAACCT TTCGCGCCTTTGTTGGTTATGGCTGATCAG GGGAGTATGGCTGGTGAGTCTGCCGTAAT GCATACCGAAAGATTTTCAGGCCGCTCTG GATGCTGACAATATTAAGGCGGTTAACGAT GACCTGAAAGAAAAGGGCGCGGGTATTA ATTCAACTTCTCTGACGGGAAGGGTGGGTT TGGTGGTCTGGAAAATATGTATGCCAGCT	Hypothetical protein	

211. StyR-355	177	G ATTCAGTCCCAGCGTGTGAAAGCAGACCAG GGGTTTCGACGGCCTGTACAACGAATTACTG CTGGAAATGGCGCGTAATCAAATCTTTCTG ATCAACGAGCGTCAGCTCTCGGTGAGCCA ACAAAGCTGGTTGCGCCACTATTTAAGCA CTATTTGCGCCAGCATATTACCCCGATT	polyphosphate kinase	
212. StyR-356	95	AATATTTATTAACCTCCCAGGTGAGATATT GCCCATGTACTCGTATCGCTAAAGAAGCCCT GACGTTTGACGACGCTCCTTGTTCCTGC TCACT	inosine-5'- monophosphate dehydrogenase	Overlap of putative 5'- UTR- 28 nt
213. StyR-357	79	ATATTGATAACAAACCGCGTTGACGAAG TAATTTTGTGATACCGCTGATGAGGTTAC GTTTCATCAGGCTGCAAACC	smpA (small membrane protein A)	Overlap of putative 3'- UTR- 47 nt
214. StyR-359	47	CTTTCTCACTGGTCAACTGTCGACACA ATGCCCGTTTTGCTTT	putative membrane protein	Overlap of putative 5'- UTR- 30 nt
215. StyR-365	158	ATCAAACGACATTTGCCAAAAGGCGAGTG CCTTGTGCAACCTTTTGTGGGTGCCGATC GGTGTCTTAAACACCGACTTTTCTCGTTAT ATCCTCGCCGATATCAACAGCGACCTTATT AGCCTCTATAACATCGTGAAGTTACGTACT GACGAGTA	DNA adenine methylase	
216. StyR-367	115	ATTGGGGATGTATCTGGATCAACAACGAG GAGCTGCATGATGAATCCACAGGCAACCA CAACTGATGAATTAACCTTTACCAGGCCGC AAGGCGAGCTGAAAAAGCAAGTCCTGA	malate synthase A	Overlap of putative 5'- UTR- 39 nt
217. StyR-368	226	GATCAGATCGCTTTTGAAAAAGTGGTCACC GCGCCGGTTGAAAAAGCGCAAGAGAAAAC CGAGGTAGCACCGGTAGCGTCTCCGGCAG TCGTTGCGCCAGCCGCAAAAAGCGCGGCC CATGAACATCATGCGGGCGTGAAAAACC TGCGCGTGAACGCGAGTCCACCAGCATTTCG CGTGGCGGTAGAGAAAGTGGATCAGCTCA TAAACCTGGTCGGCGAGTTAG	chemotaxis protein CheA	

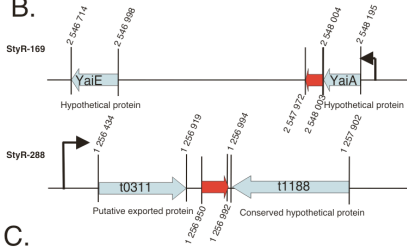
Table S3. Known npcRNAs in *E. coli* and/or other *Salmonella* strains.

