

**Table S3.** The information of target six *Salmonella enterica* subspecies enterica serovars, their amplified sequences with encompassing primers, alignments of amplified sequences, and searching SNPs on the alignment, and design SNP-based primers on the respective align genes.

| No | <i>Salmonella</i> serovars  | Catalog No. | Source strains                           |
|----|---|-------------|--|
| 1  | <i>Salmonella enterica</i> subspecies enterica serovar Typhimurium ( <i>Salmonella</i> Typhimurium) | NCCP-14760  | National Culture Collection of Pathogens |
| 2  | <i>Salmonella</i> Enteritidis   | NCCP-14545  | National Culture Collection of Pathogens |
| 3  | <i>Salmonella</i> Agona   | NCCP-12231  | National Culture Collection of Pathogens |
| 4  | <i>Salmonella enterica</i>  | NCCP-15756  | National Culture Collection of Pathogens |
| 5  | <i>Salmonella</i> Typhi   | NCCP-14641  | National Culture Collection of Pathogens |
| 6  | <i>Salmonella</i> Abony   | BA1800061   | Veterinary Culture Collection Center     |

**The PCR amplification of 1<sup>st</sup> time PCR with the primer sets (01-, 09-, 13-, 14-, 24-Sbon) are as following:**

The amplified sequences of six *Salmonella* serovars (the provided serial no. was presented in the above table: 1-6; SNP-encompassing primers, gene name) are presented below: **for example, primer name (01-Sbon-2); primer serial-short form of *Salmonella bongori*-*Salmonella* serovar serial no. (1-6)**

01. Sbon F/R, Gene Name: Conserved hypothetical protein (SBG) SBG\_RS00105

|            |                     |
|------------|---------------------|
| 01-Sbon-F: | GGGGAAATGTTGGCGGGA  |
| 01-Sbon-R: | TTATGCCCCGGTGCCATGG |

**>01-Sbon-2 (name of primer-serial no. - short form of *Salmonella bongori* -*Salmonella* serovar serial no in the above table)**

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CCCACCGTCTCAAGAACTGATTGTCTGTAGTACATCAGCAGGAGACCCTGTTACATCAACTGCTGGAGGGCGACCTGCGA
CAGCGGGTAATGGACGCGATTGTAATCGCTGCCGGAACGCGAGCAACTGGTGTTAACGCTGTATTACCAGGAAGAGCTCA
ACCTCAAAGAGATTGGCGCGGTACTGGAAGTTGGCGAATCGCGGGTCAGCCAGTTGCATAGTCAGGCCATCAAACGATTA
CGCACCAAACCTGGGTAAGTTATAGGTCGCGCATGGTCGACCCGAAAAGTGCCGCACAACGTATAGACTACCAGGAGTTC
TCATGACGGTGCAGCAACCTAAAAGGCGGCCCTTGAGCCGCTATCTTAAAGACTTTAAACACAGCCAGACGCATTGCGCG
CATTGTCACAACTGCTCGACCGCATTACGCTGGTTGCGCGTGGCAAGATCGTTAATAAAATCGCTATTTACAGCTGGA

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TATGCTACTTGACGACGCTGCCTGGCAGCGGGAGCAGAAGGAGTGGGTGGCGCTGTGTGCTTTTGCGGCGATTGCACT  
GCAAAAAGCAGAGTGATTTTTTCGATATTATCGGTTTCAAGCAGTATTTGTTTGAACAAACCGAGATGAGCCATGGCACC  
GGGGCATAAA

>01-Sbon-4

AAACCGCAAATCGAACTGAGTGTATGAGACATCAACAGGAGAACCCGTTACATCAACTGCTGGAGGGCGACCTGCGACA  
GCGGGTAATGGATGCGATTGAATCGCTGCCGGAACGCGAGCAACTGGTGTAAACGCTGTATTACCAGGAAGAGCTCAATC  
TCAAAGAGATTGGCGCGGTACTGGAAGTCGGCGAATCGCGGGTCAGCCAGTTGCATAGTCAGGCCATCAAACGATTACGC  
ACCAAACCTGGGTAAGTTATAGGTGCGCGCATGATCGCACCCGAAAAGTGCCGCACAACGTATAGACTACCAGGAGTTCTCA  
TGACGGTGCAGCAACCTAAAAGGCGGCCCTTTGAGCCGCTATCTTAAAGACTTTAAACACAGCCAGACGCATTGCGCGCAT  
TGTCACAAACTGCTCGACCGCATTACGCTGGTTCGCCGTGGCAAGATCGTTAATAAAATCGCTATTTACAGCTGGATAT  
GCTACTTGACGACGCTGCCTGGCAGCGGGAGCAGAAGGAGTGGGTGGCGCTGTGTGCTTTTGCGGCGATTGCACTGCA  
AAAAGCAGAGTGATTTTTTCGATATTATCGGTTTCAAGCAGTATTTGTTTGAACAAACCGAGATGAGCCATGGCACCGGG  
GCATAAA

>01-Sbon-5

TGTAATACCCGACTGGTGTCTGAGACATCAGCAGGAAACCCGTTACATCAACTGCTGGAGGGCGACCTGCGACAGCGGGT  
AATGGATGCGATTGAATCGCTGCCGGAACGCGAGCAACTGGTGTAAACGCTGTATTACCAGGAAGAGCTCAATCTCAAAG  
AGATTGGCGCGGTACTGGAAGTCGGCGAATCGCGGGTCAGCCAGTTGCATAGTCAGGCCATCAAACGATTACGCACCAAA  
CTGGGTAAGTTATAGGTAGCGCATGATCGCACCCGAAAAGTGCCGCACAACATATAGACTACCAGGAGTTCTCATGACGG  
TGCAGCAACCTAAAAGGCGGCCCTTGAGCCGCTATCTTAAAGACTTTAAACACAGCCAGACGCATTGCGCGCATTTGTAC  
AAATTGCTCGACCGCATTACGCTGGTTCGCCGTGGCAAGATCGTTAATAAAATCGCTATTTACAGCTGGATATGCTACT  
TGACGACGCTGCCTGGCAGCGGGAGCAGAAGGAGTGGGTGGCGTGTGTGCTTTTGCGGCGATTGCACTGCAAAAAGC  
AGAGTGATTTTTTCGATATTATCGGTTTCAAGCAGTATTTGTTTGAACAAACCGAGATGAGCCATGGCACCGGGGCATAA  
A

>01-Sbon-6

ACTGTCTTCCTCGAACTTGGTGATGAGACATCAGCAGGAAACCCGTTACATCAACTGCTGGAGGGCGACCTGCGACAGCG  
GGTAATGGATGCGATTGAATCGCTGCCGGAACGCGAGCAACTGGTGTAAACGCTGTATTACCAGGAAGAGCTCAATCTCA  
AAGAGATTGGCGCGGTACTGGAAGTCGGCGAATCGCGGGTCAGCCAGTTGCATAGTCAGGCCATCAAACGATTACGCACC  
AAACTGGGTAAGTTATAGGTAGCGCATGATCGCACCCGAAAAGTGCCGCACAACGTATAGACTACCAGGAGTTCTCATGA  
CGGTGCAGCAACCTAAAAGGCGGCCCTTGAGCCGCTATCTTAAAGACTTTAAACACAGCCAGACGCATTGCGCGCATTTGT  
CACAACTGCTCGACCGCATTACGCTGGTTCGCCGTGGCAAGATCGTTAATAAAATCGCTATTTACAGCTGGATATGCT  
ACTTGACGACGCGCCTGGCAGCGGGAGCAGAAGGAGTGGGTGGCGCTGTGTGCTTTTGCGGCGATTGCACTGCAAAA  
AGCAGAGTGATTTTTTCGATATTATCGGTTTCAAGCAGTATTTGTTTGAACAAACCGAGATGAGCCATGGCACCGGGGGC

ATAAA

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      10      20      30      40      50      60      70      80      90     100
01-Sbon-2_F  CCCACCGTCTCAAGAACTGATTGTCTGTAGTACATCAGCAGGAGACCCCTGTTACATCAACTGCTGGAGGGCGACCTGCGACAGCGGGTAATGGACGCGAT
01-Sbon-4_F  --A.A.CG.AA.TCG.AACTGA..G.A.GAG....A.....A..C.....T.....
01-Sbon-5_F  ----T..AAT.CCCGA--C.G..G.C.GAG.....A..C.....T.....
01-Sbon-6_F  ----.T.....TCCTCGAACT.G..GA..GAG.....A..C.....T.....

      110     120     130     140     150     160     170     180     190     200
01-Sbon-2_F  TGTAAATCGCTGCCGGAACCGGAGCAACTGGTGTAAACGCTGTATTACCGAGGAGAGCTCAACCTCAAAAGAGATTGGCGCGGTACTGGAAGTTGGCGAATC
01-Sbon-4_F  .....T.....C.....
01-Sbon-5_F  .....T.....C.....
01-Sbon-6_F  .....T.....C.....

      210     220     230     240     250     260     270     280     290     300
01-Sbon-2_F  GCGGGTCAGCCAGTTGCTAGTCAAGCCATCAAAAGATTACGCACCAAACTGGGTAAGTTATAGGTCGCGCATGGTCGCACCCGAAAAATGCGGCACAAAC
01-Sbon-4_F  .....A.....
01-Sbon-5_F  .....A.....A.....
01-Sbon-6_F  .....A.....A.....

      310     320     330     340     350     360     370     380     390     400
01-Sbon-2_F  GTATAGACTACCGAGTTCTCATGACGGTGCAGCAACCATAAAAGCGGCCCTTGAGCCGCTATCTTAAAGACTTTAAACACAGCCAGACGCAATTGCGCG
01-Sbon-4_F  .....T.....
01-Sbon-5_F  A.....
01-Sbon-6_F  .....

      410     420     430     440     450     460     470     480     490     500
01-Sbon-2_F  CATTGTCACAAACTGCTGACCGCATTACGCTGGTTGCGCGTGGCAAGATCGTTAATAAAATCGCTATTTACAGCTGGATATGCTACTTGAACGACGCTG
01-Sbon-4_F  .....
01-Sbon-5_F  .....T.....
01-Sbon-6_F  .....A.....

      510     520     530     540     550     560     570     580     590     600
01-Sbon-2_F  CCTGGCAGCGGGAGCAGAAAGAGTGGTGGCGCTGTGTCGCTTTTGCGGCGATTGCACTGCAAAAAGCAGAGTGATTTTTTCGATATTATCGGTTTCAA
01-Sbon-4_F  .....
01-Sbon-5_F  .....T.....
01-Sbon-6_F  .....

      610     620     630     640     650
01-Sbon-2_F  GCAGTATTTGTTTGAACAAACCGAGATGAGCCATGGCACCAGGGG-CATAAA
01-Sbon-4_F  .....
01-Sbon-5_F  .....
01-Sbon-6_F  .....G.....
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**The SNP-based primers were designed based on the above align gene (SBG) sequences (natural SNP is marked by red color and artificial mutated bases are marked by yellow color)**

SBG-2 F: TTACCAGGAAGAGCTC**G**AC

SBG-2 R: CGG TGC CAT GGC TCA TCT CG

SBG-2 (2) F: GTA AGT TAT AGG TCG CGC A**C**G G

SBG-2 R: CGG TGC CAT GGC TCA TCT CG

SBG-4 F: GTA AGT TAT AGG TCG CGC AGG **A**

SBG-4 R: CGG TGC CAT GGC TCA TCT CG

09-Sbon, Gene Name: Penicillin Binding protein gene (*mrcB*)

|           |                    |
|-----------|--------------------|
| 09-Sbon-F | GGCGTTGAAGAAGCAGCG |
| 09-Sbon-R | ACGGCCTACCCAGGTGAT |

>09-Sbon-1

CCTTGAAGTGCACGCGAGGTGGTAGTGGACGCTTTAGCGGCGAGGTGCGCGGATGGTTGGCGGGGCGGAGCCGCAGTAT  
GCCGGCTATAACCGTGCCATGCAGGCGCGCCGTTCCATCGGGTCGCTGGCGAAACCGGCGACCTATCTGACCGCGTTAAG  
TCAGCCGAACCTTATACCGTCTGAACACCTGGATTGCCGATGCGCCGATTTCTCTGCGCCAGCCGAATGGTCAGGTCTGGT  
CGCCGCAGAACGACGATCGTCGCTACAGCGAAAGCGGGAAAGTGATGCTGGTGGATGCGTTAACTCGCTCAATGAACGTA  
CCGACGGTCAATCTGGGGATGGCGTTAGGTCTACCGGCAGTAACCGATACCTGGACGAAGCTCGGCGTGCCGAAAGATCA  
GCTCAATCCGGTTCCGGCGATGCTGTTAGGGGCGCTGAACCTGACGCCGATCGAAGTGGCGCAGGCGTTCCAGACTATCG  
CCAGCGGCGGAAATCGCGCGCCGTTATCAGCGCTGCGTTCGGTTATTGCGGAAGATGGTAAAGTGTGTACCAAAGTTAT  
CCGCAAGCTGAACGCGCTGTACCGGCACAGGCGGCTTACCTGACGCTCTGGACAATGCAGCAGGTCTGCCAGCGTGGTAC  
GGGGCGTCAGCTTGCGCGGAAATATCCGGGTCTGCATCTGGCCGGTAAAACCGGGACGACAAACAACAATGTCGATACCT  
GGTTTGCCGGTATCGACGGCAGCCAGGTGACTATCACCTGGGTAGGCCGTAGAT

>09-Sbon-2

GCTGAAATGGCACGCGAGGTGGTGGTGGACGCTTTAGCGGCGAGGTGCGCGGATGGTTGGCGGGGCGGAGCCGCAGTAT  
GCCGGCTATAACCGTGCCATGCAGGCGCGCCGTTCCATCGGGTCGCTGGCGAAACCGGCGACCTATCTGACCGCGTTAAG  
TCAGCCGAACCTTATACCGTCTGAACACCTGGATTGCCGATGCGCCGATTTCTCTGCGCCAGCCGAATGGTCAGGTCTGGT  
CGCCGCAGAACGACGATCGTCGCTACAGCGAAAGCGGGAAAGTGATGCTGGTGGATGCGTTAACTCGCTCAATGAACGTA  
CCGACGGTCAATCTGGGGATGGCGTTAGGTTTACCGGCGGTAACCGATACCTGGACGAAGCTCGGCGTGCCGAAAGATCA  
GCTCAATCCGGTTCCGGCTATGCTGTTAGGGGCGCTGAACCTGACGCCGATCGAAGTGGCGCAGGCGTTCCAGACTATCG  
CCAGCGGCGGAAATCGCGCGCCGTTATCAGCGCTGCGTTCAGTTATTGCGGAAGATGGTAAAGTGTGTACCAAAGTTAT  
CCGCAAGCTGAACGCGCTGTACCGGCACAGGCGGCTTACCTGACGCTCTGGACAATGCAGCAGGTCTGCCAGCGTGGTAC  
GGGGCGTCAGCTTGCGCGGAAATATCCGGGTCTGCATCTGGCCGGTAAAACCGGGACGACAAACAACAATGTCGATACCT  
GGTTTGCCGGTATCGACGGCAGCCAGGTGACTATCACCTGGGGTAGGCCGTA

