Supplementary information

Regulation of Hfq mRNA and protein levels in *Escherichia coli* and *Pseudomonas aeruginosa* by the *Burkholderia cenocepacia* MtvR sRNA

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Supplementary Methods

Bioinformatic analysis

BLAST searches were performed using the Integrated Microbial Genomes (IMG) webserver [1], using an E-value ≤ $1e^{-50}$ as cut-off. MtvR putative targets were predicted using the sRNATarget [2], the TargetRNA [3], and the RNAPredator [4] programs, with a cut-off of 1, a minimum seed of 7 nucleotides, an hybridization target region window size of -100 to + 30 around the translation start site.

Suplementary Results

Interaction of MtvR with additional *E. coli* sequences

A Blast search within the genome of *Escherichia coli* strain K-12 sub-strain MG1655, using a low complexity match and a word size of 6 revealed 9 intergenic regions with segments with homology to the *mtvR* sequence. The non-coding region between *lysV* and REPv173 contains the Intergenic Repeat Region (IRR) rtV, and within this region, the sequence 5'-cgcggcgacggcc-3', corresponding to nt 68 to 80 of MtvR. The rlQ, also a IRR found in the non-coding region between *lysQ* and *nadA*, contains exactly the same sequence of MtvR found on rtV. A H-NS binding sequence of *E. coli* was also found in the non-coding region between yciG and trpA, sharing homology with nt 53-64 (5'-aatgccgccagc-3') of MtvR. The remaining 6 sequences had no identifiable features worth mentioning (Table S4).

This 13 nucleotide sequence match found within non-coding regions of the *E. coli* genome, together with its conservation along other enteric might represent an unidentified regulatory region in *E. coli.*

Additional sequences in *P. aeruginosa* PA14 genome with possible interaction with MtvR

Blast analysis using the MtvR encoding sequence to query the genome sequence of *P. aeruginosa* UCBPP-PA14, revealed a 100% match in a 17 nt (5'-GCCGCGCGTGCTGG-3') segment within an intergenic region 232 bp at the 5' side of a probable C4-dicarboxylate transporter and 550 bp at the 3' side of a arginine/ornithine antiporter. A thorough search revealed that this sequence is widely distributed along all organisms, including prokaryotes, eukaryotes and virus. Another search, using the complete intergenic region, revealed a 38 nt region (5’-AAATGAAGAAGCCCGGCGAACGCCGGGCTTCTTCATTT-3’) that is present only in prokaryotes, and in general, with a conservation over 80 %, found in intergenic regions. No conserved regulatory elements could be identified in this sequence. This sequence might represent a new uncharacterized regulatory region.

Table S1: Putative MtvR targets in the genome of *E. coli* predicted by TargetRNA

1 ***hofN*** protein required for the utilization of DNA as a carbon source; fimbrial assembly protein homolog

Energy: -17.32 p-value: 0.000

```
sRNA          22    CUUAC-UGGGCGGC    10
                     :||| |||||||
mRNA (hofN)   -2    UGAUGAACCCGCCA    12
```

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2 ***malS*** alpha-amylase

Energy: -16.82 p-value: 0.000

```
sRNA          18    CUGGGCGGCGG-CAGU    4
                     ||:||||||| ||:
mRNA (malS)   5     AACUCGCCGCCUGUUU    20
```

---

3 ***yidJ*** predicted sulfatase/phosphatase

Energy: -16.75 p-value: 0.000

```
sRNA          128   CGCGGGGUUAAUAAGGA    112
                     |||||||||| || ||
mRNA (yidJ)   6     ACGCCCCAAUU-UU-CU    20
```

---

4 ***yjbG*** conserved protein

Energy: -15.58 p-value: 0.000

```
sRNA          62    ACCGCCGUA    54
                     |||||||
mRNA (yjbG)   -13   AGGCGGCAA    -5
```

---

5 **nagC** DNA-binding transcriptional dual regulator, repressor of N-acetylglucosamine

Energy: -14.61 p-value: 0.001

```
sRNA          40    GCUGU-GUCCGCCC    28
                    :|||| |||||||
mRNA (nagC)   2     UGACACCAGGCGGA    15
```

---

6 ***yfiQ*** CP4-57 prophage; predicted protein

Energy: -13.77 p-value: 0.002

```
sRNA          21    UUACUGGGCGGC    10
                     ||||||||:|
mRNA (yfiQ)   -1    UAUGACCCGUCU    11
```

7 ***uhpA*** **DNA-binding response regulator in two-component regulatory system wtih UhpB**

Energy: -13.01 **p-value: 0.004**

```
sRNA           18    CUGGGCGGC     10
                      |||||||
mRNA (uhpA)   -19    UACCCGCCA    -11
```

---

8 ***yceG*** predicted aminodeoxychorismate lyase

Energy: -12.99 p-value: 0.004

```
sRNA          130    AUCGCGGGGUUAAUA    116
                      ||||||| |||||
mRNA (yceG)   -17    GAGCGCCCGAAUUAG     -3
```

---

9 ***dacD*** D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 6b)

Energy: -12.91 p-value: 0.004

```
sRNA           20    UACUGGGCGGCGGC     7
                      |||  |||||:|
mRNA (dacD)     1    UUGAAACGCCGUCU    14
```

---

10 ***csiD*** carbon starvation induced gene

Energy: -12.72 p-value: 0.005

```
sRNA           20    UAC-UGGGC-GGCGGCAG     5
                     ||| | |:| |||||||
mRNA (csiD)     4    AUGCA-CUGACCGCCGU-    20
```

---

11 ***mpaA*** murein peptide amidase A

Energy: -12.7 p-value: 0.005

```
sRNA           21    UACUGG-G--CGGCGGC     7
                     |||||| :   |||||
mRNA (mpaA)     1    AUGACCGUAACCCGCCC    17
```

Table S2: Putative MtvR targets in the genome of *E. coli* predicted by RNAPredator

<table>
<tr><th>Energy [kJ/mol]</th><th>z-Score</th><th>Interaction</th><th>mRNA [Start]</th><th>mRNA [End]</th><th>sRNA</th><th>Gene Annotation</th></tr>
<tr><td>-14.14</td><td>-1.88</td><td>(((((((((((((.((((((((&))))).......))))))))))))))))<pre>
mRNA: 5'- AAAUUAUGGCGCCGCC------ -3'
          ||||||||||||| ||
sRNA: 3'- UUUAAUAUCGCGG-GGUUAAUA -5'
</pre></td><td>-5</td><td>16</td><td>109-136</td><td>conserved protein; UPF0161 family</td></tr>
<tr><td>-13.63</td><td>-1.7</td><td>(((((((.(((((.((&)).))))).)))))))<pre>
mRNA: 5'- AGCGCCCGAAUUAGUC -3'
          ||||||| ||||| ||
sRNA: 3'- UCGCGGGGUUAAUAAG -5'
</pre></td><td>-16</td><td>-1</td><td>114-129</td><td><u>predicted aminodeoxychorismate lyase</u></td></tr>
<tr><td>-13.33</td><td>-1.59</td><td>(((((..(((..((((.((&))))))..)))..)))))<pre>
mRNA: 5'- GCCCCUCUUACACCUGCU -3'
          ||||| ||| |||| |
sRNA: 3'- CGGGGUUAAUAAGGAC-A -5'
</pre></td><td>2</td><td>20</td><td>109-126</td><td>predicted anti terminator regulatory protein</td></tr>
</table>