ERNS	cDNA (nt)	Coordinates in <i>S. Typhi ty2</i> genome	N. blot	Known npcRNA in other enterobacteria	Coordinates in <i>E.coli</i>
6S RNA	194	3070109-3070298>	NP	All Enterobacteria	<i>E. coli</i> -3054005-3054185 (from our library)
4.5S RNA	68	2463713-2463780<	NP	All Enterobacteria	<i>E. coli</i> -475709-47576 (from our library)
StyR-56	69	806323-806255<	Yes	RyeE - <i>E. coli</i>	<i>E. coli</i> -2165148-2165217 (from our library)
				OmpX- <i>S. Typhimurium</i>	<i>E.coli</i> -2165136-2165221(RyeE)
StyR-366	105	1299620-1299517<	NP	rprA - <i>E. coli</i>	<i>E.coli</i> -1768396-1768499
				rprA- <i>S. Typhimurium</i>	<i>E.coli</i> - (rprA)
StyR-7	238	251005-251242	NP	t44 - <i>E. coli</i>	<i>E. coli</i> -189711-189944 (from our library)
					<i>E. coli</i> -189712-189847 (t44)
StyR-23	138	332924-333061	Yes	SroF - <i>E. coli</i>	<i>E. coli</i> -2689345-2689217 (from our library)
					<i>E. coli</i> -2689362-2689179 (SroF)
StyR-97	83	3013177-3013259<	NP	RygB/OmrB - <i>E. coli</i>	<i>E. coli</i> -2974407-2974328 (from our library)
					<i>E. coli</i> -2974407-2974332 (RygB/OmrB)
StyR-111	86	128205-128120<	Yes	SroA - <i>E. coli</i>	<i>E. coli</i> -75523-75605 (from our library)
					<i>E. coli</i> -75516-75608 (SroA)
StyR-183	82	3330462-3330543	Yes	RyhA - <i>E. coli</i>	<i>E. coli</i> -3348664-3348745 (from our library)
					<i>E. coli</i> -3348599-3348706 (RyhA)
StyR-229	198	3205319-3205516	Yes	RyhD - <i>E. coli</i>	<i>E. coli</i> -3192776-3192922 (from our library)
					<i>E. coli</i> -3192743-3192887 (ryhD)
StyR-239	150	3721814-3721960	NP	SPORT-42/spf- <i>E. coli</i>	<i>E. coli</i> 4047885-4048030 (from our library)
					<i>E. coli</i> 4047922-4048030 (SPORT-42/spf)
StyR-290/360	64	2275510-2275575 2275539-2275627	Yes	SroC - <i>E. coli</i>	<i>E. coli</i> 685967-686032 (from our library)
					685907-686007 (from our library)
					<i>E. coli</i> -685904-686066 (SroC)
StyR-323	87	2431993-2432070	NP	SroB - <i>E. coli</i>	<i>E. coli</i> -506440-506509 (from our library)
					<i>E. coli</i> -506428-506509 (SroB)
StyR-330	64	1597142-1597225	Yes	RydC - <i>E. coli</i>	<i>E. coli</i> -1489530-1489467 (from our library)
					<i>E. coli</i> -1489529-1489468 (rydC)