>09-Sbon-3

GCGTGACCTGGACGCGAGGTGGTAGTGGACGCTTTAGCGGCGAGGTGCGCGGATGGTTGGCGGGGCGGAGCCGCAGTAT  
GCCGGCTATAACCGTGCCATGCAGGCGCGCCGTTCCATCGGGTCGCTGGCGAAACCGGCGACCTATCTGACCGCGTTAAG  
TCAGCCGAACCTTATACCGTCTGAACACCTGGATTGCCGATGCGCCGATTTCTCTGCGCCAGCCGAATGGTCAGGTCTGGT

CGCCGCAGAACGACGATCGTCGCTACAGCGAAAGCGGGAAAGTGATGCTGGTGGATGCGTTAACTCGCTCAATGAACGTA  
CCsGACGGTCAATCTGGGGATGGCGTTAGGTTTACCGGCGGTAACCGATACCTGGACGAAGCTCGGCGTGCCGAAAGATCA  
GCTCAATCCGGTTCCGGCTATGCTGTTAGGGGCGCTGAACCTGACGCCGATCGAAGTGGCGCAAGCGTTCCAGACTATCG  
CCAGCGGCGGAAATCGCGCGCCGTTATCAGCGCTGCGTTCGGTTATTGCGGAAGATGGTAAGGTGCTGTACCAAAGTTAT  
CCGCAAGCTGAACGCGCCGTACCGGCACAGGCGGCTTACCTGACGCTCTGGACAATGCAGCAGGTTCGTCCAGCGTGGTAC  
GGGGCGTCAGCTTGGCGCGAAATATCCGGGTCTGCATCTGGCGGGTAAAACCGGGACGACAAACAACAATGTCGATACCT  
GGTTTGCCGGTATCGACGGCAGCCAGGTGACTATCACCTGGGTAGGCCGTAGA

>09-Sbon-4

CCTCCACTGGTACGCGAGGTGGTGGTGGACGCTTTAGCGGCGAGGTGCGCGGATGGTTGGCGGGGCGGAGCCGCAGTAT  
GCCGGCTATAACCGTGCCATGCAGGCGCGCCGTTCCATCGGGTCGCTGGCGAAACCGGCGACCTATCTGACCGCGTTAAG  
TCAGCCGAACCTTATACCGTCTGAACACCTGGATTGCCGATGCGCCGATTCTCTGCGCCAGCCGAATGGTCAGGTCTGGT  
CGCCGCAGAACGACGATCGTCGCTACAGCGAAAGCGGGAAAGTGATGCTGGTGGATGCGTTAACTCGCTCAATGAACGTA  
CCGACGGTCAATCTGGGGATGGCGTTAGGTTTACCGGCGGTAACCGATACCTGGACGAAGCTCGGCGTGCCGAAAGATCA  
GCTCAATCCGGTTCCGGCTATGCTGTTAGGAGCGCTGAACCTGACGCCGATCGAAGTGGCGCAGGCGTTCCAGACTATCG  
CCAGCGGCGGAAATCGCGCGCCGTTATCAGCGCTGCGTTCAGTTATTGCGGAAGATGGTAAAGTGCTGTACCAAAGTTAT  
CCGCAAGCTGAACGCGCCGTACCGGCACAGGCGGCTTACCTGACGCTCTGGACAATGCAGCAGGTTCGTCCAGCGTGGTAC  
GGGGCGTCAGCTTGGCGCGAAATATCCGGGTCTGCATCTGGCCGGTAAAACCGGGACGACAAACAACAATGTCGATACCT  
GGTTTTGCCGGTATCGACGGCAGCCAGGTGACTATCACTCTGGGGTAGGCCGTAG

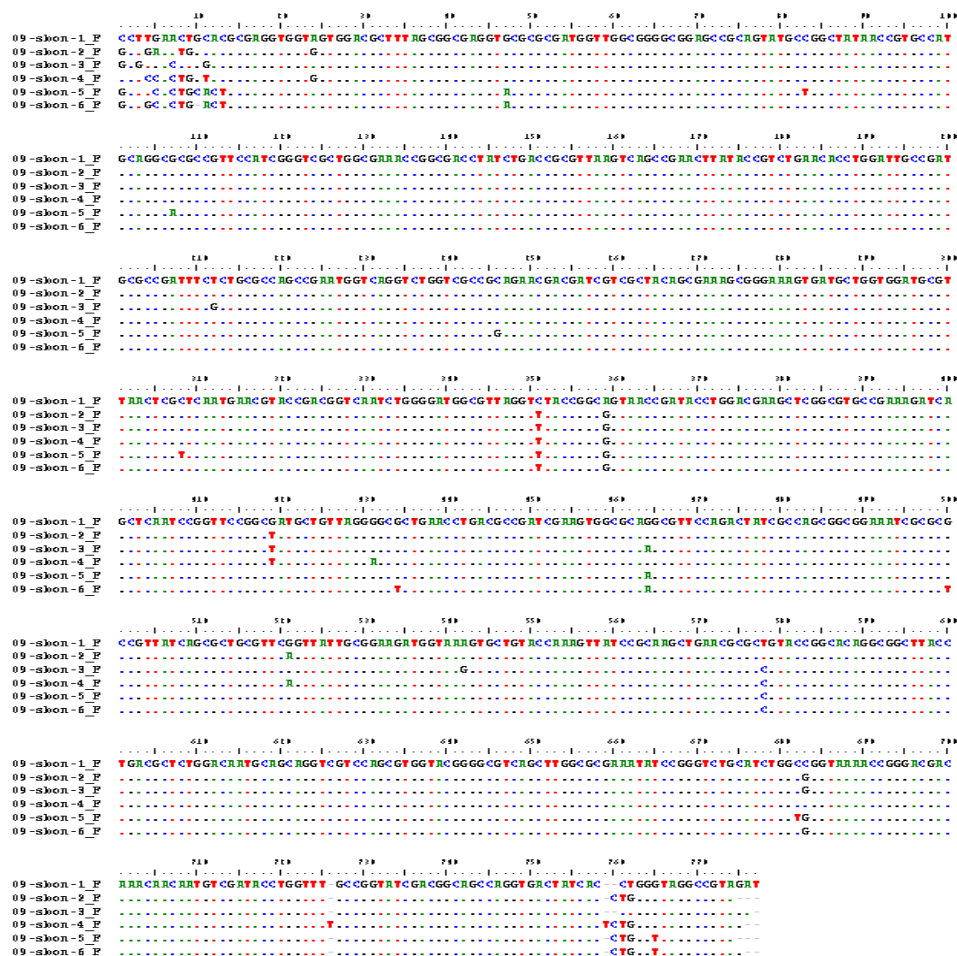
>09-Sbon-5

GCTTCACTGCACTGCGAGGTGGTAGTGGACGCTTTAGCGGCGAGGTACGCGGATGGTTGGCGGGGCGGAGCCGCAGTAT  
GCTGGCTATAACCGTGCCATGCAGGCACGCCGTTCCATCGGGTCGCTGGCGAAACCGGCGACCTATCTGACCGCGTTAAG  
TCAGCCGAACCTTATACCGTCTGAACACCTGGATTGCCGATGCGCCGATTCTCTGCGCCAGCCGAATGGTCAGGTCTGGT  
CGCCGGAGAACGACGATCGTCGCTACAGCGAAAGCGGGAAAGTGATGCTGGTGGATGCGTTAACTCGTTCAATGAACGTA  
CCGACGGTCAATCTGGGGATGGCGTTAGGTTTACCGGCGGTAACCGATACCTGGACGAAGCTCGGCGTGCCGAAAGATCA  
GCTCAATCCGGTTCCGGCGATGCTGTTAGGGGCGCTGAACCTGACGCCGATCGAAGTGGCGCAAGCGTTCCAGACTATCG  
CCAGCGGCGGAAATCGCGCGCCGTTATCAGCGCTGCGTTCGGTTATTGCGGAAGATGGTAAAGTGCTGTACCAAAGTTAT  
CCGCAAGCTGAACGCGCCGTACCGGCACAGGCGGCTTACCTGACGCTCTGGACAATGCAGCAGGTTCGTCCAGCGTGGTAC  
GGGGCGTCAGCTTGGCGCGAAATATCCGGGTCTGCATCTGGTGGGTAAAACCGGGACGACAAACAACAATGTCGATACCT  
GGTTTGCCGGTATCGACGGCAGCCAGGTGACTATCACCTGGGTAGGCCGTA

>09-Sbon-6

GCTGCACTGACTGCGAGGTGGTAGTGGACGCTTTAGCGGCGAGGTACGCGGATGGTTGGCGGGGCGGAGCCGCAGTATG  
CCGGCTATAACCGTGCCATGCAGGCGCGCCGTTCCATCGGGTCGCTGGCGAAACCGGCGACCTATCTGACCGCGTTAAGT

CAGCCGAAC TTATACCGTCTGAACACCTGGATTGCCGATGCGCCGATTTCTCTGCGCCAGCCGAATGGTCAGGTCTGGTC  
 GCCGCAGAACGACGATCGTCGCTACAGCGAAAGCGGGAAAGTGATGCTGGTGGATGCGTTAACTCGCTCAATGAACGTAC  
 CGACGGTCAATCTGGGGATGGCGTTAGGTTTACCGGCGGTAACCGATACCTGGACGAAGCTCGGCGTGCCGAAAGATCAG  
 CTCAATCCGGTTCCGGCGATGCTGTTAGGGGCTCTGAACCTGACGCCGATCGAAGTGGCGCAAGCGTTCCAGACTATCGC  
 CAGCGGCGGAAATCGCGCTCCGTTATCAGCGCTGCGTTTCGGTTATTGCGGAAGATGGTAAAGTGCTGTACCAAAGTTATC  
 CGCAAGCTGAACGCGCCGTACCGGCACAGGCGGCTTACCTGACGCTCTGGACAATGCAGCAGGTCTGCCAGCGTGGTACG  
 GGGCGTCAGCTTGGCGCGAAATATCCGGGTCTGCATCTGGCGGGTAAAACCGGGACGACAAACAACAATGTCGATACCTG  
 GTTGGCCGGTATCGACGGCAGCCAGGTGACTATCACCTGGGTTAGGCCGTAG



The SNP-based primers were designed based on the above align gene (*mrcB*) sequences (natural SNP is marked by red color and artificial mutated bases are marked by yellow shaded)

mrcB-1-F: TGGCGTTAGGTCTACCGTCA

mrcB-1-R: TTG TCG TCC CGG TTT TAT CG

mrcB-3-F : TTG CCG ATG CGC CGA TTG CG

mrcB-3-R : GGA TAA CTT TGG TAC AGC CCC

mrcB-4-F : GTT CCG GCT ATG CTG TTA **A**GA

mrcB-4-R : TTG TCG TCC CGG TTT TAT CG

mrcB-5-F : GGC GGA GCC GCA GTA **T**AC T

mrcB-5-R : TGT CGT CCC GGT TTT AC**T** CA

mrcB-6-F : ACGCTTTAGCGGCGAG**A**TA

mrcB-6-R : TGT CGT CCC GGT TTT AC**T** CA

### 13-Sbon, Gene Name: Pyrimidine-specific ribonucleoside hydrolase (*rihB*)

|             |                    |
|-------------|--------------------|
| 013-Sbon-F: | GCTGTACCTGCCGACTGG |
| 13-Sbon-R:  | GTTCCCCACGGGCTATGG |

>13-Sbon-1

CAAAGCTTTTTTTAGTTTCTTGCAAGTAAATGCAATTGCAGCATTAACGAAGAAGGAAGTGATCTGGTTAACTACTGTAAT  
GTAAAAAATGGGTAACGATACGGTTTTATCATGTTGTTGTGTTGTTAATTACGGTAAAGGTGTTATAGAAACAAAATGTA  
ACATCTCTCTGGAACACCCAAACGGACAACAACATATGAATAAATCAGGGAAATACCTCGTCTGGACAGCGCTCTCAGTAT  
TGGGTGCGTTTGCCCTGGGCTATATTGCGTTAAATCGTGGGGAACAGATCAACGCGCTATGGATCGCACTGGGCGTCGGT  
CTGTGTCTATCTTATTGCGTATCGTTTTTATGGGCTCTATATCGCCAAAAAAGTGCTGGCGGTTGACCCAACGCGTATGA  
CGCCCGCGGTACGTCATAATGATGGTCTGGATTATGTCCGACCGATAAGAAAGTGCTTTTTTGGTCACCATTTTGCGGCC  
ATTGCTGGCGCAGTCCGCTGGCCTGGCCGGTACTGGCGGCGCAGATGGGCTATCTGCCGGGGATGATCTGTTTGCT

>13-Sbon-4

TTCACACCATAGTATCTTGGAATAAATTGCATTGCAGCATTAACGAAGAAAGGAAGTGTTCTGGTTAGACTGTAATGAA  
AAATGGGAAATTTTCGAATAATTTGTGTGGTGTTAATTACGGTAAGGCTCCTTGAAACAAAATGAACATCTCTCTGGAAC  
ACCCAAACGTACAACACTACTATGAATAAATCACGCAAAT

>13-Sbon-6

CACCGGGTAGGTAATTCTTGCAAGTAAATGCATTGCAGCATTAACGAAGAAAGGAAGTGATCTGGTTAACTACTGTAATGT  
AAAAAATGGGTAATAATTCGGATGTATCATGTTGTTGTGTTGTTAATTACGGTAAAGGTGTTATAGAAACAAAATGTAACA  
TCTCTCTGGAACACCCAAACGGACAACAGCTATGAATAAATCAGGGAAATACCTCGTCTGGACAGCGCTCTCAGTATTGG  
GTGCGTTTGGCCTGGGCTATATTGCGTTAAATCGTGGGGAACAGATCAACGCGCTATGGATCGTGGTGTCTTTTTTCTG  
TGTTTATCTTATTGCGTATCGTTTTTATGGGCTCTATATCGCCAATAAAGTGCTGGCGGTTGACCCTACGCGTATTA