Table S3: Putative MtvR targets in the genome of *E. coli* predicted by sRNATarget

```
______________
    1   nfuA_b3414     predicted gluconate transport associated protein
    Probability = 1
    sRNA(sRNA1)         11 ggCGGGUCAUucuau 25
                           .|||.||||  ||
    Target(nfuA_b3414)  10 auGCCUAGUAucauu -5
_____________

    2   amiA_b2435     N-acetylmuramoyl-l-alanine amidase I
    Probability = 1
    sRNA(sRNA1)         74 gACGGCCUGu 83
                           ||||||||
    Target(amiA_b2435)   1 aUGCCGGACu -9
_____________

    3   gpmM_b3612     phosphoglycero mutase III, cofactor-independent
    Probability = 1
    sRNA(sRNA1)         68 cGCGGCGACg  77
                           |||.|.||
    Target(gpmM_b3612)  -1 aCGCUGUUGg -10
    Probability = 1
    sRNA(sRNA1)         71 gGCGACGGCCUg  82
                           |||||..|||
    Target(gpmM_b3612)  -1 aCGCUGUUGGAg -12
_____________

    4   pmrD_b2259     polymyxin resistance protein B
    Probability = 1
    sRNA(sRNA1)         90 cGCAUCGCAa 99
                           ||||||||
    Target(pmrD_b2259)  72 uCGUAGCGUc 63
    Probability = 1
    sRNA(sRNA1)         10 cggcggGUCAUUCUAUc 26
                           |.| .|.|||||.||
    Target(pmrD_b2259)  16 acugguCGGUAAGGUAa -1
    Probability = 1
    sRNA(sRNA1)         55 uGCCGCCAGCA-cgcg 69
                           |||||||||| |||
    Target(pmrD_b2259)  79 gCGGCGGUCGUagcgu 64
_____________
```

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5   *uhpA* b3669   DNA-binding response regulator in two-component regulatory system wtih UhpB

```
Probability = 1
sRNA(sRNA1)         70 cGGCGACGGc 79
                       |||.||||
Target(uhpA_b3669)  16 cCCGUUGCCa  7
Probability = 1
sRNA(sRNA1)          3 uugacGGCGGCGG--gucau--ucuaucacccg  31
                       |.| |||..|||  .||||  |||     ||
Target(uhpA_b3669)  20 uauucCCGUUGCCacuaguaccagaaca--gga -11
```

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6   *yfcP*_b2333   predicted fimbrial-like adhesin protein

```
Probability = 1
sRNA(sRNA1)         28 cCCGCCUGUg  37
                       ||.||.||.
Target(yfcP_b2333)  -7 aGGUGGGCAu -16
```

____

7   *fliE*_b1937   flagellar basal-body component

```
                 Probability = 1
sRNA(sRNA1)         18 cauucuaucac-ccgCCUGUGUCGCc 42
                       |..|. |||  || |||||.||||
Target(fliE_b1937)  30 uuggggaaguuagg-GGACAUAGCGa  6
```

____

8   *frsA*_b0239   hydrolase, binds to enzyme IIA(Glc)

```
Probability = 1
sRNA(sRNA1)         30 cGCCUGUGUCg 40
                       |||||||||
Target(frsA_b0239)  12 aCGGACACAGu  2
Probability = 1
sRNA(sRNA1)         102 aAGUGUUGA-----caggaa 116
                       ||.||.||     |||||
Target(frsA_b0239)   69 aUCGCAGCUccaaaguccua  50
Probability = 1
sRNA(sRNA1)          26 cACCCGCCUGu  36
                       |||||||||
Target(frsA_b0239)  -38 uUGGGCGGACu -48
Probability = 1
sRNA(sRNA1)         102 aaguguuga-----caggaauaaUUGGGGCGc 128
                       ||.||.||     |||||    ||...|||
Target(frsA_b0239)   69 aucgcagcuccaaaguccuaca-AAUUUCGCc  39
```

____

9 *mntR*_b0817 DNA-binding transcriptional regulator of mntH

```
Probability = 1
sRNA(sRNA1)         32 cCUGUGUCGCc 42
                       |||.|||.|
Target(mntR_b0817)  46 uGACGCAGUGa 36
Probability = 1
sRNA(sRNA1)         66 cGCGCGGCGACg 77
                       |||||.||||
Target(mntR_b0817)  15 aCGCGCUGCUGa  4
```

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10 *relE*_b1563 Qin prophage; toxin of the RelE-RelB toxin-antitoxin system

```
Probability = 1
sRNA(sRNA1)         77 gGCCUGUUUGc 87
                       |||.|.|.|
Target(relE_b1563)  33 aCGGGCGAGCa 23
Probability = 1
sRNA(sRNA1)         19 auucuaucacccgccugugucgccaaaagac-GGGAAUGCcgccag 63
                              |||.|. ||| |||||    |..|||.| ||||
Target(relE_b1563)  42 aaggaaauca--cgggcg-agcaguuuuagguCUUUUAUG-cggua  1
```

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11 *ymcE*_b0991 cold shock gene

```
Probability = 1
sRNA(sRNA1)         85 uGCGGCGCAUc 95
                       |||||||||
Target(ymcE_b0991)  10 uCGCCGCGUAc -1
Probability = 1
sRNA(sRNA1)          6 aCGGCGGCG---ggucau 20
                       |.||||||   |||||
Target(ymcE_b0991)  12 gGUCGCCGCguaccaguc -6
```

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12 *hybA*_b2996 hydrogenase 2 4Fe-4S ferredoxin-type component

```
Probability = 1
sRNA(sRNA1)         74 gacggcCUGUUUGCGGc 90
                       |||  |||||  |||
Target(hybA_b2996)  13 augca-GACAAGUGCCa -3
```

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13 *apaH*_b0049 diadenosine tetraphosphatase

```
Probability = 1
sRNA(sRNA1)           7 cggCGGCGGGUCa  19
                       ..|||||.|||
Target(apaH_b0049)  -24 cuuGCCGCUCAGc -36
```

```
    Probability = 1
    sRNA(sRNA1)         33 cUGUGUCGCCAa 44
                           |.||||||||
    Target(apaH_b0049)  12 cAUACAGCGGUa  1
    Probability = 1
    sRNA(sRNA1)         36 uGUCGCCAA-aaga 48
                           |||||||| |||
    Target(apaH_b0049)  25 gCAGCGGUUauucc 12
____________

    14  lamB_b4036     maltose outer membrane porin (maltoporin)
    Probability = 1
    sRNA(sRNA1)            7 cGGCGGCGGGuca   19
                           ||||||.||.|
    Target(lamB_b4036)  -141 aCCGCCGUCCggc -153
    Probability = 1
    sRNA(sRNA1)         15 ggUCAUUCUAUCacccgccugugucg  40
                           .||||||||||     |||| |||
    Target(lamB_b4036)   6 guAGUAAGAUAGa----ggacucagu -16
____________

    15  srmB_b2576     ATP-dependent RNA helicase
    Probability = 1
    sRNA(sRNA1)         120 uUGGGGCGCU 129
                           |||||||||
    Target(srmB_b2576)  -14 cACCCCGCGA -23
____________

    16  dusC_b2140     tRNA-dihydrouridine synthase C
    Probability = 1
    sRNA(sRNA1)           7 cgg-CGGCGGGUc  18
                           || |.||||.|
    Target(dusC_b2140)  -42 accaGUCGCCUAa -54
    Probability = 0.997
    sRNA(sRNA1)         22 cuAUCACCCGCc  33
                           .|||||||||
    Target(dusC_b2140)  -2 agUAGUGGGCGu -13
____________
```