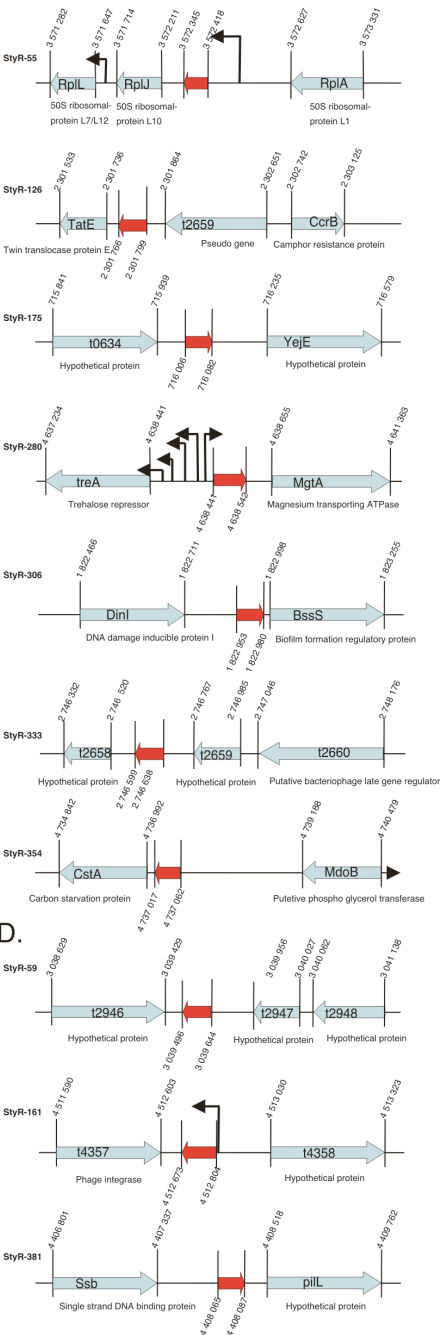
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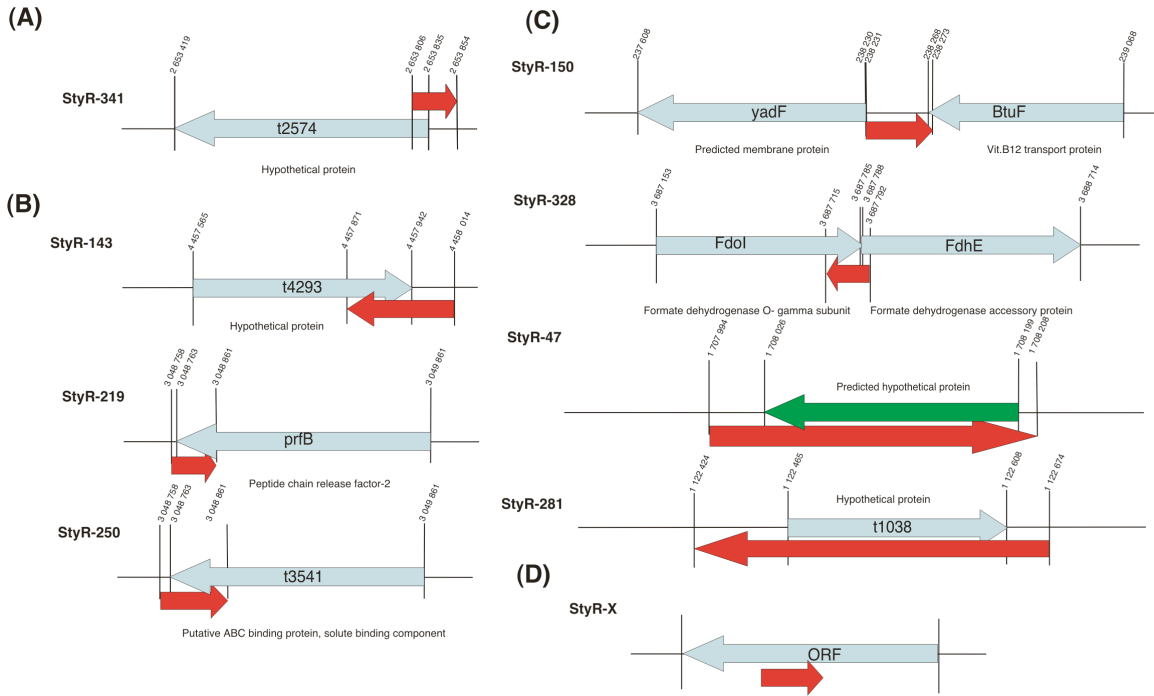
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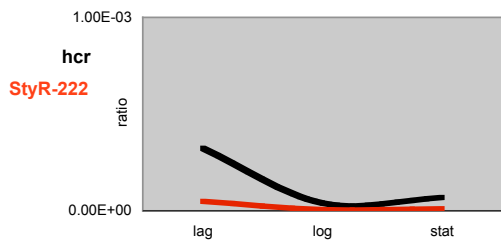
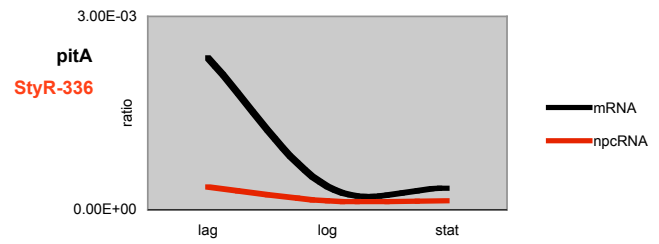
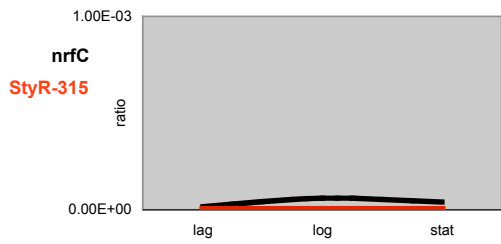
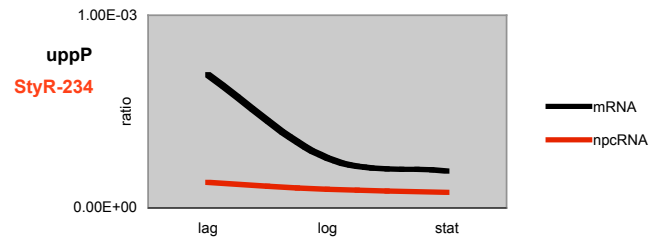