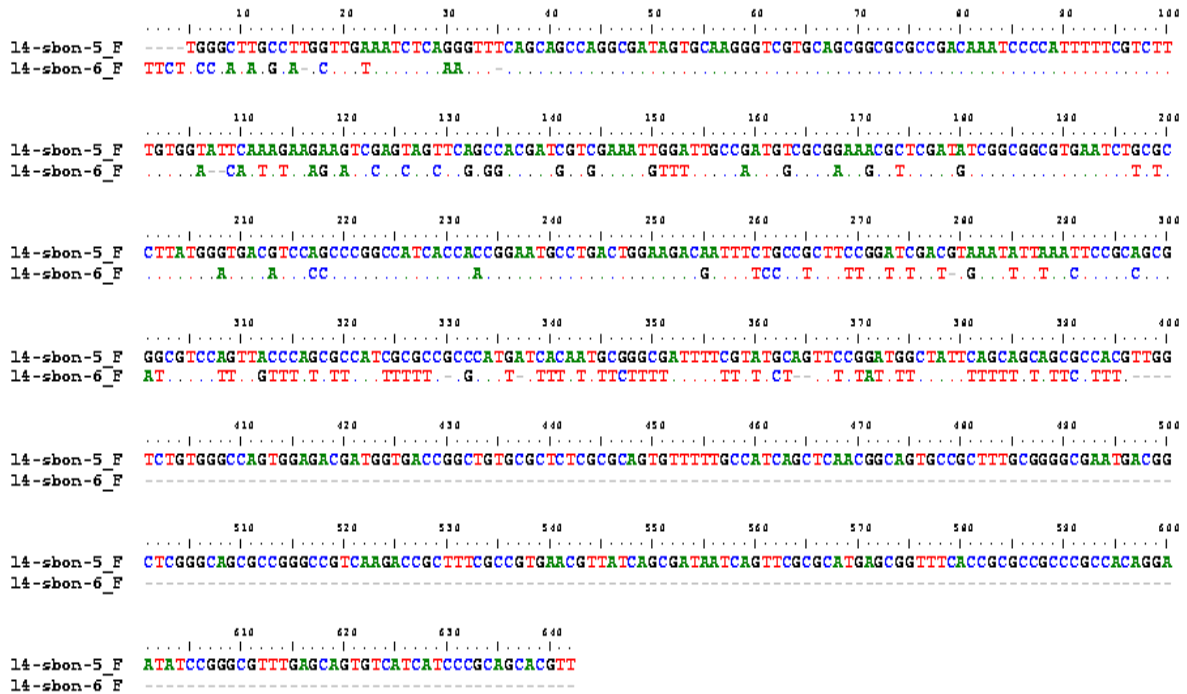
The above align gene (rihB) did not produce the good quality gene sequences of all target Salmonella, where we did not find any suitable SNPs. Second PCR was conducted, and the sequence was showed it latter

|                  |                           |
|------------------|---------------------------|
| <b>14-Sbon-F</b> | <b>TCCCCTGTGTTTCGACGC</b> |
| <b>14-Sbon-R</b> | <b>ACGCCGATAAGACGCTG</b>  |

TGGGCTTGCCTTGGTTGAAATCTCAGGGTTTTCAGCAGCCAGGCGATAGTGCAAGGGTCGTGCAGCGGGCGCCGACAAAT  
CCCCATTTTTTCGTCTTTGTGGTATTCAAAGAAGAAGTCGAGTAGTTACGCCACGATCGTCGAAATTGGATTGCCGATGTC  
GCGGAAACGCTCGATATCGGGCGGCTGAATCTGCGCCTTATGGGTGACGTCCAGCCCGGCCATCACCACCGGAATGCCTG  
ACTGGAAGACAATTTCTGCCGCTTCCGGATCGACGTAAATATTAAATTCCGCAGCGGGCGTCCAGTTACCCAGCGCCATC  
GCGCCGCCCATGATCACAATGCGGGCGATTTTCGTATGCAGTTCGGGATGGCTATTCAGCAGCAGCGCCACGTTGGTCTG  
TGGGCCAGTGGAGACGATGGTGACCGGCTGTGCGCTCTCGCGCAGTGTTTTTGCCATCAGCTCAACGGCAGTGCCGCTTT  
GCGGGGCGAATGACGGCTCGGGCAGCGCCGGGCCGTCAAGACCGCTTTCGCCGTGAACGTTATCAGCGATAATCAGTTTCG  
CGCATGAGCGGTTTTCACCGCGCCGCCGCCACAGGAATATCCGGGCGTTTGAGCAGTGTATCATCCCCGAGCACGTT

TTCTTCCGATAGGCAGCTTGTAATCTCAAAGTTCAGCAGCCAGGCGATAGTGCAAGGGTCGTGCAGCGGCGCGCCGACAA  
ATCCCCATTTTTCTGCTTTGTGGACAATATAAAGAATCCAGCAGCTCGGGGACGATGGTGGAAATGTTTTTGCCAATGGC

GCGAAAGCGTTCGATGTCGGCGGCGTGAATCTTCTCCTTATGGATGACATCCCCCGGCCATCACCAACGGAATGCCTG  
 ACTGGAAGACGATTTTCCCCTCTTTTGGTTTGATTGAATTTTAACTCCGCCGCGATCGTCCTTTTGTATTCTTCATTT  
 TTTCCGCATTTTTTATTTCTTTTATTTTTTTCTTTTCTATTTTCTATTTTTTGTATTCCTTTG



The above alignment of gene, Pyrimidine-specific ribonucleoside hydrolase (rihA) did not produce the all target sequences of *Salmonella*, where we did not find any suitable SNPs.

## 24-Sbon, Gene Name: Candidate type three secretion system effector protein (sopA)

|           |                    |
|-----------|--------------------|
| 24-Sbon-F | GTAGTGTGGCGGGCTGAG |
| 24-Sbon-R | CTGGTAAGCGTGCTGGCC |

>24-sbon-1

TGAGGTAGGGTCAAAATGGTGGCAGACGCGACACTGAGGCATCATCAATCAACTTCACGGTGGAATGTTTCTGGTTTCGTG  
 GCGGCAATAAACTGCTGGTTTCAGCTCCCCGTGCTCTTCAGTGCTGAGGATGATATCAATCAGCTCCCCAAAGCGTCGCTG  
 CGTGGCCTGCTGATTAAATGCGGCGAGAAACACCGGAAAGTCATGACGGAATAACTCTACCGGAGAGATTTGCGCGGTGG  
 AAACGTTCTCTCCGGCTCGCAGCAGGTAAAAGTTGTCCCATGCAGTGTGAGGAGTAGGGTTTAGCATTGTTAACAGCGTG  
 TCAGTGGAGAGCATCATCGCCGTGTCTGAATCCTGGGAGGAAAGCAGCAGGAAATTATCTGCAGCGCGGGTTGTCCAGTC  
 CGGGATGCCGTCATAATTGCCGAAGAGCCCATATGGATGTGGGGAGACACCGCCGGGTGAGCAAGATACTGTTTCATAAA  
 GCGCTGCAGCTTTCTGGCGGGTGCCATCAGTGCAGTCCACGCCTGTCATACAGTGTAATAACCTGATTAAAGAGTCCG  
 CTGTGAGTGGTCATGGCGGCGCTGTTCTGTCAAACGAATCCAGCAACACAGGCAGTATGCGCTGCTGATAATATGTGTC

AGGAGTCGGCAGGGGAACGTCATTATAGGTCTGGCACTGGTGGGCAAAAAACGTTCTGAACAGGCCCGAGCCACTCGC  
GGATAAGCGCACTTTTTCGTATAGGGGAGGGTGGGCCAGCACGCCTCACTCAGACAAATTACTATTTTCGCCTGTTGTCCC  
TTGTTTCGATTCTTGGCCTCTTATTATCTGTCTGGTATATCGTCTTTTGTCTTTTTTTCTTCTTTATAGGCATAATTCC  
TCCCCCCTCACCTGACAATGTTTTT

>24-sbon-2

GACGGTAGGAGCAATGGTGGCAGACGCGACACTGAGGCATCATCAATCAACTTCACGGTGGAATGTTTCTGGTTCGTGGC  
GGCAATAAACTGCTGGTTCAGCTCCCCGTGCTCTTCAGTGCTGAGGATGATATCAATCAGCTCCCCAAAGCGTCGCTGCG  
TGGCCTGCTGATTAAATGCGGCGAGAAACACCGGAAAGTCATGACGGAATAACTCTACCGGAGAGATTTGCGCGGTGGAA  
ACGTTCTCTCCGGCTCGCAGCAGGTAAAAGTTGTCCCATGCAGTGTGAGGAGTAGGGTTTAGCATTGTTAACAGCGTGTC  
AGTGGAGAGCATCATCGCCGTGTCTGAATCTTGGGAGGAAAGCAGCAGGAAATTATCTGCAGCGCGGGTTGTCCAGTCCG  
GGCTGCCGTCATAATTGCCGAAGAGCCCATTATGGATGTGGGGAGACACCGCCGGGTGAGCAAGATACTGTTTCATAAAGC  
GCTGCAGCTTTCTGGCGGGTGCCATCAGTGCAGTCCACGCCTGTCATACAGTGTAATAACCTGATTAAAGAGTCCGCT  
GTGAGTGGTCATGGCGGCGCTGTTCTGTCAAACGAATCCAGCAACACAGGCAGTATGCGCTGCTGATAATATGTGTCAG  
GAGTCGGCAGGGGAACGTCATTATAGGTCTGGCACTGGTGGGCAAAAAACGTTCTGAACAGGCCCGAGCCACTCGCGG  
ATAAGCGCACTTTTCGTATAGGGAGGGTGGGCCAGCACGCTTTACCCAGAAAAACCTATATTGACGTTGCCCCTTGCTT  
CGACTTCTGACCCAAATAATCAGCAGAGCAAAACGGTCGGGTGTTGTGTATTATCTTTTCATAGAGAAACACCTCTCTTT  
CTTACTTCAAGCTTTTCTATGTATTGTATTCTCTTCATCGAGGAGGGCTGAG

>24-sbon-3

CTAAGTCTGGGTCAAATGGTGGCAGACGCGACACTGAGGCATCATCAATCAACTTCACGGTGGAATGTTTCTGGTTCGTG  
GCGGCAATAAACTGCTGGTTCAGCTCCCCGTGCTCTTCAGTGCTGAGGATGATATCAATCAGCTCCCCAAAGCGTCGCTG  
CGTGGCCTGCTGATTAAATGCGGCGAGAAACACCGGAAAGTCATGACGGAATAACTCTACCGGAGAGATTTGCGCGGTGG  
AAACGTTCTCTCCGGCTCGCAGCAGGTAAAAGTTGTCCCATGCAGTGTGAGGAGTAGGGTTTAGCATTGTTAACAGCGTG  
TCAGTGGAGAGCATCATCGCCGTGTCTGAATCTTGGGAGGAAAGCAGCAGGAAATTATCTGCAGCGCGGGTTGTCCAGTC  
CGGGCTGCCGTCATAATTGCCGAAGAGCCCATTATGGATGTGGGGAGACACCGCCGGGTGAGCAAGATACTGTTTCATAAA  
GCGCTGCAGCTTTCTGGCGGGTGCCATCAGTGCAGTCCACGCCTGTCATACAGTGTAATAACCTGATTAAAGAGTCCG  
CTGTGATTAGTCATGGCGGCGCTGTTCTGTCAAACGAATCCAGCAACACAGGCAGTATGCGCTGCTGATAATATGTGTC  
AGGAGCCGGCAGGGGAACGTCATTATAGTTTTTGGCACTGGTGGGCAATAAAACGTTTCTGATCAGGTCCGTTCTCTTT  
CGCTGATAAGTGACTTTGTTGTATAC

>24-sbon-4

CCCAAATGGGTCAAATGGTGGCAGACGCGACACTGAGGCATCATCAATCAACTTCACGGTGGAATGTTTCTGGTTCGTG  
GCGGCAAGAAACTGCTGGTTCAGCTCCCCGTGCTCTTCAGTGCTGAGGATGATATCAATCAGCTCCCCAAAGCGTCGCTG  
CGTGGCCTGCTGATTAAATGCGGCGAGAAACACCGGAAAGTCATGACGGAATAACTCTACCGGAGAGATTTGCGCGGTGG

AAACGTTCTCTCCGGCTCGCAGCAGGTAAAAGTTGTCCCATGCAGTGTGAGGAGTAGGGTTTAGCATTGTTAACAGCGTG  
TCAGTGGAGAGCATCATCGCCGTGTCTGAATCCTGGGAGGAAAGCAGCAGGAAATTATCTGCAGCGCGGGTTGTCCAGTC  
CGGGCTGCCATCATAATTGCCGAAGAGCCCATTATGGATGTGGGGAGACACCGCCGGGTGAGCAAGATACTGTTTCATAAA  
GCGCTGCAGCTTTCTGGCGGGTGCCATCAGTGCAGTCCACGCCTGTCATACAGTGTAAAAATCACCTGATTAAAGAGTCCG  
CTGTGAGTGGTCATGGCGGCGCTGTTCCCTGTCAAACGAATCCAGCAACACAGGCAGTATGCGCTGCTGATAATATGTGTC  
AGGAGCCGGCAGGGGAACGTCATTATAGGTCTGGCACTGGTGGGCAAAAAAACGTTCCCTGAACAGGCCCCGAGCCACTC  
GCTGATTAAAGCGCACTTTGCGTATAGGGGGGGTGTGCCAGCAGCTTACCAGATTACAACCATTCTGCCGTGTACCTTG  
CTGGTTCCTTGTCCCAATTGTAACGCCTGGACACCGTTTGTTTACTCCTTTGCTCCCTGAAGTACAACCCCCCCCCGCCCT  
CTCCTTTCTAATTCTTTTCTCT

>24-sbon-5

AATGTCTTTAGTCAAATGGTGTTTCTGAGACGCGACACTGAGGCATCATCAATCAACTTCACGGTGAATGTTTCTGGGTCGT  
GGCGGCAATAAACTGCTGGTTCAGCTCCCCGTGCTCTTCAGCGCTGAGGATGATATCAATCAGTTCCCCAAAGCGTCGCT  
GCACGGCCTGCTGATTAAATGCGGCGAGAAACACCGGAAAGTCATGACGGAATAACTCTACCGGAGAGATTTGCGCGGTG  
GAAACGTTCTCTCCGGCTCGCAGCAGGTAAAAGTTGTCCCATGCAGTGTGAGGAGTAGGGTTTAGCATTGTTAACAGCGT  
GTCAGTGGAGAGCATCATCGCCGTGTCTGAATCCTGGGAGGAAAGCAGCAGGAAATTATCTGCAGCGCGGGTTGTCCAGT  
CCGGGCTGCCGTGATAATTGCCGAAGAGCCCATTATGGATGTGGGGAGACACCGTTGGGTGAGCAAGATATCGTTCATAA  
AGCGCTGCAGCTTTCTGGCGGGTGCCATCAGTGCAGCCACGCCTGTCATACAGTGTAAAAATCACCTGATTAAAGAGTCC  
GTTGTGAGTGGTCATGGCGGCGTTGTTCCCTGTCAAACGAATCCAGCAACACAGGCCGTATGCGCTGCTGATAATATGTGT  
CAGGAGCCGGCAGGGGAACGTCATTATAGGTCTGGCACTGGTGGGCAAAAAAACGTTCCCTGAACAGGCCCCGAACCAC  
TCGCTGATAAAGCGTACTTCTGCGGTATAGGGGGGGTTTCTGACCGCTTACCCAGAAAAAACTATTAATGGAGGGTTCT  
CCCCTTGCCGGTTTTCTGACCTATTTTAACCACATTCAATTACCGTTCTCTTTCTGTGTGATTCTTTATAGAACACAC