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_________________
    17  metC_b3008     cystathionine beta-lyase, PLP-dependent
    Probability = 1
    sRNA(sRNA1)          85 ugc-GGCGCAUCg  96
                           || ||||||||
    Target(metC_b3008)  -52 gcgcCCGCGUAGg -64
    Probability = 1
    sRNA(sRNA1)         28 cccgcCUGUGUCG-----cca  43
                           ||| |..|||||     ||
    Target(metC_b3008)   8 aggc-GGUACAGCccuaagga -12
_____________

    18  lpxT_b2174     undecaprenyl pyrophosphate phosphatase
    Probability = 1
    sRNA(sRNA1)          8 gGCGGCGGGUcauucuaucac 28
                           |||||...|      ||||
    Target(lpxT_b2174)  20 aCGCCGUUUAaaaau-uagua  1
    Probability = 1
    sRNA(sRNA1)         74 gacggc-CUGUUUGCGGCg 91
                           .||..| ||.||||||||
    Target(lpxT_b2174)  32 uuguuguGAUAAACGCCGu 14
_____________

    19  hypC_b2728     protein required for maturation of hydrogenases 1 and 3
    Probability = 1
    sRNA(sRNA1)         48 aCGGGAAUGCCg 59
                           ||||||.|||
    Target(hypC_b2728)  20 gGCCCUUGCGGa  9
    Probability = 1
    sRNA(sRNA1)            5 gACGGCGGCGGGUCAuucua   24
                           |||||..|.|||||  ||
    Target(hypC_b2728)  -130 aUGCCGUUGUCCAGUu-gaa -148
_____________
```

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20 *idnK*_b4268   D-gluconate kinase, thermosensitive

```
Probability = 1
sRNA(sRNA1)          87 cGGCGCAUCGCa   98
                       |||.||||.|
Target(idnK_b4268)  -93 uCCGUGUAGUGc -104
Probability = 1
sRNA(sRNA1)         24 aUCACCCGCCu 34
                       |||||||||
Target(idnK_b4268)  12 aAGUGGGCGGu  2
Probability = 0.995
sRNA(sRNA1)         66 cgCGCGGCGACg 77
                       .||||||.||
Target(idnK_b4268)  77 uuGCGCCGUUGg 66
```

---

21 *zitB*_b0752   zinc efflux system

```
Probability = 1
sRNA(sRNA1)         10 cGGCGGGUCAUUCu  23
                       |.||.|||||.|.
Target(zitB_b0752)   1 aCUGCUCAGUAGGg -13
```

---

22 *yjeS*_b4166   predicted Fe-S electron transport protein

```
Probability = 1
sRNA(sRNA1)         3 uugacggcGGCGGGUCAUu  21
                       ||||.  |.|||  |||
Target(yjeS_b4166)  7 gacugua-CUGCCUGGUAu -11
```

---

23 *ydjJ*_b1774   predicted oxidoreductase, Zn-dependent and NAD(P)-binding

```
Probability = 1
sRNA(sRNA1)         16 gucauucuaucacCCGCCUGUGUc  39
                       |||||       ||.||.||.|
Target(ydjJ_b1774)   5 aaguaaaacuua-GGUGGGCAUAa -18
```

---

24 *fliM*_b1945   flagellar motor switching and energizing component

```
Probability = 1
sRNA(sRNA1)         29 cCGCCUGUGUCGc 41
                       ||||..|||||
Target(fliM_b1945)   8 aGCGGGUACAGCa -5
```

---

25 *recE*_b1350 Rac prophage; exonuclease VIII, 5' -> 3' specific dsDNA exonuclease

```
Probability = 1
sRNA(sRNA1)         107 uUGACAGGAAuaauuggggc---gcua 130
                         |.|||||||    |||      |||
Target(recE_b1350)   28 cAUUGUCCUUcuc-accaaaacacgag   3
```

---

26 *hrpB*_b0148 predicted ATP-dependent helicase

```
Probability = 1
sRNA(sRNA1)          3 uugaCGGCGGCGGGucau 20
                        .| |.||..||||.
Target(hrpB_b0148)  26 ugccGUCGUUGCCCguu- 10
Probability = 1
sRNA(sRNA1)          4 uGACGGCGGCg 14
                        ||||||.||
Target(hrpB_b0148)  28 uCUGCCGUCGu 18

Probability = 1
sRNA(sRNA1)          6 aCGGCGGCGg 15
                        |..||.||
Target(hrpB_b0148)  13 cGUUGCUGCu  4
Probability = 1
sRNA(sRNA1)          4 ugACGGCGGC---------------gggu---cauucua  24
                        .|||.||.|               ||||   ||||||
Target(hrpB_b0148)  12 guUGCUGCUGuguuuugcgaggucucccaauuguaagaa -27
Probability = 0.999
sRNA(sRNA1)          7 cGGCGGCGGg 16
                        |.||||.|
Target(hrpB_b0148)  28 uCUGCCGUCg 19
```

---

27 *yhdH*_b3253 predicted oxidoreductase, Zn-dependent and NAD(P)-binding

```
Probability = 1
sRNA(sRNA1)         120 uUGGGGCGCuauaau 134
                         ||..|||| ||||
Target(yhdH_b3253)  -76 uACUUCGCGuuauuu -90
Probability = 0.996
sRNA(sRNA1)         19 auucuaucacc--CGCCUGUGUc 39
                        |||||         ||||||..|
Target(yhdH_b3253)  22 caagauuuucauuGCGGACGUAu -1
```

---

28 *creB*_b4398 DNA-binding response regulator in two-component regulatory system with CreC

```
Probability = 1
sRNA(sRNA1)           71 ggcg-ACGGCCUGUu   84
                         .||| |||.|||||
Target(creB_b4398)  -126 ucgcgUGCUGGACAu -140
Probability = 1
sRNA(sRNA1)         36 ugucgccaaaagacgggaaUGCCGCCA--gca  65
                        .|||||            ||||||||  ||
Target(creB_b4398)  -2 uuagcggagacaaua----ACGGCGGUgccgu -29
```

29 *yahD*_b0318 predicted transcriptional regulator with ankyrin domain

```
Probability = 1
sRNA(sRNA1)          9 gCGGCGGGU--------------cauuc-uaucacccg  31
                        ||||.|||              ||||| .||  |||
Target(yahD_b0318)  26 aGCCGUCCAucuaaaaaauaugaguaaguguaagggga -12
Probability = 1
sRNA(sRNA1)         22 cUAUCACCCgccugugucgccaaa 45
                        ||||||||   ||||. |||||
Target(yahD_b0318)  56 uAUAGUGGGacaacacgucgguua 33
```

30 ***fepB* b0592 iron-enterobactin transporter subunit**

```
Probability = 1
sRNA(sRNA1)          4 uga-cggcGGCGGGUCa 19
                        || ||| ||||.|||
Target(fepB_b0592)  19 ucucgcc-CCGCUCAGa  4
Probability = 1
sRNA(sRNA1)          46 agacgggaaugccGCCAGCACg   67
                         || |||||.   ||||||||
Target(fepB_b0592)  -98 acuccccuugu--CGGUCGUGa -117
```

31 *polB*_b0060 DNA polymerase II

```
Probability = 1
sRNA(sRNA1)         76 cggCCUGUUUGCGgcgca 93
                        ..||||..|||| |.|
Target(polB_b0060)  17 uuuGGACGGACGCggugc -1
Probability = 1
sRNA(sRNA1)         12 gcgggucauucuaucacccGCCUGUGUCGCc 42
                        |||||     ||  ||| |||||.|.|.|
Target(polB_b0060)  30 agcccaauucuauuuuggaCGGACGCGGUGc -1
```