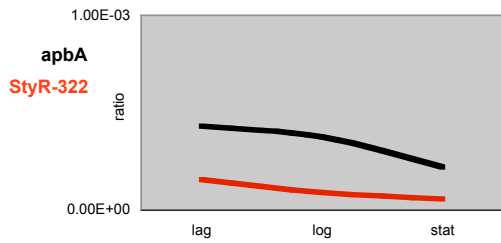
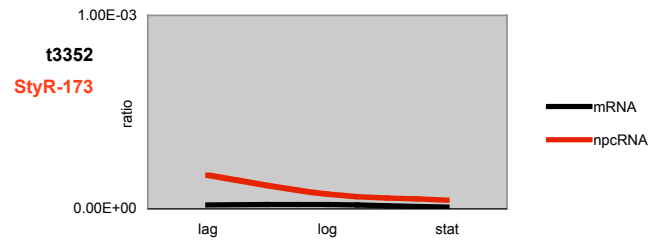
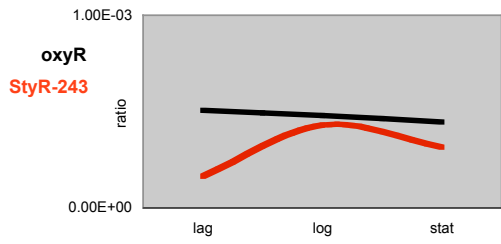
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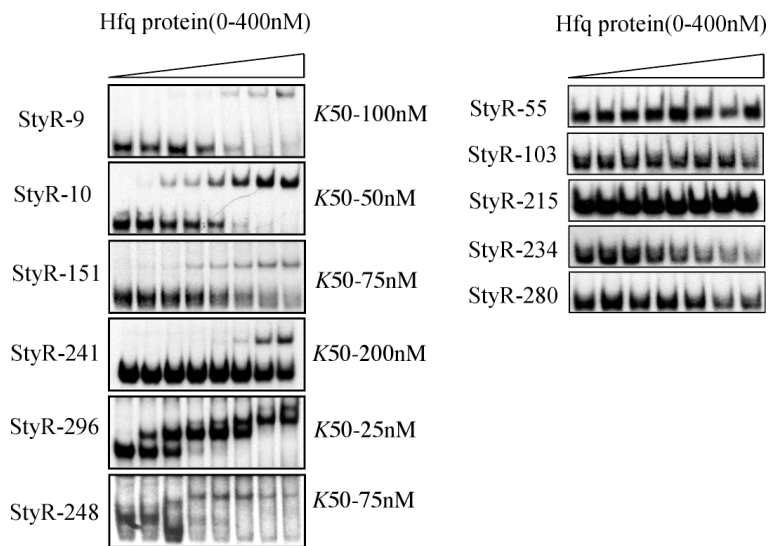
Supplementary Figure S1



Supplementary Figure S2



Supplementary Figure S3



Supplementary Figure S4