>24-sbon-6

GAAGTGGTATTCGTTCAAATGGTGGCAGACGCGACACTGAGGCATCATCAATCAACTTCACGGTGAATGTTTCTGGTTC  
GTGGCGGCAATAAACTGCTGGTTCAGCTCCCCGTTATCTTCAGTGTGAGGATGATATCAATCAGCTCCCCAAAGCGTCG  
CTGCGTGGCCTGCTGATTAAATGCGGCGAGAAACACCGGAAAGTCATGACGGAATAACTCTACTGGAGAGATTTGCGCGG  
TAGAAACGTTCTCTCCGGCTCGCAGCAGGTAAAAGTTGTCCCATGCAGTGTGAGGAGTAGGGTTTAGCATTGTTAACAGC  
GTGTGAGTGGAGAGCATCATCGCCGTGTCTGAATCCTGGGAGGAAAGCAGCAGGAAATTATCTGCGGCGCGGGTTGTCCA  
GTCCGGGCTGCCGTGATAATTGCCGAAGAGCCCATTATGGATGTGGGGAGACACCGCCGGGTGAGCAATATACTGTTTAT  
AATGCGCTGCAGCTTTCTGGGGGGTGCCATCAATGCAATACCACACCTGTTATTTTTTTTTTTTTTTTTTTTTTTTATTA

SBG(2)\_1F : TTT CTG GTT CGT GGC GGC AAT  
SBG(2)\_1R : TCT TCG GCA ATT ATG ACG GTA T  
SBG(2)\_2F : TTT CTG GTT CGT GGC GGC GAT  
SBG(2)\_2R : TTC CTG CTG CTT TCC TCC TAA  
SBG(2)\_4F : TTC TGG TTC GTG GCG GCG AG  
SBG(2)\_4R : ATG GGC TCT TCG GCA ATT ATA AT  
SBG(2)\_5F : TTC CCC AAA GCG TCG CTG TAC  
SBG(2)\_5R : GCT GCA GCG CTT TAT GAG CGA  
SBG(2)\_6F : GCT GGT TCA GCT CCC CAT TA  
SBG(2)\_6R : CGG ACT GGA CAA CCC GCT CC

The PCR amplification of 2<sup>nd</sup> time with the primer sets (11-, 12-, 13-, 14-, 15-, 16-, 18-, 19-, 21-Sbon) are as following:

11-Sbon, Gene Name: tRNA (Ile)-lysidine synthase (*mesI*)

---

|                  |                           |
|------------------|---------------------------|
| <b>11-Sbon-F</b> | <b>TTCTGGCCAGCGACCTTG</b> |
|------------------|---------------------------|

|                  |                           |
|------------------|---------------------------|
| <b>11-Sbon-R</b> | <b>TGCCAGTTTCAGCCACCC</b> |
|------------------|---------------------------|

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>11-Sbon-3

GGTGACGAGGATTGCGGCTTTTTCCTTTATTGTCCGATGAAGCGATGTACGGCGGGCGGCGATTGCGTCGCTGGCTGGC  
GATGCGTAATGCGCCGATGCTCTCTCGCGACGCGCTGGAACGTATCTGGCAGGAGGTGGCGCTGGCGCGCGACGATGCCT  
CTCCCTGTTTACGTTTTTGGCGATCGCGAGATTGCGCGTTATCAGTCGCAACTGTGGTGGATTAAATCCGTGGCCGGACAA  
CACGAAACGACGGTCGCCTGGCCCGTCTGGCAAACACCGCTGGCGCTGCCTGCCGGCTTAGGGACGGTACAGCTCGTTCC  
TGGCGGCGAACTGCGCCGACCGCGAGAGGAAGAATCCGTACGATTTCGGTTTAAGGCGCCAGGGTTGCTACACATTGTGG  
GACGTCACGGCGGACGTAAATTAAAGAAAATCTGGCAGGAGCAGGGGATCCCGCCCTGGCGACGAGACACCACGCCGCTG  
TTGTTTTACGGCGAAACGCTGATTGCGGCTGCGGGTGTTTTTGTGACGCGTGAGGGAGCAGCAGAAGATAAAGAAGGGGT  
GAGTCTGGTTTGGCATGCCTGATGGCGCTGCGCTTATCAGGCCTACGTATCGCATGGAACGTAGGCCGGATAAGGTGCTT  
GCACCACCATCCGGCAACAAAATACTCAGGATTCGCTAACTACCACGGTACCAATTTCCGGGTGGTGAAAACTGGGCAA

>11-Sbon-4

GGCTTTCGGAAGGATTGCGGCTCTCTCCTTTATGTCGATGAAGCGATGTACGGCGGGCGGCGATTTTTCGTCGCTTGGCT  
TGGCGATGCGTAATGCGCCGATGCCCTCTCGCGACGCGCTGGAACGTATCTGGCAGGAGGTGGCGCTGGCGCGCGACGAT  
GCCTCTCCCTGTTTACGCTTTGGCGATCACGAGATTGCGCGTTACAGTCGCAACTGTGGTGGATTAAATCCGTGGCCGG  
ACAACACGAAACGACGGTCGCCTGGCCCGTCTGGCAAACACCGCTGGCGCTGCCTGCCGGCTTAGGGACGGTACAGCTCG  
TTCCTGGTGGCGAACTGCGCCGACCGCGAGAGGAAGAATCCGTACGATTTCGTTTTAAAGCGCCAGGCGTGTTACATATT  
GTCGGGCGTAACGGTGGACGTAAATTAAAGAAAATCTGGCAGGAGCAGGGGATCCCGCCCTGGCGACGAGATACCACGCC  
GCTGTTGTTTTACGGCGAAACGCTGATTGCGGCTGCGGGTGTTTTTGTGACGCGTGAGGGAGCAGCAGAAGATAAAGAAG  
GGGTGAGTCTGGTTTGGCATGCCTGATGGCGCTGCGCTTATCAGGCCTACGTATCGCATGGAACGTAGGCCGGATAAGGT  
GCTTGCAACCACCATCCGGCAACAAAATACTCAGGATTCGCTAACTACCACGGTACCAATTTCCGGGTGCGAAAAACCTGG  
CCACGGCCGGATGTCCGGCATCCGATCCCATGCCACTTCGCCGATCACCGAACAGCATTCCATGCTCTTCCATCCATG  
CCTCATATTGTCGTGTACGTCCCCCATCCGCTTATTGCATTTTCTTACGATTACGTGGTACATGGCTATTTCTCTGCTGA  
CGATCAGTCTA

>11-Sbon-5

CTTTACGAGTAATTGCGGCATTACTTATGTCGACAGCGAGTGCGGCGGGCGGCGACTTGCGCGCTGGTTGGCGAGCGAAAG  
CGTCATCTTATCGCGAGCGCTGGAACGTACTGGCAGGAGGTGGCGCTGGCGCGCGAGATCCCTCTTGTTTACGTTTGGCG  
AGCACGAGAGTCGCGTTATCAGTCGCAATGTGGTGGATAAAACCGTACCGGACAACACGAAACGACGGTCGCCTGGCCCCG

TCTGGCAAACACCGCTGGCGCTGCTGCCGGTTAGGGACGGTACAGCTCGTTCCTGGCGGCGAATGCGCCGACCGCGAGAG  
GAAGATCCGTCAGCATTTCGGTTTAAAGCGCCGGGTTGCTACACATTGTGGGACGTCACGGCGGACGTAAATTAAAGAAAA  
TCTGGCAGGAGCAGGGGATCCCGCCCTGGCGACGAGACACCACGCCGCTGTTGTTTTACGGCGAACGCTGATTGCGGCTG  
CGGGTGTTTTTGTGACGCGTGAGGGAGCAGCAGAAGATAAAGAAGGGTGAGTCTGGTTTGGCATGCCTGATGGCGCTGCG  
CTTATCAGGCCTACGTATCGCATGGAACGTAGCCGGATAAGGTGCTTGCAACCACCATCCCGGCAACAAAATACTCAGGAT  
TCGCTAACTACCACGGTACCATTTCCGGTGGA AAAAATGGGAAA

>11-Sbon-6

CCGGATACGAGTAAGTGGCGCATTACTCAATGTCGATGAAGCGATGACGGCGGGCGCGTTTTGCGTCGTTGGTTGGCGAT  
GCGTAATGCGTCGACCTTACTCGCGACGCGCTGGAACGTATCTGGCAGGAGGTGGCGCTGGCGCGCGACGATCTTCTCTT  
GTTTACGTTTTTGGCGATCGCGAGAGTCGCCGTATCAGTCGAACTGTGGTGGATTAAATCCGTGGCCGGACAACACGAAAC  
GACGGTCGCTGGCCCGTCTGGCAAACACCGCTGGCGCTGCTGCCGGCTTAGGGACGGTACAGCTCGTCCTGGCGGCGAA  
CTGCGCCGACCGCGAGAGGAAAAATCCTCAGCATTTCGGTTAAAGCGCCGGCGTATTACATATTGTCGGGCGTAACGGGGAC  
GTAATTAAGAAATCTGGCAGGACAGGGGATCCCGCCCTGGCACAGTACCACGCCCTTTGTTTACGGCAACGCTATTGCGG  
CTGCGGTGTTTTGTGACGCGTGAGGGACACAAAATAGAAGGGTGATCTGGTTGCATGCCTGATGGCGCTGCGCTTATCAG  
CCTACTATCGCTGGACGAGCGGAAAGGTTGCCCCCTCCGGCACAAATACTCAGATCCTACTACCACGTCCTTTCCGTGAA

|           |     |     |     |     |     |     |     |     |     |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|           | 10  | 20  | 30  | 40  | 50  | 60  | 70  | 80  | 90  |
| 11-Sbon-3 | T   | G   | C   | G   | G   | C   | T   | T   | T   |
| 11-Sbon-4 | C   |     |     |     |     |     |     |     |     |
| 11-Sbon-5 | A   |     |     |     |     |     |     |     |     |
| 11-Sbon-6 |     |     |     |     |     |     |     |     |     |
|           | 100 | 110 | 120 | 130 | 140 | 150 | 160 | 170 | 180 |
| 11-Sbon-3 | C   | T   | C   | T   | C   | T   | C   | T   | C   |
| 11-Sbon-4 | C   |     |     |     |     |     |     |     |     |
| 11-Sbon-5 | T   | C   | T   | A   |     |     |     |     |     |
| 11-Sbon-6 |     |     |     |     |     |     |     |     |     |
|           | 190 | 200 | 210 | 220 | 230 | 240 | 250 | 260 | 270 |
| 11-Sbon-3 | A   | T   | T   | C   | G   | C   | C   | T   | T   |
| 11-Sbon-4 |     |     |     |     |     |     |     |     |     |
| 11-Sbon-5 | G   |     |     |     |     |     |     |     |     |
| 11-Sbon-6 |     |     |     |     |     |     |     |     |     |
|           | 280 | 290 | 300 | 310 | 320 | 330 | 340 | 350 | 360 |
| 11-Sbon-3 | C   | T   | G   | C   | C   | T   | G   | C   | C   |
| 11-Sbon-4 |     |     |     |     |     |     |     |     |     |
| 11-Sbon-5 |     |     |     |     |     |     |     |     |     |
| 11-Sbon-6 |     |     |     |     |     |     |     |     |     |
|           | 370 | 380 | 390 | 400 | 410 | 420 | 430 | 440 | 450 |
| 11-Sbon-3 | T   | T   | A   | A   | G   | G   | C   | C   | A   |
| 11-Sbon-4 |     |     |     |     |     |     |     |     |     |
| 11-Sbon-5 | A   |     |     |     |     |     |     |     |     |
| 11-Sbon-6 |     |     |     |     |     |     |     |     |     |
|           | 460 | 470 | 480 | 490 | 500 | 510 | 520 | 530 | 540 |
| 11-Sbon-3 | C   | G   | A   | C   | G   | A   | C   | A   | C   |
| 11-Sbon-4 |     |     |     |     |     |     |     |     |     |
| 11-Sbon-5 |     |     |     |     |     |     |     |     |     |
| 11-Sbon-6 |     |     |     |     |     |     |     |     |     |
|           | 550 | 560 | 570 | 580 | 590 | 600 | 610 | 620 | 630 |
| 11-Sbon-3 | A   | A   | G   | A   | A   | G   | G   | G   | T   |
| 11-Sbon-4 |     |     |     |     |     |     |     |     |     |
| 11-Sbon-5 |     |     |     |     |     |     |     |     |     |
| 11-Sbon-6 |     |     |     |     |     |     |     |     |     |
|           | 640 | 650 | 660 | 670 | 680 | 690 |     |     |     |
| 11-Sbon-3 | T   | G   | C   | A   | C   | A   | C   | A   | T   |
| 11-Sbon-4 |     |     |     |     |     |     |     |     |     |
| 11-Sbon-5 |     |     |     |     |     |     |     |     |     |
| 11-Sbon-6 |     |     |     |     |     |     |     |     |     |

The above alignment of gene, tRNA(Ile)-lysidine synthase (mesJ) did not produce all target sequences of Salmonella, where we did not find any suitable SNPs.