```
__________________
    32  yfcS_b2336    predicted periplasmic pilus chaperone
    Probability = 1
    sRNA(sRNA1)         13 cGGGUCAUUCu---aucacc  29
                           ||.||||||.   |||||
    Target(yfcS_b2336)   1 aCCUAGUAAGgaauuagugc -19
    Probability = 1
    sRNA(sRNA1)         105 uguug--ACAGGAAUAauuggggc 126
                           |.||  ||||.||.|   ||||
    Target(yfcS_b2336)  -29 ucgacuuUGUCUUUGUc--ccccu -50
    Probability = 1
    sRNA(sRNA1)           66 cGCGCGGCGacggccuguuugc-ggcg   91
                           |||||.||   ||||   ||| |||
    Target(yfcS_b2336)  -114 cCGCGCUGCaa-cggaaauacgaccgu -139
______________

    33  fhuE_b1102    ferric-rhodotorulic acid outer membrane transporter
    Probability = 1
    sRNA(sRNA1)         100 aAAAGUGUUgacaggaauaa-uuggg 124
                           ||||..||    |.|||   ||||
    Target(fhuE_b1102)    8 cUUUCGUAAa---cuuuagagaacca -15
______________

    34  uhpC_b3667    membrane protein regulates uhpT expression
    Probability = 1
    sRNA(sRNA1)          91 gcaucgcaaaaaaguguuGACAGGAAu 117
                           .|| |||      |||. ||||||||
    Target(uhpC_b3667)  -41 ugu-gcgcacgg-cacguCUGUCCUUu -65
    Probability = 1
    sRNA(sRNA1)          4 ugACGGCGGCgggucauucuauca  27
                           .|||||..|  .||||.  |.|
    Target(uhpC_b3667)  12 uuUGCCGUUG--uaguaguuugga -10
    Probability = 1
    sRNA(sRNA1)         87 cGGCGCAUCG-caaaaaaguguugacaggaau 117
                           ||||||||| ||     |.|.|  |||.||.
    Target(uhpC_b3667)  36 aCCGCGUAGCcguc----cgcgaaagucuuug   9
    Probability = 1
    sRNA(sRNA1)          34 ugugucgccaaa-AGACGGGAA----------ugccgcc-agca  65
                           |.|| |||    ||||.||||          ||||.|| |||
    Target(uhpC_b3667)  -44 gcgca-cggcacgUCUGUCCUUuacacauuacacggugggucgc -86
_______________
```

```
_______________
    35  galF_b2042     predicted subunit with GalU
    Probability = 1
    sRNA(sRNA1)         15 ggucauucuaucacCCGCCUGUg  37
                          ||||||   ||| ||.|||||.
    Target(galF_b2042)   6 gcaguaauaaaguaGGUGGACAu -17
_____________

    36  yeaP_b1794     predicted diguanylate cyclase
    Probability = 1
    sRNA(sRNA1)         106 guugaca-GGAAUAAUU---gg----ggcgc 128
                          .||||| ||||.||.|   ||    ||||
    Target(yeaP_b1794)    8 agacugugCCUUGUUGAgguccuaugccgcc -23
    Probability = 1
    sRNA(sRNA1)           8 ggCGGCGGGUc  18
                          .||||||||
    Target(yeaP_b1794)  -16 auGCCGCCCAu -26
_____________

    37  recQ_b3822     ATP-dependent DNA helicase
    Probability = 1
    sRNA(sRNA1)         79 cCUGUUUGCGgcgcau-cgca 98
                          |.|..|||| |.||| |.|
    Target(recQ_b3822)  14 aGGCGGACGCgguguaagugg -7
    Probability = 1
    sRNA(sRNA1)         12 gcgggucauucuaucac--CCGCCUGUGUCGCc 42
                          |.|.|   ||   |||  |||||||.|.|.|
    Target(recQ_b3822)  28 ggucua---aguu-gugaaGGCGGACGCGGUGu -1
_____________

    38  rpiB_b4090     ribose 5-phosphate isomerase B/allose 6-phosphate isomerase
    Probability = 1
    sRNA(sRNA1)         16 gucauucuauca--cccgccugugu-------cgc---CAAAAGACg  50
                          |||||| |||   |||| |.|||.       |.|   |||||.||
    Target(rpiB_b4090)   5 aaguaag-uagaaggggcaggcacguuuugaaguguuaGUUUUUUGu -41
_____________

    39  deoC_b4381     2-deoxyribose-5-phosphate aldolase, NAD(P)-linked
    Probability = 1
    sRNA(sRNA1)          56 gccgcCAGCACGCg  69
                          ||| ||.|||.|
    Target(deoC_b4381)  -66 aggc-GUUGUGUGa -78
    Probability = 1
    sRNA(sRNA1)         12 gcgggucauucua-ucacccgccug---UGUCGCCAAa  45
                          |.|.||| ||   |||    ||||   |||||||||
    Target(deoC_b4381)  13 agucuagucaguaaaguaagaggaccgaACAGCGGUUa -25
```

```
_____________

    40  wzc_b2060      protein-tyrosine kinase
    Probability = 1
    sRNA(sRNA1)        15 gGUCAUUCUaucacccgc-cugug-ucg  40
                           ||||||||   ||| || |||.| ||
    Target(wzc_b2060)   6 aCAGUAAGAauauggacgagacgcaagu -22
_____________

    41  rph_b3643      defective ribonuclease PH
    Probability = 1
    sRNA(sRNA1)        71 ggcgACGGCCUGUUugcggcgcauc 95
                           || ||||||||.|   |.|||||
    Target(rph_b3643)  22 acgaUGCCGGACGAc--cugcguau -1
_____________

    42  cueR_b0487     DNA-binding transcriptional activator of copper-responsive regulon genes
    Probability = 1
    sRNA(sRNA1)         65 aCGCGCGGCGacggccuguu  84
                            |||||..||    |||||
    Target(cueR_b0487)  -4 aGCGCGUUGCgga-ggacac -22
_____________


    43  yeeF_b2014     predicted amino-acid transporter
    Probability = 1
    sRNA(sRNA1)         8 ggcggcg-GGUCAUUCUa  24
                           |||.|. |||||||||
    Target(yeeF_b2014)  8 acgcuguaCCAGUAAGAg -10
_______________

    44  sdhA_b0723     succinate dehydrogenase, flavoprotein subunit
    Probability = 1
    sRNA(sRNA1)         19 auucuaucacccg-CCUGUGUCGCc  42
                            ||| ||||| |. ||..  .|.|
    Target(sdhA_b0723)   6 aaag-uagugugugGGGUGUGGUGu -18
_____________
```

45 *fliK*_b1943 flagellar hook-length control protein

```
Probability = 1
sRNA(sRNA1)         103 aguguugaca--ggaa-UAAUUGGGG-cgcuau 131
                         ||||  ||   ||   ||||  .|| |||||
Target(fliK_b1943)   42 ccacaguugcagccgccAUUAGUUCCcgcgauu  10
Probability = 1
sRNA(sRNA1)         103 aGUGUUGACa--ggaa-uaauug-gggcgcuau 131
                         ||||  ||   ||   ||||.. ||||||||
Target(fliK_b1943)   42 cCACAGUUGcagccgccauuaguucccgcgauu  10
Probability = 1
sRNA(sRNA1)         103 aguguugaca--ggaa-uaauug-GGGCGCUAu 131
                         ||||  ||   ||   ||||.. ||||||||
Target(fliK_b1943)   42 ccacaguugcagccgccauuaguuCCCGCGAUu  10
```

46 *sirA*_b3470 conserved protein required for cell growth

```
Probability = 1
sRNA(sRNA1)         47 gacgggaaugc-cgccagca-cgcgcggcgacggccuguuuGCGGCGCAucgcaaaaaaguguugacaggaauaauuggggcg 127
                        ||||   ||| |.||| || |.| |||   |||       ||.|||||  ||      |.||.||         |..||||
Target(sirA_b3470)  90 gugccaaaacgcgugguaguagug-gccaaggcc-------CGUCGCGUc-cgguucg-cgcagcucacacacc-agucccga  19
```

47 *fliO*_b1947 flagellar biosynthesis protein

```
Probability = 1
sRNA(sRNA1)         73 cgacggccuguuuGCGGCGCAU-cgca  98
                        .|||||      ||||||||| |||
Target(fliO_b1947)  -4 auugccgaguc--CGCCGCGUAagcga -28
```

48 *sgrT*_b4662 Inhibitor of glucose uptake

```
Probability = 0.999
sRNA(sRNA1)         102 aaguguugacaggaauaau---UGGGGCGCu 129
                         ||||.||| |..|        ||||||.|.
Target(sgrT_b4662)   23 aucacgacuauuuugacugcguACCCCGUGg  -8
```

49 *pcnB*_b0143 poly(A) polymerase I

```
Probability = 0.998
sRNA(sRNA1)         90 cgcaucgcaaaaaAGUGUUGA--------caggaa 116
                        .||.|       |||||..|        |||||
Target(pcnB_b0143)  -3 auguggagcca--UCACAGUUuguaguaaguccug -35
```

50 *mscS*_b2924   mechanosensitive channel

```
Probability = 0.995
sRNA(sRNA1)          1 -UAUUGACGGCgg-cgggucauucuauc 26
                        |||.|||..|.  |...|| |||.||
Target(mscS_b2924)  26 gAUAGCUGUUGuaaguuuag-aagguaa -1
```

51 *mak*_b0394   manno(fructo)kinase

```
Probability = 0.99
sRNA(sRNA1)        34 uGUGUCGCCaaaagacgggaaugccgccagcacgcgcggcgacgg-ccug  82
                       |||.|||| |||  ||   ||.||      ||||.|||  ||   |||
Target(mak_b0394)  30 cCACGGCGGauuua-gc---uauggaua---ugcgugcca-ugagaggaa -12
```

52 *dapA*_b2478   dihydrodipicolinate synthase

```
Probability = 0.99
sRNA(sRNA1)         67 gCGCGGCGAcgg--ccuguuugc---ggcgcauc------gcaaaaaaguguugaca-ggaauaauugg---ggcgc 128
                        ||||.|.|     ||.||  .|   ||| ||||      ||||| ||||||.     || |.  ||||   |||.
Target(dapA_b2478)  25 aGCGCUGUUaugaagggcacuuguacccg-guaggagacacguuuguucacagaguuaccaugcaaaccauaccgua -51
```

Table S4: regions with homology to within the genome of *E. coli*

1- (2662273..2662285) non-coding region between *suhB* and *yfhR*

```
 Score = 26.3 bits (13), Expect = 7.0
 Identities = 13/13 (100%)
 Strand = Plus / Minus

Query: 23      tatcacccgcctg 35
               |||||||||||||
Sbjct: 2662285 tatcacccgcctg 2662273
_____________
```

2- (2519454..2519466) non-coding region between *lysV* and *REPv173*

```
 Score = 26.3 bits (13), Expect = 7.0
 Identities = 13/13 (100%)
 Strand = Plus / Plus

Query: 68      cgcggcgacggcc 80
               |||||||||||||
Sbjct: 2519454 cgcggcgacggcc 2519466
_____________
```

3- (780979..780991) non-coding region between *lysQ* and *nadA*

```
 Score = 26.3 bits (13), Expect = 7.0
 Identities = 13/13 (100%)
 Strand = Plus / Plus

Query: 68     cgcggcgacggcc 80
              |||||||||||||
Sbjct: 780979 cgcggcgacggcc 780991


_____________
```

3- (3325770..3325781) non-coding region between *rlmE* and *yhbY*

```
 Score = 24.3 bits (12), Expect =    28
 Identities = 12/12 (100%)
 Strand = Plus / Minus

Query: 13      cgggtcattcta 24
               ||||||||||||
Sbjct: 3325781 cgggtcattcta 3325770


_____________
```

5- (1877381..1877392) non-coding region between *yeaQ* and *yoaG*

```
 Score = 24.3 bits (12), Expect =    28
 Identities = 12/12 (100%)
 Strand = Plus / Minus

Query: 92      catcgcaaaaaa 103
               ||||||||||||
Sbjct: 1877392 catcgcaaaaaa 1877381
_____________
```

6- (1500400..1500411) non-coding region between *tehB* and *ydcL*

```
 Score = 24.3 bits (12), Expect =    28
 Identities = 12/12 (100%)
 Strand = Plus / Minus

Query: 98      aaaaaagtgttg 109
               ||||||||||||
Sbjct: 1500411 aaaaaagtgttg 1500400
```

7- (1405859..1405870) non-coding region between *ydaM* and *ydaN*

```
 Score = 24.3 bits (12), Expect =    28
 Identities = 12/12 (100%)
 Strand = Plus / Plus

Query: 93      atcgcaaaaaag 104
               ||||||||||||
Sbjct: 1405859 atcgcaaaaaag 1405870
```

8- (1314409..1314420) non-coding region between *yciG* and *trpA*

```
 Score = 24.3 bits (12), Expect =    28
 Identities = 12/12 (100%)
 Strand = Plus / Plus

Query: 53      aatgccgccagc 64
               ||||||||||||
Sbjct: 1314409 aatgccgccagc 1314420
```

9- (741938..741949) non-coding region between *dtpD* and *ybgI*

```
 Score = 24.3 bits (12), Expect =    28
 Identities = 12/12 (100%)
 Strand = Plus / Minus

Query: 39     cgccaaaagacg 50
              ||||||||||||
Sbjct: 741949 cgccaaaagacg 741938
```

Table S5: Putative MtvR targets in the genome of *P. aeruginosa* UCBPP-PA14 predicted by TargetRNA

1 PA14_15920 major facilitator transporter

Energy: -21.91 p-value: 0.000

```
sRNA              21  UUACUGGGCGGCGGC   7
                       |||| ||||||||
mRNA
(PA14_15920)      -1  CAUGA-CCGCCGCCA   13
```

2 PA14_39850 MFS transporter

Energy: -21.71 p-value: 0.000

```
sRNA              21  UAC---U-GGGCGGCGGCAGU   4
                      |||   | ||||||||| ||
mRNA
(PA14_39850)      1   AUGACCACCCCGCCGCCCUC-   20
```

3 katA catalase

Energy: -21.03 p-value: 0.000

```
sRNA              24  AUCUUACUGGGCGGC   10
                       |||| ||||||||
mRNA (katA)       7   GAGAA-GACCCGCCU   20
```

4 fepB iron-enterobactin transporter periplasmic binding protein

Energy: -20.33 p-value: 0.000

```
sRNA              19  ACUGGGCGGCGGCA   6
                       ||||||||||||
mRNA (fepB)       5   CGACCCGCCGCCGC   18
```

5 PA14_69340 ABC transporter ATP-binding protein

Energy: -20.29 p-value: 0.000