12-Sbon, Gene Name: methionine import ATP-binding protein (*metN*)

|           |                    |
|-----------|--------------------|
| 12-Sbon-F | ATTGGCACGCTGTCAGCT |
| 12-Sbon-R | TGCCGGTAAAAGCACGCT |

>12-Sbon-1

GATGCCTATAGCGCCTGGTATCTTCCGGATGTCCAGGTGCAGAGTGGACTGAATAAACTTCTGCGCCAGCGGCGTTTTAG  
GGTGCGAGAAGACTTCGCTGACCGTATCCTGCTCAATAAGCTCGCCATTACTGATGACGGCAACGCAGTCGCAGATACGT  
TTTACGACATCCATTTTCATGAGTGATAAGCAGAATCGTCAACCCAGACGACGGTTGATATCTTTCAGCAATTCAGAAT  
CGAACGGGTCGTTGCGGGATCAAGCGCGCTGGTGGCTTCATCGCACAGCAACACTTTTGGATTACTGGCTAACGCGCGGG  
CAATCGCGACACGCTGTTTCTGACCGCCGGAAGATTTGCCGGATAGCTGTCGTGCTTGTGCGCAAGACCGACTAAATCC  
AGCAGCTCTGTGACACGGCGTTTGATCTCTTCCTTTGGTGTGTTATCCAGTTCAGCGGCAACGCGACGTTGCCAAACAC  
GGTACGGGAAGAGAGCAGGTTAAAATGTTGGAAAATCATGCCGATTTGACGGCGAGCTTTGGTCAACTCAGACTCTGAAA  
GCGTTGTCAGCTCCTGACCGCCGACCTGAACGCTACCTTCGGTTGGGCGTTCAAGTAAGTTAACGCAGCGGATAAGCGTG  
TTTTTTACCCGCAAAAAATTTCCGGGGGTCAAGAACTCGCTCTGCTCCCCGCTTGGCCCGTTTTTCGTGGGATATAGTACC  
CAAAATGTCTTTGAGCAATGAAACACCTAACGCTAGATCCCGATTGACGTGTTGCATACTTGTACTTGCAGAGGTGGTC  
AACCGTCTCCTGGGGTGACTATCCTACTATTATTCATGCAGTGGAATGCCGTAGTTACTTACCTG

>12-Sbon-2

GAGGCTTACCGCGCTGGTATCTTCCGGATGTCCAGGTGCAGAGTGGACTGAATAAACTTCTGCGCCAGCGGCGTTTTAGG  
GTGCGAGAAGACTTCGCTGACCGTATCTTGCTCAATAAGCTCGCCATTACTGATAACGGCAACGCAGTCGCAGATACGTT  
TTACGACATCCATTTTCATGAGTGATAAGCAGAATCGTCAACCCAGACGACGGTTGATATCTTTCAGCAATTCAGAATC  
GAACGGGTCGTCGCGGGATCAAGCGCGCTGGTGGCTTCATCGCACAGCAACACTTTTGGATTACTGGCTAACGCGCGGGC  
AATCGCGACACGCTGTTTCTGACCGCCGGAAGATTTGCCGGATAGCTGTCGTGCTTGTGCGCAAGACCGACTAAATCCA  
GCAGCTCTGTGACACGGCGTTTGATCTCTTCCTTTGGTGTGTTATCCAGTTCAGCGGCAACGCGACGTTGCCAAACACG  
GTACGGGAAGAGAGCAGGTTAAAATGTTGGAAAATCATGCCGATTTGACGGCGAGCTTTGGTCAACTCAGACTCTGAAAG  
CGTTGTCAGCTCCTGACCGCCGACCTGAACGCTACCTTCGGTTGGACGTTCAAGTAAGTTAACGCAGCGGATAAGCGTGT  
TTTTACCCGGCA

>12-Sbon-3

GTGGCTTACGGCGCTGGTATCTTCCGGATGTCCAGATGCAGAGTGGACTGAATAAACTTCTGCGCCAGCGGCGTTTTAGG  
GTGCGAGAAGACTTCGCTGACCGTATCTTGCTCAATAAGCTCACCATTACTGATGACGGCAACGCAGTCGCAGATACGTT  
TTACGACATCCATTTTCATGAGTGATAAGCAGAATCGTCAACCCAGACGACGGTTGATATCTTTCAGCAATTCAGAATC  
GAACGGGTCGTCGCGGGATCAAGCGCGCTGGTGGCTTCATCGCACAGCAACACTTTTGGATTACTGGCTAACGCGCGGGC  
AATCGCGACACGCTGTTTCTGACCGCCGGAAGATTTGCCGGATAGCTGTCGTGCTTGTGCGCAAGACCGACTAAATCCA

GCAGCTCTGTGACACGGCGTTTGATCTCTTCCTTTGGTGTGTTATCCAGTTCAGCGGCAACGCGACGTTGCCAAACACG  
GTACGGGAAGAGAGCAGGTTAAAATGTTGGAAAATCATGCCGATTTGACGGCGAGCTTTGGTCAACTCAGACTCTGAAAG  
CGTTGTCAGCTCCTGACCGCCGACCTGAACGCTACCTTCGGTTGGGCGTTCAAGTAAGTTAACGCAGCGGATAAGCGTGC  
TTTTACCGGCAA

>12-Sbon-4

TATGCGCTACCGCGCTGGTATCTTCCGGATGTCCAGATGCAGAGTGGACTGAATAAACTTCTGCGCCAGCGGCGTTTTAG  
GATGCGAGAAGACTTCGCTGACCGTATCCTGCTCAATAAGCTCGCCATTACTGATAACGGCAACGCAGTCGCAGATACGT  
TTCACGACATCCATTTTCATGAGTGATAAGCAGAATCGTCAACCCAGACGACGGTTGATATCTTTCAGCAATTCCAAAAT  
CGAACGGGTCGTTGCGGGATCAAGCGCGCTGGTGGCTTCATCGCACAGCAACACTTTTGGATTACTGGCTAACGCGCGGG  
CAATCGCGACACGCTGTTTCTGACCGCCGGAAGATTTGCCGGATAGCTGTCGTGCTTGTGCGCAAGACCGACTAAATCC  
AGCAGCTCTGTGACACGGCGTTTGATCTCTTCCTTTGGTGTGTTATCCAGTTCAGCGGCAACGCGACGTTGCCAAACAC  
GGTACGGGAAGAGAGCAGGTTAAAATGTTGGAAAATCATGCCGATTTGACGGCGAGCTTTGGTCAACTCAGACTCTGAAA  
GCGTTGTTAGCTCCTGACCGCCGACCTGAACGCTACCTTCGGTTGGGCGTTCAAGTAAGTTAACGCAGCGGATAAGCGTG  
TTTTTTACCGGCAAATATTTCCGGGCGGTTATAATCTGCCGGTTCCCGTTGCCCGGTTTGGTGGCCGTTTTTTCTTCTAG  
TTTTTCTGTTGCGATGAAAACCCCTTGC

>12-Sbon-5

GAAGCATTCGCGCTGGTATCTTCCGGATGTCCAGATGCAGAGTGGACTGAATAAACTTCTGCGCCAGCGGCGTTTTAGG  
ATGCGAGAAGACTTCGCTGACCGTATCCTGCTCAATAAGCTCGCCATTACTGATGACGGCAACGCAGTCGCAGATACGTT  
TTACGACATCCATTTTCATGAGTGATAAGCAGAATCGTCAACCCAGACGACGGTTGATATCTTTCAGCAATTCCAGAATC  
GAACGGGTCGTCGCGGGATCAAGCGCGCTGGTGGCTTCATCGCACAGCAACACTTTTGGATTACTGGCTAACGCGCGGGC  
AATCGCGACACGCTGTTTCTGACCGCCGGAAGATTTGCCGGATAGCTGTCGTGCTTGTGCGCAAGACCGACTAAATCCA  
GCAGCTCTGTGACACGGCGTTTGATCTCTTCCTTTGGTGTGTTATCCAGTTCAGCGGCAACGCGACGTTGCCAAACACG  
GTACGGGAAGAGAGCAGGTTAAAATGTTGGAAAATCATGCCGATTTGACGGCGAGCTTTGGTCAACCCGGACTCTGAAAG  
CGTTGTCAGCTCCTGACCGCCTACCATACGCTTCCTTCAGTAGGACGTTCAAGTAAGTTTACGCAGCGAATGAGCGTGC  
TTTTTACCGGCAA

>12-Sbon-6

GAGGCTTTCACGCGCCTGGTATCTTCCGGATGTCCAGGTGCAGAGTGGACTGAATAAACTTCTGCGCCAGCGGCGTTTTAG  
GATGCGAGAAGACTTCGCTGACCGTATCCTGCTCAATAAGCTCGCCATTACTGATAACGGCAACGCAGTCGCAGATACGT  
TTCACGACATCCATTTTCATGAGTGATAAGCAGAATCGTCAACCCAGACGACGGTTGATATCTTTCAGCAATTCCAGAAT  
CGAACGGGTCGTCGCGGGATCAAGCGCGCTGGTGGCTTCATCGCACAGCAATACTTTTGGATTGCTGGCTAACGCGCGGG  
CAATCGCGACACGCTGTTTCTGACCGCCGGAAGATTTGCCGGATAGCTGTCGTGCTTGTGCGCAAGACCGACTAAATCC  
AGCAGTTCTGTGACACGGCGTTTGATCTCTTCCTTTGGTGTGTTATCCAGTTCAGCGGCAACGCGACGTTGCCAAACAC  
GGTACGGGAAGAGAGCAGGTTAAAATGTTGGAAAATCATGCCGATTTGACGGCGAGCTTTGGTCAACCCGGACTCTGAAA

GC GTTGT CAGCTCCTGACCGCCTACCATTACGCTTCCTTCAGTAGGACGTTCAAGTAAGTTTACGCAGCGAATGAGCGTG

TTTTTACCGGCAAA

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      10      20      30      40      50      60      70      80      90
12-Sbon-1  CCGCTGGTATCTTCCGGATGTCAGGTGCGAGTGGACTGAATAAACTTCTGCCAGCGGGCTTTTAGGGTGCAGAGACTTCGCTGA
12-Sbon-2  .....
12-Sbon-3  .....
12-Sbon-4  .....
12-Sbon-5  .....
12-Sbon-6  .....

      100     110     120     130     140     150     160     170     180
12-Sbon-1  CCGTATCCTGCTCAATAAGCTCGCCATTACTGATGACGGCAACGCGATCGCAGATACGTTTTACGACATCCATTTCATGATGATAAGCA
12-Sbon-2  .....T.....A.....
12-Sbon-3  .....T.....A.....
12-Sbon-4  .....A.....C.....
12-Sbon-5  .....
12-Sbon-6  .....A.....C.....

      190     200     210     220     230     240     250     260     270
12-Sbon-1  GAATCGTCAACCCCGACGACGGTTGATATCTTTCAGCAATTCAGAAATCGAACGGGTCTGTTGCGGGATCAAGCGCGCTGGTGGCTTCAT
12-Sbon-2  .....C.....
12-Sbon-3  .....C.....
12-Sbon-4  .....A.....
12-Sbon-5  .....C.....
12-Sbon-6  .....C.....

      280     290     300     310     320     330     340     350     360
12-Sbon-1  CGCACGCAACACTTTTGGATTACTGGCTAACGCGGGGCAATCGCGACCGCTGTTTCTGACCGCGGAAAGATTTGCCGGATAGCTGT
12-Sbon-2  .....
12-Sbon-3  .....
12-Sbon-4  .....
12-Sbon-5  .....
12-Sbon-6  .....T.....G.....

      370     380     390     400     410     420     430     440     450
12-Sbon-1  CGTGCTTGTCCCAAGACCGACTAAATCCAGCAGCTCTGTGACACGGCGTTTGATCTCTTCTTTGGTGTGTTATCCAGTTCCAGCGGCA
12-Sbon-2  .....
12-Sbon-3  .....
12-Sbon-4  .....
12-Sbon-5  .....
12-Sbon-6  .....T.....

      460     470     480     490     500     510     520     530     540
12-Sbon-1  ACGCGACGTTGCCAAACACGGTACGGGAAGAGAGCAGGTTAAATGTTGGAAATCATGCCGATTTGACGGCGAGCTTTGGTCAACTCAG
12-Sbon-2  .....
12-Sbon-3  .....
12-Sbon-4  .....
12-Sbon-5  .....C.G.
12-Sbon-6  .....C.G.

      550     560     570     580     590     600     610     620     630
12-Sbon-1  ACTCTGAAAGCGTTGTCAGCTCCTGACCGCGACCTGAAACGCTACCTTCGGTTGGGCGTTCAAGTAAGTTAAGCAGCGGATAGCGTGT
12-Sbon-2  .....A.....
12-Sbon-3  .....C.....
12-Sbon-4  .....T.....
12-Sbon-5  .....T...ATT...T...A..A..A...T...A..G...C
12-Sbon-6  .....T...ATT...T...A..A..A...T...A..G...-

      640
12-Sbon-1  TTTTACCGGCA
12-Sbon-2  ...AC..G...
12-Sbon-3  ...-..G...
12-Sbon-4  ...G...
12-Sbon-5  ...G...
12-Sbon-6  ...G...

```

The designed SNP-based primers are based on the above align gene (*metN*) sequences (natural SNP is marked by red color and artificial mutated bases are marked by yellow shaded)

metN\_F1: GACTTCGCTGACCGTA<sup>CC</sup>

metN\_R1: GCT GCG TTA ACT TAC TTG AAT<sup>T</sup> GC

metN\_F3: CCG TAT CTT GCT CAA TAA GC**C** CA  
metN\_R3: GCC CAA CCG AAG GTA GCG T  
metN\_F4: GGT TGA TAT CTT TCA GCA ATT C**T**A A  
metN\_R4: GGT CGG CGG TCA GGA G**T**T A  
metN\_F5: CGC ACA GCA ACA CTT TTG GAT TA  
metN\_R5: CCT ACT GAA GGA AGC GTA ATG **A**TA  
metN\_F6: CGC ACA GCA ATA CTT TTG GA**C** TG  
metN\_R6: CCT ACT GAA GGA AGC GTA ATG **A**TA

### 13-Sbon, Gene Name: Pyrimidine-specific ribonucleoside hydrolase (*rihB*)

|           |                    |
|-----------|--------------------|
| 13-Sbon-F | GCTGTACCTGCCGACTGG |
| 13-Sbon-R | GTTCCCCACGGGCTATGG |

>13-Sbon-1

GAGCGATAGTGTCTGGCAAGTAAATGCATTGCAGCATTAACGAAGAAAGGAAGTGATCTGGTTAACTGTAATGTAAAA  
AATGGGTAACGATACGGTTTTATCATGTTGTTGTGTTGTTAATTACGGTAAAGGTGTTATAGAAACAAAATGTAACATCT  
CTCTGGAACACCCAAACGGACAACAACATATGAATAAATCAGGGAAATACCTCGTCTGGACAGCGCTCTCAGTATTGGGTG  
CGTTTGCCCTGGGCTATATTGCGTTAAATCGTGGGGAACAGATCAACGCGCTATGGATCGTGGTGGCGTCGGTCTGTGTC  
TATCTTATTGCGTATCGTTTTTATGGGCTCTATATCGCCAAAAAAGTGCTGGCGGTTGACCCAACGCGTATGACGCCCGC  
GGTACGTCATAATGATGGTCTGGATTATGTCCGACCGATAAGAAAGTGCTTTTTGGTCACCATTTTGCGGCCATTGCTG  
GCGCAGGTCCGCTGGTCCGGCCGGTACTGGCGGCGCAGATGGGCTATCTGCCGGGGATGATCTGGCTGCTGGCGGGCGTC  
GTGCTGGCGGGAGCGGTGCAGGACTTTATGGTGTCTGTTGCTCTCGACCCGGCGCGATGGGCGTTCGCTTGCGGAGCTGGT  
TAAAGAGGAGATGGGCGCGACGGCAGGGGTGATCGCGTGGTGGCCTGCTTTATGATCATGGTGATCATTTCTGGCCGTCC  
TGGCGATGATCGTGGTGAAAGCGCTGACCCATAGCCGGGGGGGGGAAACAACAGCACCATAAAGTCCTGCACCGGCTGT  
CTTTCCCGCACGAAAAACACCCCGCCCCGGGCACATATAATAAATTAATGGCGCAAGATGCCACTTTCCTCTCCGGGTC  
CGGTCCGGACAGGAGGATATTTCTCCCCATTGGGCCCGCAAAAATGGTTAACAAAAAGAGCTATTTTCTTTAGTCGGG  
GGAGGTATATTTCATCACACTACCATTCTATATTTAACGGTAGCGGGCGCGTCAATACGGCGGTTTGGGCGTCCACCCCG  
TCTTGCTGTTTTTTTGGGCGATTTACAGCTCAATGAATACCGATCGCAATTATAAATGAACACAGCACCGACCTCCGCGA  
CGATTCTTAGTCGGCTGTGGATTTGTTTCCTCACGATTTACGGCATATAGTCTATGGGCTGATACGCCATCGAACGATGG  
CGCTTTTCCGAACCTAGGCTATTTTCGCTGTGAACTGTATGATCA

>13-Sbon-2

AACCCTTGGGTTATTTCTGGCAGTAAATGCAATTGCAGCATTAACGAAGAAAGGAAGTGATCTGGTTAACTGTAATGT  
AAAAAATGGGTAACAATCCGGTTTTATCATGTTGTTGTGTTGTTAATTACGGTAAAGGTGTTATAGAAACAAAATGTAAC  
ATCTCTCTGGAACACCCAAACGGACAACAACATATGAATAAATCAGGGAAATACCTCGTCTGGACAGCGCTCTCAGTATTG

GGTGCGTTTGGCCCTGGGCTATATTGCGTTAAATCGTGGGGAACAGATCAACGCGCTATGGATCGTGGTGGCGTCGGTCTG  
TGTCTATCTTATTGCGTATCGTTTTTATGGGCTCTATATCGCCAAAAAAGTGCTGGCGGTTGACCCAACGCGTATGACGC  
CCGCGGTACGTATAATGATGGTCTGGATTATGTCCCGACCGATAAAAAAGTGCTGTTTCGGTCACCATTTTGCGGCCATT  
GCTGGCGCAGGTCCGCTGGTCGGGCCGGTACTGGCGGCGCAGATGGGCTATCTGCCGGGGATGATCTGGCTGCTGGCGGG  
CGTCGTGCTGGCGGGAGCGGTGCAGGACTTTATGGTGTCTTCGTCTCGACCCGGCGCGATGGGCGTTTCGCTTGGCGAGC  
TGGTTAAAGAGGAGATGGGCGCGACGGCAGGGGTGATCGCGCTGGTGGCCTGCTTTATGATCATGGTGATCATTTCTGGCC  
GTCCTGGCGATGATCGTGGTGAAAGCGCTGACCCATAGCCGTGGGGGAACAAACAGCACCATAAAGTCCCTGCACCGGCT  
TCTCTCTCCACTGTCTT

>13-Sbon-6

GAGCCTTATTATTGTTCTGGCAAGTAAATGCAATTGCAGCATTAACGAAGAAAGGAAGTGATCTGGTTAACTACTGTAATG  
TAAAAAATGGGTAACAATCCGGTTTTATCATGTTGTTGTGTTGTTAATTACGGTAAAGGTGTTATAGAAACAAAATGTAA  
CATCTCTCTGGAACACCCAAACGGACAACAACCTATGAATAAATCAGGGAAATACCTCGTCTGGACAGCGCTCTCAGTATT  
GGGTGCGTTTGGCCCTGGGCTATATTGCGTTAAATCGTGGGGAACAGATCAACGCGCTATGGATCGTGGTGGCGTCGGTCT  
GTGTCTATCTTATTGCGTATCGTTTTTATGGGCTCTATATCGCCAAAAAAGTGCTGGCGGTTGACCCAACGCGTATGACG  
CCCGCGGTACGTATAATGATGGTCTGGATTATGTCCCGACCGATAAGAAAGTGCTTTTTTGGTCACCATTTTGCGGCCAT  
TGCTGGCGCAGGTCCGCTGGTCGGGCCGGTACTGGCGGCGCAGATGGGCTATCTGCCGGGGATGATCTGGCTGCTGGCGG  
GCGTTGTGCTGGCGGGAGCGGTGCAGGACTTTATGGTGTCTTCGTCTCGACCCGACGCGATGGGCGTTTCGCTTGGCGAG  
CTGGTTAAAGAGGAGATGGGCGCGACGGCAGGGGTGATCGCCCTGGTGGCCTGCTTTATGATCATGGTGATCATTTCTGGC  
CGTCCTGGCGATGATCGTGGTGAAAGCGCTGACCCATAGCCCGTGGGGGAAACACACAGCACCATAAAAGTCCTGCACCG  
CTTCTTCCCTCTAATATTATTCTTGCTTCTGTACCTTAAAAATATCTAACACGGTGTATGCTAATTCCCTCTCCCGTACGT  
CCAACCATATGAATTTTCCTCCCATTTGGCCCCAAATGGTTAACAAAAGCTCTTTTTTTTTTGTGGGGTGGTAAATCAAC  
CCAATCTATTAAATATTTACCGTAGCCGTGGTGACTCATAAGTCGGTGGGGTCCTCCTGCTTTTATTTTTTATGGTCTAA  
TTTGCATCCCCTTTTGTACTGAC

```

      10      20      30      40      50      60      70      80      90
13-Sbon-1  CTGGCAAGTAAATGCA TTGCAGCATTAACTAAAGAAAGGAGT GATCTGTTAAACACTGTAATGTAAAAAATGGGTAACTATACGGTTT
13-Sbon-2  .....A.....A.C.....
13-Sbon-6  .....A.....A.C.....

     100     110     120     130     140     150     160     170     180
13-Sbon-1  ATCATGTTGTTGTTGTTTAAATACGGTAAAGGTGTTATAGAAACAAATGTAAACATCTCTCTGGACACCCAAACGGAACAACACTATG
13-Sbon-2  .....
13-Sbon-6  .....

     190     200     210     220     230     240     250     260     270
13-Sbon-1  AATAAATCAGGGAAATACCTCTGCTGGACAGCGCTCTCAGTATTGGGTGGCTTGGCCTGGGCTATATTGGCTTAAATCTGGGGAAACAG
13-Sbon-2  .....
13-Sbon-6  .....

     280     290     300     310     320     330     340     350     360
13-Sbon-1  ATCAACGCGCTATGGATCTGTTGGCTCGGTCTGTGCTATCTTATTGGGTATCTTTTATGGGCTCTATATCGCCAAAAAGTGCTG
13-Sbon-2  .....
13-Sbon-6  .....

     370     380     390     400     410     420     430     440     450
13-Sbon-1  GCGGTTGACCCAAAGCGTATGACGCCCGCGGTACGTCTAATGATGGTCTGGATTATGTCGACCGGATAAGAAAGTGCTTTTGGTCAC
13-Sbon-2  .....A.....G..C.....
13-Sbon-6  .....

     460     470     480     490     500     510     520     530     540
13-Sbon-1  CATTTTGGGCCATTGCTGGCGCAGGTCCGGTGGTGGGGCCGGTACTGGGGCCAGATGGGCTATCTGCCGGGATGATCTGGCTGCTG
13-Sbon-2  .....
13-Sbon-6  .....

     550     560     570     580     590     600     610     620     630
13-Sbon-1  GCGGGCTGCTGCTGGCGGAGCGGTGCAGGACTTTATGGTGGCTGCTCGACCCGGCGGATGGGCGTTGCTTGGCAGCTGGTT
13-Sbon-2  .....
13-Sbon-6  .....T.....A.....

     640     650     660     670     680     690     700     710     720
13-Sbon-1  AAAAGAGAGATGGGCGCGACGGCAGGGGTGATCGGCTGGTGGCTGCTTTATGATCATGGTGATCAATCTGGCCGTCCTGGCGATGATC
13-Sbon-2  .....
13-Sbon-6  .....C.....

     730     740     750     760     770     780
13-Sbon-1  GTGGTAAAGCGCTGACCCATAGCGGGGGGGGAAACAAACAGCACCATAAAGTCC-TGCACCGG
13-Sbon-2  .....T.....C.....
13-Sbon-6  .....C.T.....C.....AGT.C.....

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The above alignment of gene(rihB) did not produce the all target sequences of Salmonella, where we did not find any suitable SNPs.

#### 14-Sbon, Pyrimidine-specific ribonucleoside hydrolase (rihA)

|           |                    |
|-----------|--------------------|
| 14-Sbon-F | TCCCCTGTGTTTCGACGC |
| 14-Sbon-R | ACGCCGATAAGACGCTG  |

>14-Sbon-1

```

CGGATGGAAAGGGTGCAATCTCGGGCTGGAGCAGCCAGGCGATGGTGCACGGGTCTGTGCAGCGGTGCGCCGACGAATCCC
CATTTTTCGTCTTTGTGGTACTCCATAAAGAAGTCCAGCAGTTCCGGCGACGATGGTGGAAATCGGGTTACCGATGGCGCG
AAAGCGTTCGATATCGGCGGCGTGAATCTGTGCCTTATGAGTGACGTCCAGCCCGGCCATCACCACCGGAATGCCTGACT
GGAAGACAATTTCTGCCGCTTCCGGGTCGACGTAAATATTAAATTCCGCAGCGGGCGTCCAGTTACCCAGCGCCATCGCG
CCGCCCATGATCACAATACGGGCGATTTTCGTATGCAGTTCGGATGGCTATTACAGCAGCAGCGCCACGTTGGTCTGTGG
GCCAGTGGAGACGATGGTGACCGGCTGTGAGCTCTCGCGCAGTGTTTTTGCATCAGCTCAACGGCAGTGCCGCTTTGCG

```

GGGCGAATGACGGCTCGGGCAGCGCCGGGCCGTCGAGGCCGCTTTCGCCGTGAACGTTATCGGGCGATAATCAGTTCGCGC  
ATGAGAGGTTTACCGCGCCGCCGCCACCGGAATATCCGGGCGTTTGAGCAGTGTGAGCATCCGCAGCACGTTGCGCAG  
CGTCTTATCCGGCGTATGGGGAATTTTCTTGATTGCTTACTTTTCTCTGTTTCTTACTTTTCGTGTAATTTTTTTTTTG  
TGATTTGATTTTTCGATTATTATGGAGGATCGCCTG

>14-Sbon-3

TTGGGCTTGCGGGGTAAATCTCGGGTTTCAGCAGCCAGGCGATGGTGCACGGGTCGTGCAGCGGCGGCCGACAAATCC  
CCATTTTTCGTCTTTGTGATACTCCATAAAGAAGTCCAGCAGTTCGGCGACGATGGTGAAATCGGGTTACCGATGGCGC  
GGAAACGCTCGATATCGGCGGCGTGAATCTGCGCCTTATGGGTGACGTCCAGCCCGGCCATCACCACCGGAATGCCTGAC  
TGGAAGACAATTTCTGCCGCTTCCGGGTGACGTAAATATTAATTGTTAATCCGCAGCGGGCGTCCAGTTCCCCAATCC  
CATTGCGCCGCCCATGATCACAATGCGCGCATTTTCGTGTCAGTCCGGTGGTATCGGTATCACACACGACACGCCACGTG  
GGCTGGGGCAGGAGGAGACGATGGTGACTTGGCTGTGAGCTCTCACGCAGTGTTTTTGCCATCAGCTCAACGGCAGTG  
CCGCTTTGCGGGGCGAATGACGGCTCGGGCAGCGCCGGGCCGTCGAGGCCGCTTTCGCCGTGAACGTTATCGGGCGATAAT  
CAGTTCGCGCATGAGAGGTTTACCGCACCGCCGCCACCGGAATATCCGGGCGTTTGAGCAGCGTCAGCATCCGCAGCA  
CGTTGCGCAGCGTCTATCCGGCGT

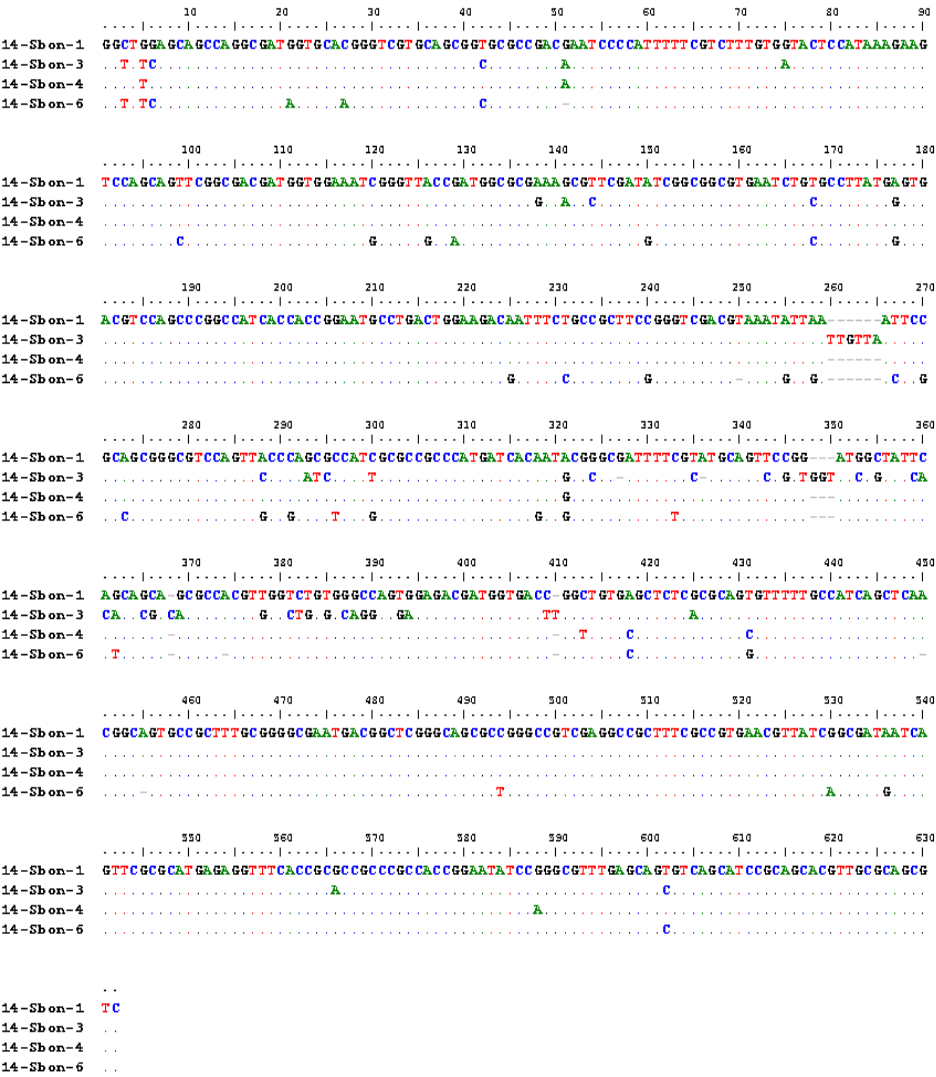
>14-Sbon-4

GGGGTATTTGAGCTGAAATCTCGGGCTTGAGCAGCCAGGCGATGGTGCACGGGTCGTGCAGCGGTGCGCCGACAAATCCC  
CATTTTTTCGTCTTTGTGGTACTCCATAAAGAAGTCCAGCAGTTCGGCGACGATGGTGAAATCGGGTTACCGATGGCGCG  
AAAGCGTTCGATATCGGCGGCGTGAATCTGTGCCTTATGAGTGACGTCCAGCCCGGCCATCACCACCGGAATGCCTGACT  
GGAAGACAATTTCTGCCGCTTCCGGGTGACGTAAATATTAATTTCCGCAGCGGGCGTCCAGTTACCCAGCGCCATCGCG  
CCGCCCATGATCACAATGCGGGCGATTTTCGTATGCAGTTCGGGATGGCTATTCAGCAGCAGCGCCACGTTGGTCTGTGG  
GCCAGTGAGACGATGGTGACCGGTTGTGCGCTCTCGCGCAGCGTTTTTGCCATCAGCTCAACGGCAGTGCCGCTTTGCG  
GGGCGAATGACGGCTCGGGCAGCGCCGGGCCGTCGAGGCCGCTTTCGCCGTGAACGTTATCGGGCGATAATCAGTTCGCGC  
ATGAGAGGTTTACCGCGCCGCCGCCACCGGAATATCCAGGCGTTTGAGCAGTGTGAGCATCCGCAGCACGTTGCGCAG  
CGTCTTTAATCACGGCGTA