```
sRNA              17  UGGGCGGCGGC   7
                       :||||||||
mRNA
(PA14_69340)      -10 CUCCGCCGCCA   1
```

6 PA14_18050 hypothetical protein

Energy: -20.18 p-value: 0.000

```
sRNA              17  UGGGCGGCGGCA   6
                       ||||||||||
mRNA              -20 CCCCGCCGCCGA   -9
```

(PA14_18050)

---

7 **PA14_69880** LysR family transcriptional regulator

Energy: -19.74 p-value: 0.000

```
sRNA              22  CUUACUGGGCGGCGGC   7
                       |||||||||:||||
mRNA
(PA14_69880)      -2  CAAUGACCCGUCGCCU   14
```

---

8 **modA** molybdate-binding periplasmic protein precursor modA

Energy: -18.98 p-value: 0.000

```
sRNA              21  UUACUGG-GCGGCGGC   7
                       |||||| | |||||
mRNA (modA)       -1  CAUGACCAC-CCGCCU   14
```

---

9 **ureD** urease accessory protein

Energy: -18.81 p-value: 0.000

```
sRNA              21  UUACUGGGCGGCGGCAGU   4
                      :|||| |||||||| ||
mRNA (ureD)       -2  GAUGA-CCGCCGCCCUCC   16
```

---

10 **PA14_56960** hypothetical protein

Energy: -18.31 p-value: 0.000

```
sRNA              20  UACUGGG--CGGCGGCAGU   4
                      |||||||  |||||||||
mRNA
(PA14_56960)       1  AUGACCCAGGCCGCCGUCC   19
```

---

11 **gacA** **response regulator GacA**

Energy: -17.85 **p-value: 0.000**

```
sRNA              71  GC--G--CGCACGACCGCCGU   55
                      :|  :  | |||||||:||:
mRNA (gacA)        1  UGAUUAAG-GUGCUGGUGGU-   20
```

---

12 **PA14_53090** transcriptional regulator

Energy: -17.85 p-value: 0.000

```
sRNA              19  ACUGGGCGGCGGC   7
                       |||||||| ||
mRNA
(PA14_53090)       7  CGACCCGCC-CCA   18
```

13 PA14_12610 transporter

Energy: -17.78 p-value: 0.000

```
sRNA                 130   AUCGCGGGGUU   120
                            |||||||||
mRNA (PA14_12610)     -9   AAGCGCCCCAU     2
```

14 **PA14_28980** Fe^{2+}-dicitrate sensor

Energy: -17.7 p-value: 0.000

```
sRNA                  21   UACUGGGCGGCGGC    7
                           |||||||||:|||
mRNA (PA14_28980)    -20   AUGACCCGCUGCCU   -7
```

15 **fadH1** 2,4-dienoyl-CoA reductase

Energy: -17.64 p-value: 0.000

```
sRNA             20   UACUGGGCGGCGGCAGU    4
                      |||| ||||||||||:
mRNA (fadH1)     -1   AUGA-CCGCCGCCGUUC   16
```

16 **PA14_53920** transcriptional regulator

Energy: -17.63 p-value: 0.000

```
sRNA                  21   UACUGGG-C---GGCGGC    7
                           ||||||| |   |||||
mRNA (PA14_53920)      1   AUGACCCAGAACCCGCCC   18
```

17 **PA14_18060** hypothetical protein

Energy: -17.58 p-value: 0.000

```
sRNA                  18   CUGGGCGGCGGC    7
                            |:|||||||:
mRNA (PA14_18060)      6   CAUCCGCCGCUA   17
```

18 **aceK** bifunctional isocitrate dehydrogenase kinase/phosphatase

Energy: -17.53 p-value: 0.000

```
sRNA            130   AUCGCGGGGUUA   119
                       |||||||||:
mRNA (aceK)       9   GAGCGCCCCAGC    20
```

19 **PA14_15280** hypothetical protein

Energy: -16.95 p-value: 0.000

```
sRNA           21   UUACUGGGCGGCGG    8
                     ||||||| ||||
mRNA           -1   CAUGACCCACCGCA    13
(PA14_15280)
```

20 **PA14_20491** acetyltransferase

Energy: -16.87 p-value: 0.000

```
sRNA           83   UGUCCGGCAGCGGC    70
                     ||| ||||||||
mRNA            6   CCAGACCGUCGCCA    19
(PA14_20491)
```

21 **PA14_50850** hypothetical protein

Energy: -16.5 p-value: 0.000

```
sRNA           23   UCUUACUGGGCGGC    10
                     ||||||||| ||
mRNA           -3   CGAAUGACCC-CCU    10
(PA14_50850)
```

22 **PA14_22280** pirin-related protein

Energy: -16.39 p-value: 0.000

```
sRNA           21   UUACUGGGCGGCGGCA    6
                     |||||||||: ||||
mRNA           -1   CAUGACCCGCUACCGU    15
(PA14_22280)
```

23 **PA14_44770** guanine deaminase

Energy: -16.34 p-value: 0.000

```
sRNA           21   UUACUGGGCG--GCGGC    7
                     |||||||||   ||||
mRNA           -1   CAUGACCCGCAACGCC-    15
(PA14_44770)
```

24 **PA14_29090** periplasmic spermidine/putrescine-binding protein

Energy: -15.88 p-value: 0.000

```
sRNA           23   UCUUACUGGGCG--GCGGC           7
                     ||| |||||||  |||:
mRNA            2   UGAA-GACCCGCAUCGCUU           19
(PA14_29090)
```

---

25 **PA14_40280** hypothetical protein

Energy: -15.57 p-value: 0.000

```
sRNA              23    UCUU--ACUGGGCGGCGGCA    6
                         ||:  |  ||| ||||||
mRNA
(PA14_40280)       2    UGAGCCUUUCCC-CCGCCGA    20
```

---

26 **PA14_31070** hypothetical protein

Energy: -15.57 p-value: 0.000

```
sRNA              77    GCAGCGGCGCGCACGACCGCC    57
                        :||||:|||||||||  |: |
mRNA
(PA14_31070)       2    UGUCGUCGCGCGUGC-AGU-G    20
```

---

27 *fepC* ferric enterobactin transport protein FepC

Energy: -15.5 p-value: 0.000

```
sRNA            21    UUACUGGGCGGCGGC    7
                       ||||||| :||||
mRNA (fepC)     -1    CAUGACCCAUCGCCU    14
```

---

28 **PA14_38950** hypothetical protein

Energy: -15.49 p-value: 0.000

```
sRNA              18    CUGGGC-GGCGGCAG    5
                         :|||| |||||||
mRNA
(PA14_38950)       2    UGCCCGACCGCCGUA    16
```

---

29 **pykA** pyruvate kinase

Energy: -15.45 p-value: 0.000

```
sRNA            81    UCCGGC-AGCGGCGC    68
                       | ||| |||||||
mRNA (pykA)      2    UGUCCGUUCGCCGCA    16
```

---

30 **phaD** poly(3-hydroxyalkanoic acid) depolymerase

Energy: -15.26 p-value: 0.001

```
sRNA            15    GCGGCGGCA        6
                      ||||||||
mRNA (phaD)    -20    CGCCGCCGA        -12
```

31 **PA14_29760** chemotaxis transducer

Energy: -15.25 p-value: 0.001

```
sRNA            17   UGGGCGGCGG-CAGU   4
                      ::||||||| |||
mRNA
(PA14_29760)     7   CUUCGCCGCCUGUC-   20
```

---

32 **PA14_26350** hypothetical protein

Energy: -15.08 p-value: 0.001