>14-Sbon-6

GGCTTCGACGTGGTGAATCTCAGGTTTCAGCAGCCAGGCGATAGTGCAAGGGTCGTGCAGCGGCGGCCGACAAATCCCCA  
TTTTTCGTCTTTGTGGTACTCCATAAAGAAGTCCAGCAGCTCGGCGACGATGGTGAAATGGGGTTGCCAATGGCGCGAA  
AGCGTTCGATGTGCGCGGCGTGAATCTGCGCCTTATGGGTGACGTCCAGCCCGGCCATCACCACCGGAATGCCTGACTGG  
AAGACGATTTCCGCCGCTTCGGGGTCGACGAAATGTTGAACTCGGCCGCGGGCGTCCAGTTGCCGAGCGTCATGGCGCCG  
CCCATGATCACGATGCGGGCGATTTTTGTATGCAGTTCGGGATGGCTATTCATCAGCAGCGCCCGTTGGTCTGTGGGCCA  
GTGGAGACGATGGTGACCGGCTGTGCGCTCTCGCGCAGGGTTTTTGCCATCAGCTCACGGCGTGCCGCTTTGCGGGGCGA  
ATGACGGCTCGGGCAGCGCTGGGCCGTCGAGGCCGCTTTCGCCGTGAACGTTATCAGCGATGATCAGTTCGCGCATGAGA

GGTTTCACCGCGCCGCCGCCACCGGAATATCCGGGCGTTTGAGCAGCGTCAGCATCCGCAGCACGTTGCGCAGCGTCTT  
AAACCAAGCGTA



The above alignment of gene (rihA) did not produce the all target sequences of Salmonella, where we did not find any suitable SNPs.

15-Sbon, Gene Name: Molybdate-binding periplasmic protein (*modA*)

|           |                    |
|-----------|--------------------|
| 15-Sbon-F | GCGGGAAACTCCTGTGCT |
| 15-Sbon-R | CAACACCCGGCAGCAAAC |

>15-Sbon-1

AAACTGTAAGCGTCGTATCATACCGGTACGCGTTCCGCCAGTGGCAGCCCCGTCTGGTGTGGAGTTGCCTGGCATTATA  
TGTCGTTTTTCTTACCGCGCTGGAGCTCAGGCAAGAGTTATGGGGACTGGTGTGGTGGCGGCTGGGTTTATTGTGCTGG

CGCGCAGGGTGATAGTCAGCGTGGACTGGACGCTGCTGCTGGTATTTATGGCGATGTTTATTGATGTCCATCTGCTAACG  
CAATTGCCGGCGTTGCAGGGCGTTTTCAACCAGGTTGGCGCACTGTCTCACCTGGGGCTTTGGCTAACCGCTATCGGCCCT  
GTCGCAGGTTATCAGTAATGTGCCCAGTACCATTCTCCTGCTGAACTATGTACCGGCCTCGACGTTGCTGGCGTGGGCGG  
TGAATATCGGCGGGTTTGGTTTGCTGCCGGGTGTT

>15-Sbon-2

ATCAAATGTAGGGCGTTCGTATCATACCGGTACGCGTTCGCCGCAGTGGCAGCCCCGTCTGGTGTGGAGTTGCCTGGCAT  
TATATGTCGTTTTTCTTACCGCGCTGGAGCTCAGGCAAGAGTTATGGGGACTGGTGTGGTGGCGGCTGGGTTTATTGTG  
CTGGCGCGCAGGGTGATAGTCAGCGTGGACTGGACGCTGCTGCTGGTATTTATGGCGATGTTTATTGATGTCCATCTGCT  
AACGCAATTGCCGGCGTTGCAGGGCGTTTTCAACCAGGTTGGCGCACTGTCTCACCTGGGGCTTTGGCTAACCGCTATCG  
GCCTGTGCGCAGGTTATCAGTAATGTGCCCAGTACCATTCTCCTGCTGAACTATGTACCGGCCTCGACGTTGCTGGCGTGG  
GCGGTGAATATCGGCGGGTTTGGTTTGCTGCCGGATGTTGAAGACTACTGAACATCATCGCAATGCTTTTAGCTGCCGGG  
TGTTTTGTTTTTTTTTTTTTACTGTTAATACGGTGTGGGGGGGTGTGTTCAAATCCCCCCCCCCCCACATATAAAAC  
TTTT

>15-Sbon-3

ATAGCATAGTAGGCGTTAGTATCATACCGGTACGCGTTCGCCGCAGTGGCAGCCCCGTCTGGTGTGGAGTTGCCTGGCAT  
TATATGTCGTTTTTCTTACCGCGCTGGAACTCAGGCAAGAGTTATGGGGATTGGTGTGGTGGCGGCTGGGTTTATTGTG  
CTGGCGCGCAGGGTGATAGTCAGCGTGGACTGGACGCTGCTGCTGGTATTTATGGCGATGTTTATTGATGTCCATCTGCT  
AACGCAATTGCCGGCGTTGCAGGGCGTTTTCAACCAGGTTGGCGCACTGTCTCACCTGGGACTTTGGCTAACCGCTATCG  
GCCTGTGCGCAGGTTATCAGTAATGTGCCCAGTACCATTCTCCTGCTGAACTATGTACCGGCCTCGACGCTGCTGGCGTGG  
GCGGTGAATATCGGCGGGTTTGGTTTGCTCCCGGTGTTGAAGAAATCGGATGTGGTTGAATTCAGTCAATTTGGTGTATT  
TTTTTTTTTTTTTTTTTTTTCCCGGTATTAGTTGTGGGGGTGTGTTGTTTATCTCCCCCCTCCTAGAGTTTTTTTTT

>15-Sbon-4

GGTCTCCCTAGGGCGTTCAGTATCATACCGGTACGCGTTCGCCGCAGTGGCAGCCCCGTCTGGTGTGGAGTTGCCTGGCA  
TTATATGTCGTTTTTCTTACCGCGCTGGAGCTCAGGCAAGAGTTATGGGGACTGGTGTGGTGGCGGCTGGGTTTATTGT  
GCTGGCGCGCAGGGTGATAGTCAGCGTGGACTGGACGCTGCTGCTGGTATTTATGGCGATGTTTATTGATGTCCATCTGC  
TAACGCAATTGCCGGCGTTGCAGGGCGTTTTCAACCAGGTTGGCGCACTGTCTCACCTGGGGCTTTGGCTAACCGCTATC  
GGCCTGTGCGCAGATTATCAGTAATGTGCCCAGTACCATTCTCCTGCTGAACTATGTACCGGCCTCGACGCTGCTGGCGTG  
GGCGGTGAATATCGGCGGGTTTGGTTTGCTGCCGGGTGTTGAAGAACTCCCGCACGACGCTCTGATTGCCACAATTTGTG  
AGTTTTTTTGTTTTTTTTTTTTTTAAATCTTTTGAATGGTTGGGGGGGGTGTGTTCTCCCCCCCCCTGTATACTTTTT  
TTTT

>15-Sbon-5

GAAGCGGCTAAGGCGTTCGTATCATACCGGTACGCGTTCGCCGCAGTGGCAGCCCCGTCTGGTGTGGAGTTGCCTGGCAT

>15-Sbon-6

10 20 30 40 50 60 70 80 90

15-Sben-1 G T A T C A T A C C G G T A C G C G T T C G C C G C A G T G G C A G C C C C G T C T G G T G T G A G T T G C C T G G C A T T A T A T G T C G T T T T T C T T A C C G C G C T G G A

15-Sben-2

15-Sben-3

15-Sben-4

15-Sben-5

15-Sben-6

100 110 120 130 140 150 160 170 180

15-Sben-1 G C T C A G G C A A G A G T T A T G G G G A C T G G T G T T G G T G G C G G G T G G G T T T A T T G T G C T G G C C G C G A G G G T G A T A G T C A G C G T G G A C T G G A C G C T

15-Sben-2

15-Sben-3 A . . . . . T . . . . .

15-Sben-4

15-Sben-5

15-Sben-6

190 200 210 220 230 240 250 260 270

15-Sben-1 G C T G C T G G T A T T T A T G G C G A T G T T T A T T G A T G T C C A T C T G C T A A C G C A A T T G C C G G C G T T G C A G G G C G T T T T C A A C C A G G T T G G C G C A C T

15-Sben-2

15-Sben-3

15-Sben-4

15-Sben-5

15-Sben-6

280 290 300 310 320 330 340 350 360

15-Sben-1 G T C T C A C C T G G G G C T T T G G C T A A C C G C T A T C G G C C T G T C G C A G G T T A T C A G T A A T G T G C C C A G T A C C A T T C T C C T G C T G A A C T A T G T A C C

15-Sben-2

15-Sben-3 . A . . . . .

15-Sben-4 . . . . . A . . . . .

15-Sben-5 . . . . . A . . . . .

15-Sben-6

370 380 390 400 410 420

15-Sben-1 G G C C T C G A C G T T G C T G G C G T G G G C G G T G A A T A T C G G C G G G T T T G G T T T G C T G C C G G G T G T T

15-Sben-2

15-Sben-3 . . . . . C . . . . . C . . . . .

15-Sben-4 . . . . . C . . . . . G . . . . .

15-Sben-5 . . . . . C . . . . . G . . . . .

15-Sben-6

16-Sbon, Gene Name: Molybdate-binding periplasmic protein (*modA*)

|                  |                           |
|------------------|---------------------------|
| <b>16-Sbon-F</b> | <b>ACGGTCTGGGTGAGGTGT</b> |
| <b>16-Sbon-R</b> | <b>CCACCGCATCAGAACCGT</b> |

>16-Sbon-1

TCAAAACGGTTCGGGTCAGAGACAGTCCAGACAGAACCGCTGATTTCCCCAAACGCCCGCTCAGTCGGGCGTTTTTGTTA  
CTCAAGATCCTGCTTTTCCTGCCGATATTTTCTGTGTTTAATCGTTAATGGGTATGAATAACCGCTGGGAAACCCCTGAG  
ATTATCGTTATATTGTCGTTTACATAACGAAACACACAAGGAGTTACAGATGGCGCATTCCTGGTTACGCCTGGTCGCAG  
GGGCGACATTATCTTTTCGTCATCGCTGGTCATGCGCTGGCGGATGAAGGCAAGATCACCGTATTTGCCGCCGCGTCGCTA  
ACGAACGCGATGCAAGACATTGCGGCAGAATATAAAAAAGAGAAAAATGTGGATGTGGTCTCCTCATTCGCCTCCTCTTC  
AACGCTGGCGCGCCAGATAGAAGCGGGCGCGCCGGCGGATCTGTTTCATCTCTGCTGACCAGAAATGGATGGATTACGCAG  
CCGATAAAAAAGCGGTGGATACCACGACGCGCGAAACATTGCTTGGCAATCGCCTGGTGGTGGTGGCGCCGAAAGCCAGC  
GAGCAGAAACCGTTTACCATCGACAACAAAACGGACTGGATTCTGCTCTGCTGAACGGCGGACGCTCTGGCAGTGGGCGATCC  
GCAACACGTACCGGCGGGAATTTATGCCAAAGAAGCGCTGCAAAGCTGGGCGCATGGCATACGCTTGAACCGAAACTGG  
CGCCGGGCGAGGATGTGCGCGGCGCGTTGTGCTGGTCGAACGTAACGAAGCGTCTTTGGGCAT

>16-Sbon-2

CCATACGGGTCGGTCAGAGACAGTCCAGACAGAACCGCTGATTTCCCCAAACGCCCGCTCAGTCGGGCGTTTTTGTACT  
CAAGATCCTGCTTTTCCTGCCGATATTTTCTGTGTTTAATCGTTAATGGGTATGAATAACCGCTGGGAAACCCCTGAGAT  
TATCGTTATATTGTCGCTTACATAACGAAACACACAAGGAGTTACAGATGGCGCATTCCTGGTTACGCCTGGTCGCAGGG  
GCAACATTATCTTTTCGTCATCGCCGGTCATGCGCTGGCGGATGAAGGCAAGATCACCGTATTTGCCGCCGCGTCGCTAAC  
GAACGCGATGCAAGACATTGCGGCAGAATATAAAAAAGAGAAAAATGTGGATGTGGTCTCCTCATTCGCCTCCTCTTCAA  
CGCTGGCGCGCCAGATAGAAGCGGGCGCGCCGGCGGACCTGTTTCATCTCTGCTGATCAGAAATGGATGGATTACGCAGCC  
GATAAAAAAGCGGTGGATACCACGACGCGCGAAACATTGCTTGGCAATAGCCTGGTGGTGGTGGCGCCGAAAGCCAGCGA  
GCAGAAACCGTTTACCATCGACAACAAAACGGACTGGATTCTGCTCTGTTGAACGGCGGGCGTCTGGCAGTGGGCGATCCGC  
AACACGTACCGGCGGGAATTTATGCCAAAGAAGCGCTGCAAAGCTGGGCGCATGGCAAACGCTTGAACCGAAACTGGCG  
CCGGGCGAGGATGTGCGCGGCGCGTTGGCGCTGGTCGAACGTAACGAAGCGCCTTTGGGCATTGTATACGGTTCGATAGG  
CCGGGTGGGAA

>16-Sbon-3

CAAATTGGTACGGTCAGAAGACCAGTCCAGACAGAACCGCTGATTTCCCCAAACGCCCGCTCAGTCGGGCGTTTTTGTTA  
CTCAAGATCCTGCTTTTCCTGCCGATATTTTCTGTGTTTAATCGTTAATGGGTATGAATAACCGCTGGGAAACCCCTGAG  
ATTATCGTTATATTATCGTTTACATAACGAAACGCACAAGGAGTTACAGATGGCGCATTCCTGGTTACGCCTGGTCGCAG  
GGGCGACATTATCTTTCATCATCGCTGGTCATGCGCTGGCGGATGAAGGCAAGATCACCGTATTCGCCGCCGCGTCGCTA  
ACGAACGCGATGCAAGACATTGCGGCAGAATATAAAAAAGAGAAAAATGTGGATGTGGTTTCCTCATTCGCCTCCTCTTC