```
sRNA            75   AGCGGCGCGC   66
                      ||||||||
mRNA
(PA14_26350)   -20   ACGCCGCGCA   -11
```

---

33 **algF** alginate o-acetyltransferase AlgF

Energy: -15.01 p-value: 0.001

```
sRNA            22   CUUACUGGGCGGCG   9
                      :|||||||||||
mRNA (algF)      8   CGAUGACCCGCCG-   20
```

---

34 **PA14_15190** hypothetical protein

Energy: -15 p-value: 0.001

```
sRNA            17   UGGGCGGCGGCAGUU   3
                      |||  :|||||||
mRNA
(PA14_15190)    -4   UCCC-AUGCCGUCAU   10
```

---

35 **PA14_43650** hypothetical protein

Energy: -14.84 p-value: 0.001

```
sRNA            76   CAGCGGCGCGCACGA   62
                      ||||: |||||||
mRNA
(PA14_43650)     7   AUCGCUUCGCGUGC-   20
```

36 **PA14_17990** hypothetical protein

Energy: -14.83 p-value: 0.001

```
sRNA          21   UUACUGGGCGGCGGC   7
                    ||||||| |:|||
mRNA          -1   CAUGACCC-CUGCCA   13
(PA14_17990)
```

37 **PA14_53210** hypothetical protein

Energy: -14.56 p-value: 0.001

```
sRNA          19   ACUGGGCGGCGGCA   6
                    || |||||||||
mRNA          7    GGAACCGCCGCCGA   20
(PA14_53210)
```

38 **PA14_03490** hypothetical protein

Energy: -14.47 p-value: 0.001

```
sRNA          21   UUACUGG-GCGGCGGCAG-U   4
                    |||||| | ||||| || |
mRNA          -1   CAUGACCAC-CCGCC-UCGA   17
(PA14_03490)
```

39 **PA14_46360** two-component response regulator

Energy: -14.41 p-value: 0.001

```
sRNA          24   AUCUUACUGGGCGGCG   9
                    ||||||||: ||||
mRNA          -4   AAGAAUGACUGGCCG-   11
(PA14_46360)
```

40 **PA14_15720** transglycosylase

Energy: -14.25 p-value: 0.001

```
sRNA          71   GCGCGCACGACCGCCG   56
                    |||||||| |  ||
mRNA          -5   AGCGCGUGCAGAAGG-   10
(PA14_15720)
```

41 **pilF** type 4 fimbrial biogenesis protein PilF

Energy: -14.24 p-value: 0.001

```
sRNA          78   GGCAGCGGCGCGC   66
                    || ||||||||
mRNA (pilF)   9    ACG-CGCCGCGCU   20
```

42 recO DNA repair protein RecO

Energy: -14.18 p-value: 0.001

```
sRNA            19     ACUGGGCGGCGGCAGU      4
                        ||||||||  :|||
mRNA (recO)     -9     CGACCCGCC-AUGUCC      6
```

---

43 PA14_20880 hypothetical protein

Energy: -14.12 p-value: 0.002

```
sRNA            17     UGGG---CGGCGGCAGUU    3
                        |||   ||||||| ||
mRNA
(PA14_20880)    -16    CCCCUGAGCCGCCGACAU    2
```

---

44 PA14_26260 hydrolase

Energy: -14.03 p-value: 0.002

```
sRNA            27     ACUAUCUUACUGG-GCGGC   10
                        || |||||||||  |||
mRNA
(PA14_26260)    -6     AGA-AGAAUGACCGAGCCU   12
```

---

45 nosF NosF protein

Energy: -13.92 p-value: 0.002

```
sRNA            17     GGGCGGCGGCA    6
                       |||||||| |
mRNA (nosF)     -20    CCCGCCGCGGA    -10
```

---

46 PA14_11650 hypothetical protein

Energy: -13.81 p-value: 0.002

```
sRNA            17     GGGCGGCGGCAGUUA-      2
                       |||||||||  ||:|
mRNA
(PA14_11650)    -20    CCCGCCGCC--CAGUG      -7
```

---

47 PA14_12670 hypothetical protein

Energy: -13.74 p-value: 0.002

```
sRNA            66     CACG-ACCGCCGUAAGGGC   49
                        |||  |||||||  |:|
mRNA
(PA14_12670)    1      AUGCGCGGCGGCAAGCUCU   19
```

48 **PA14_49720** hypothetical protein

Energy: -13.64 p-value: 0.002

```
sRNA           20     UACUG-GGCGGCGGCAG     5
                      ||| | |:||||||||
mRNA
(PA14_49720)   1      AUGUCACUGCCGCCGUA     17
```

---

49 **PA14_68920** LysR family transcriptional regulator

Energy: -13.57 p-value: 0.002

```
sRNA           19     ACUGG--GCGGCGGC     7
                       ||||  |||||||
mRNA
(PA14_68920)   6      CGACCUACGCCGCCU     20
```

---

50 **PA14_40650** hypothetical protein

Energy: -13.31 p-value: 0.003

```
sRNA           23     UCUUAC-UGGGCGGCGGC     7
                       |:| | ||||||| ||
mRNA
(PA14_40650)   -15    CGGA-GAACCCGCC-CCA     1
```

---

51 **PA14_46310** hypothetical protein

Energy: -13.25 p-value: 0.003

```
sRNA           23     UCUUACUGGGCGGC-GGCA     6
                       | |||||||| :| |||
mRNA
(PA14_46310)   -3     CGCAUGACCCG-UGACCG-     14
```

---

52 **PA14_42920** hypothetical protein

Energy: -13.18 p-value: 0.003

```
sRNA           39     CUGUGUCCGCCCACUA     24
                      |:|| ||||||||||
mRNA
(PA14_42920)   -20    GGCA-AGGCGGGUGAC     -6
```

---

53 **PA14_29210** **MFS transporter**

Energy: -13.17 p-value: 0.003

```
sRNA           19     AC-UGGGCGGCGGC     7
                       | ||||||||||
mRNA
(PA14_29210)   6      CGCACCCGCCGCCU     19
```

54 **PA14_37910** LysR family transcriptional regulator

Energy: -13.14 p-value: 0.003

```
sRNA           19   ACUGGGC-GGCGGCAGUUA   2
                     ||||:|  :||||||||
mRNA
(PA14_37910)   3    GGACCUGAAUGCCGUCAA-   20
```

55 **PA14_58440 ABC transporter permease**

Energy: -13.12 p-value: 0.003

```
sRNA           24   AUCUUACUGGGCGGC   10
                     :||:| |||||||
mRNA
(PA14_58440)   -17  AGGAGUUACCCGCCA   -3
```

56 **PA14_16740** hypothetical protein

Energy: -13.11 p-value: 0.003

```
sRNA           19   ACU-GGGCGGCGGC   7
                     || |||||||||
mRNA
(PA14_16740)   -13  GGAGCCCGCCGCCA   1
```

57 **PA14_05040** coproporphyrinogen III oxidase

Energy: -13.1 p-value: 0.003

```
sRNA           17   UGGGC--GGCGGCAGUU   3
                     ||||  ||||||| |
mRNA
(PA14_05040)   -12  CCCCGCCCCGCCGUGAC   5
```

58 **PA14_71100** hypothetical protein

Energy: -13.09 p-value: 0.003

```
sRNA           18   CUGGGCGGCGGCAGUUA   2
                     |||| || |||||||
mRNA
(PA14_71100)   6    CACCCUCC-CCGUCAA-   20
```

59 **napF** ferredoxin protein NapF

Energy: -13.02 p-value: 0.004

```
sRNA           80   CCGGCAGCGG--CGCGC   66
                     || ||||||  | ||
mRNA (napF)    4    AGCAGUCGCCGAGAGCU   20
```

60 **PA14_06460** hypothetical protein

Energy: -12.99 p-value: 0.004

```
sRNA            75      GCGGCGCGC            66
                        ||||||||
mRNA
(PA14_06460)   -20      CGCCGCGCA           -12
```

61 **adhA** alcohol dehydrogenase

Energy: -12.97 p-value: 0.004

```
sRNA            27      CUAUCU--UACUGGG-CGGCGG     8
                        ||| ||  ||||||| ||| |
mRNA (adhA)     -7      GAU-GACCAUGACCCUGCCACA    14
```

62 **PA14_61990** hypothetical protein

Energy: -12.84 p-value: 0.004

```
sRNA            19      ACUGGGCGGCGGCA        6
                         |||||||:  ||
mRNA
(PA14_61990)    8       AGACCCGCU-ACGG       20
```

63 **PA14_60550** ATP-dependent protease

Energy: -12.77 p-value: 0.004

```
sRNA            79      CGGCAGCGGCGC         68
                         |||||||:||
mRNA
(PA14_60550)    10      UCCGUCGCUGC-         20
```

64 **PA14_58110** Maf-like protein

Energy: -12.65 p-value: 0.005

```
sRNA            83      UGUCCGGCAGCGGCGC     68
                         || ||||||||:|:
mRNA
(PA14_58110)    -2      CCAUGCCGUCGCUGUA     14
```

Table S6: Putative MtvR targets in the genome of *P. aeruginosa* UCBPP-PA14 predicted by RNAPredator

Energy [kJ/mol]	z-Score	Interaction	mRNA [Start]	mRNA [End]	sRNA	Gene Annotation
-16.06	-2.49	(((.(.(((((((..(((((((((&)))))))))))))))).).))) mRNA: 5'- GAUCGCAUGACCCAGGCCGCCG -3' ||| | ||||||| ||||||| sRNA: 3'- CUAUCUUACUGGG--CGGCGGC -5'	-6	17	5-26	hypothetical protein 56960
-16.04	-2.48	((((((...(((((((((((&)))))))))))..)))))) mRNA: 5'- GAUGGACUGGACCCGCCGC -3' |||||| |||||||||| sRNA: 3'- CUAUCUUA-CUGGGCGGCG -5'	-1	18	8-26	transcriptional regulator
-15.91	-2.43	(((((((..((.(((((((.((((((&))))))))))))).))..))))))) mRNA: 5'- GCGGGUGCCGGCAUGACCCAGCCGC -3' ||||||| || ||||||| ||||| sRNA: 3'- CGCCCACUAUCUUACUGGG-CGGCG -5'	-12	13	8-32	hypothetical protein 34940
-15.49	-2.28	(((((....(((((((((..(((((((&)))))))..))).....))))))))))) mRNA:5'- GUAGCCCAUGC-----CCCA-UCCCAU -3' ||||| || || |||||| sRNA:3'- UAUCG----CGGGGUUAA-UAAGGACA -5'	-6	20	104-131	putative hydrolase
-15.39	-2.24	((((((.((.((((((((((((&)))))))))))))))).)))) mRNA: 5'- CGUG-GCAUGAGCGGCAUUCC -3' |||| | || ||||||||||| sRNA: 3'- GCGCAC-GA-CCGCCGUAAGG -5'	-5	16	49-69	phenazine biosynthesis protein **PhzD**

<table>
<tr><th>Energy [kJ/mol]</th><th>z-Score</th><th>Interaction</th><th>mRNA [Start]</th><th>mRNA [End]</th><th>sRNA</th><th>Gene Annotation</th></tr>
<tr><td>-14.54</td><td>-1.94</td><td>(((((((((....(((&))).....)))))))))<pre>
mRNA: 5'- AGCGCCCCAUGAG-UC -3'
          ||||||||| ||
sRNA: 3'- UCGCGGGGUUAAUAAG -5'
</pre></td><td>-7</td><td>8</td><td>113-129</td><td>putative transporter</td></tr>
<tr><td>-14.39</td><td>-1.88</td><td>((((((((((((&))))))).....)))))<pre>
mRNA: 5'- CCCCA-----UC -3'
          ||||| ||
sRNA: 3'- GGGGUUAAUAAG -5'
</pre></td><td>-13</td><td>-2</td><td>109-125</td><td>hypothetical protein 70860</td></tr>
<tr><td>-14.27</td><td>-1.84</td><td>((.(((((.((((((.(((((((&)))))))..)))))).)))))))<pre>
mRNA: 5'- GGAGUGA-UUGAAU-GAAUGCCG -3'
          || |||| ||||| |||||||
sRNA: 3'- CC-CACUA-UCUUACUGGGCGGC -5'
</pre></td><td>-3</td><td>19</td><td>8-30</td><td>endonuclease III</td></tr>
<tr><td>-14.22</td><td>-1.82</td><td>((((((((((((.((&))))))))))))))<pre>
mRNA: 5'- GACCCGCCGCCGCU -3'
          |||||||||||| |
sRNA: 3'- CUGGGCGGCGGC-A -5'
</pre></td><td>6</td><td>20</td><td>5-18</td><td>**iron enterobactin transporter periplasmic binding protein**</td></tr>
</table>

Energy [kJ/mol]	z-Score	Interaction	mRNA [Start]	mRNA [End]	sRNA	Gene Annotation
-13.54	-1.57	(((((((((((((&)))))))).....))))) mRNA: 5'- GCCCU-----UUC -3' ||||| ||| sRNA: 3'- CGGGGUUAAUAAG -5'	-11	1	109-126	3 dehydroquinate synthase
-13.29	-1.48	(((((((((((&))))))))))) mRNA: 5'- CGAUGCGCCGC -3' ||||||||||| sRNA: 3'- GCUACGCGGCG -5'	-2	8	86-96	hypothetical protein
-13.11	-1.42	(((((..((.((.(((((((((((((((((&))).)))))))))))))).)).)).))))) mRNA: 5'- GCGGGAGG-AA-GGCAUGAUCCGCUG-UCG -3' ||||| | | ||||||||||||| ||| sRNA: 3'- CGCCCA-CU-AU-CUUACUGGGCGGCGGCA -5'	-13	16	3-32	hypothetical protein 38270
-13.05	-1.40	((.(((((((((((.(((..(((((.((&)).)))))))).))))))).)))))) mRNA: 5'- GGAGUG-AAGAAUGAGCCGUACC-GC -3' || ||| ||||||| ||| ||| | sRNA: 3'- CC-CACUAUCUUACUGGG--CGGCG- -5'	-10	17	5-30	putative secreted lipoprotein

Supplementary References

1. Markowitz VM, Chen IMA, Palaniappan K, Chu K, Szeto E, et al. (2010) The integrated microbial genomes system: an expanding comparative analysis resource. Nucleic Acids Res 30: D382-D390.
2. Zhao Y, Li H, Hou Y, Cha L, Cao Y, et al. (2008) Construction of two mathematical models for prediction of bacterial sRNA targets. Biochem Biophys Res Commun 372: 346-350.
3. Tjaden B, Goodwin SS, Opdyke JA, Guillier M, Fu DX, et al. (2006) Target prediction for small, noncoding RNAs in bacteria. Nucleic Acids Res 34: 2791-2802.
4. Eggenhofer F, Tafer H, Stadler PF, Hofacker IL (2011) RNApredator: fast accessibility-based prediction of sRNA targets. Nucleic Acids Res 39: W149-W154.