AACGCTGGCGGCCAGATAGAAGCGGGCGCGCCGGCGGATCTGTTTCATCTCTGCTGACCAGAAATGGATGGATTACGCAG  
CCGATAAAAAAGCGGTGGATACCACGACGCGCGAAACATTGCTTGGCAATAGCCTGGTGGTGGTGGCGCCGAAAGCCAGC  
GAGCAGAAACCGTTTACCATCGATAACAAAACGGACTGGATTCTGCTGCTGAACGGCGGGCGTCTGGCGGTGGGCGATCC  
GCAACACGTACCGGCGGGAATTTATGCCAAAGAAGCGCTGCAAAAGTTGGGCGCATGGCAAACGCTTGAACCGAAACTGG  
CGCCGGGCGAGGATGTGCGCGGCGCGTTGGCGCTGGTGAACGTAACGAAGCGCCTTTGGGCATTGTATACGGTTCGAAA  
>16-Sbon-4

CAATTATAGTACGGTCAGAAGACAGTCCAGACAGAACCGCTGATTTCCCCAAACGCCCGCTCAGTCGGGCGTTTTTGTTA  
CTCAAGATCCTGCTTTTCCTGCCGATATTTTCTGTGTTTAATCGTTAATGGGTATGAATAACCGCTGGGAAACCCCTGAG  
ATTATCGTTATATTATCGTTTACATAACGAAACGCACAAGGAGTTACAGATGGCGCATTCCTGGTTACGCCTGGTTCGCAG  
GGGCAACATTATCTTTTCGTCATCGCCGGTCATGCGCTGGCGGATGAAGGCAAGATCACCGTATTTGCCGCCGCGTCGCTA  
ACGAACGCGATGCAAGACATTGCGGCAGAATATAAAAAAGAGAAAAATGTGGATGTGGTCTCCTCATTCGCCTCCTCTTC  
AACGCTGGTGCGCCAGATAGAAGCGGGCGCGCCGGCGGATCTCTTCATCTCTGCTGATCAGAAATGGATGGATTACGCAG  
CCGATAAAAAAGCGGTGGATACCACGACGCGCGAAACATTGCTTGGCAATAGCCTGGTGGTGGTAGCGCCGAAAGCCAGC  
GAGCAGAAACCGTTTACCATCGACAACAAAACGGACTGGATTCTGCTGCTGAACGGCGGACGTCTGGCGGTGGGCGATCC  
GCAACACGTACCGGCGGGAATTTATGCCAAAGAAGCGCTGCAAAAGTTGGGCGCATGGCAAACGCTTGAACCGAAACTGG  
CGCCGGGCGAGGATGTGCGCGGCGCGTTGGCGCTGGTGAACGTAACGAAGCGCCTTTGGGGCATTGTATACGGTTCTAA  
TAGGCGGGGGGGGAAA

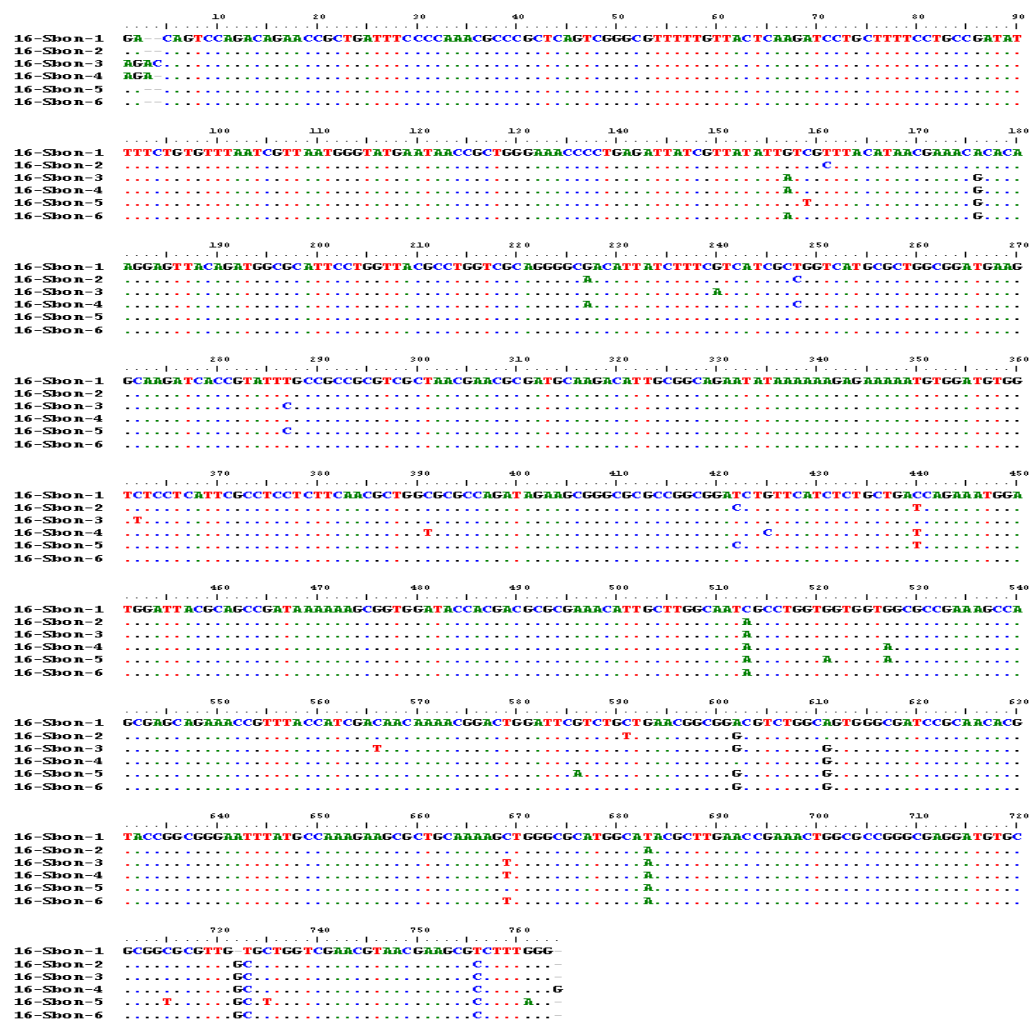
>16-Sbon-5

CCCTTAAAGGGTTCGGGTCAGAGACAGTCCAGACAGAACCGCTGATTTCCCCAAACGCCCGCTCAGTCGGGCGTTTTTGT  
TACTCAAGATCCTGCTTTTCCTGCCGATATTTTCTGTGTTTAATCGTTAATGGGTATGAATAACCGCTGGGAAACCCCTG  
AGATTATCGTTATATTGTGTTTACATAACGAAACGCACAAGGAGTTACAGATGGCGCATTCCTGGTTACGCCTGGTTCGC  
AGGGGCGACATTATCTTTTCGTCATCGCTGGTCATGCGCTGGCGGATGAAGGCAAGATCACCGTATTCGCCGCCGCGTCGC  
TAACGAACGCGATGCAAGACATTGCGGCAGAATATAAAAAAGAGAAAAATGTGGATGTGGTCTCCTCATTCGCCTCCTCT  
TCAACGCTGGCGGCCAGATAGAAGCGGGCGCGCCGGCGGACCTGTTTCATCTCTGCTGATCAGAAATGGATGGATTACGC  
AGCCGATAAAAAAGCGGTGGATACCACGACGCGCGAAACATTGCTTGGCAATAGCCTGGTAGTGGTAGCGCCGAAAGCCA  
GCGAGCAGAAACCGTTTACCATCGACAACAAAACGGACTGGATTCTGCTGCTGAACGGCGGGCGTCTGGCGGTGGGCGAT  
CCGCAACACGTACCGGCGGGAATTTATGCCAAAGAAGCGCTGCAAAAGCTGGGCGCATGGCAAACGCTTGAACCGAAACT  
GGCGCCGGGCGAGGATGTGCGCGGTGCGTTGGCGTTGGTGAACGTAACGAAGCGCCTTTAGGCATTGTATACGGTTCGA  
AAGGCCGGGTGAG

>16-Sbon-6

CCAAATTAGGGTCGGTCAGAGACAGTCCAGACAGAACCGCTGATTTCCCCAAACGCCCGCTCAGTCGGGCGTTTTTGTTA  
CTCAAGATCCTGCTTTTCCTGCCGATATTTTCTGTGTTTAATCGTTAATGGGTATGAATAACCGCTGGGAAACCCCTGAG

ATTATCGTTATATTATCGTTTACATAACGAAACGCACAAGGAGTTACAGATGGCGCATTCCTGGTTACGCCTGGTCGCAG  
GGGCGACATTATCTTTTCGTCATCGCTGGTCATGCGCTGGCGGATGAAGGCAAGATCACCGTATTTGCCGCCGCGTCGCTA  
ACGAACGCGATGCAAGACATTGCGGCAGAATATAAAAAAGAGAAAAATGTGGATGTGGTCTCCTCATTCGCCTCCTCTTC  
AACGCTGGCGCGCCAGATAGAAGCGGGCGCGCCGGCGGATCTGTTTCATCTCTGCTGACCAGAAATGGATGGATTACGCAG  
CCGATAAAAAAGCGGTGGATACCACGACGCGCGAAACATTGCTTGGCAATAGCCTGGTGGTGGTGGCGCCGAAAGCCAGC  
GAGCAGAAACCGTTTACCATCGACAACAAAACGGACTGGATTTCGTCTGCTGAACGGCGGGCGTCTGGCGGTGGGCGATCC  
GCAACACGTACCGGCGGAATTTATGCCAAAGAAGCGCTGCAAAAGTTGGGCGCATGGCAAACGCTTGAACCGAAACTGG  
CGCCGGGCGAGGATGTGCGCGGCGCGTTGGCGCTGGTCGAACGTAACGAAGCGCCTTTGGGCATTGTATACGGTTCTAAA  
TGGGCGGGTGAGA



The designed SNP-based primers are based on the above align gene (*modA*) sequences (natural SNP is marked by red color and artificial mutated bases are marked by yellow shaded)

ModA-1-F: ACC CCT GAG ATT ATC GTT ATA **CTG**

ModA-1-R: ATC GCC CAC TGC CAG **ATG** T

ModA-2-F: CTG AGA TTA TCG TTA TAT TGT **CGC**

ModA-2-R: CCA GAC GCC CGC CGT **TTA** **A**

ModA-3-F: TCG CAG GGG CGA CAT TAT CTT **CCA**

ModA-3-R: AGA CGA ATC CAG TCC GTT TTG **CTA**

ModA-4-F: TTA CGC CTG GTC GCA GGG **ACA**

ModA-4-R: CAT TTC TGA TCA GCA GAG ATG **GAG**

ModA-5-F: CCT GAG ATT ATC GTT ATA TTA **TT**

ModA-5-R: ACG CCC GCC GTT CAG CAA **AT**

## 18-Sbon, Gene Name: Formimidoylglutamase (*hutG*)

|                  |                           |
|------------------|---------------------------|
| <b>18-Sbon-F</b> | <b>GCATCTGGATCTGCGCCA</b> |
| <b>18-Sbon-R</b> | <b>TCGGCGACAAAGGTTCCC</b> |

>18-Sbon-1

AAAGCGTAACCGAGCTAGCGTGTCTCACTGCCGCAGCTATGCGACGCGCAGAGCCGCGCGTTACATTATGCCTGGTTTCG  
GCGTGAGCCCGTGCGGCGAATACGCAGGCGTTGTGGCGGGAAGCGCAGTGGCGGAATGTTACCGTGGTGGAGGATCTGGAC  
TGCCATGACGCGCTGGCGCAATATGACGCACATTATCGACAAGGTGGATAAAATTTATCTGACTATCGATCTCGACGTAT  
TGCCTGTCTGGGAAATGCCGGCCGTCTCCGCTCCCGCAGCGCTGGGCGTGCCGCTGATACAGGTTCTGCGTTTAATTGAG  
CCGGTTTGCCGCAGCGGAAAATTACAGGCGGCGGATCTGGTTGAATTTAATCCACGCTTTGATGAAGATGGCGCAGCGGC  
GCGCGTGGCGGCGCGGCTTGGCTGGCAAATCGCGCACTGGTGGCGTTAATCTGTTCATCCGAAAAACATTATCCGCATAAG  
GAAGGCTTCACGCATGTATTTCATCCCGCTCCCGTTCTGCACCTGCGCCTTTTACGAAACGGTGAAACAGGACATCTGTA  
AAAAAATAGCCGGCGGCGTCTGGCAGCCGCACGATCGCATTCGTCGGAAGCAGAACTGGTCGCCCAGTATGGCTTTAGC  
CGAATGACCATCAATCGGGCGCTGCGTGAGCTGACGGATGAAGGGTGGCTGGTGCCTTTACAGGGCGTGGGAACCTTTTTT  
CCCCCGA

>18-Sbon-2

ATGCCCATCGAGCTAGCGACGTCTCACTGCGCGCACTCTATGCGACGCGCAGAGCGCGCGGCGTTACTTTATGCCTGGT  
TCGGCGCGAGCCGTGCGGCGAATACGCAGGCGTTGTGGCGGGAAGCGCAGTGGCGGAATGTTACCGTGGTGGAGGATCTT  
GACTGCCATGACGCGCTGGCGCAAATGACATGCATTATCGACAAGGTGGATAAAATTTATCTGACTATCGATCTCGACGT  
ATTGCCTGTCTGGGAAATGCCGGCCGTCTCCGCTCCCGCAGCGCTGGGCGTGCCGCTGATACAGGTTCTGCGTTTAATTG  
AGCCGGTTTGCCGCAGCGGAAAATTACAGGCGGCGGATCTGGTTGAGTTAATCCACGCTTTGATGAAGATGGCGCAGCG  
GCGCGCTGGCGGCGCGGCTTGGCTGGCAAATCGCGCACTGGTGGCGTTAATCTGTTCATCCGAAAAACACTCTCCGCATA

AGGAAGGCTTCACGCATGTATTCATCCCGCTCCCGTTCTGCACCTGCGCCTTTTTACGAAACGGTGAAACAGGACATCTG  
TAAAAAATAGCCGGCGCGTCTGGCAGCCGCACGATCGCATTCCTCGGAAGCTGAACTGGTCGCTCAGTATGGCTTTA  
GCCGAATGACCATCAACCGGGCGCTGCGTGAGCTGACGGATGAAGGGTGGCTGGTGCCTTTACAGGGCGTGGGAACCTTT  
GGTCGCCGAA

>18-Sbon-3

GTGCCCATCGAGCTAGCGTTTCGTCACTGGCGCAGCTATGCGACGCGCAGAGCCGCGCGTTTCATTATGCCTGTTTCGGC  
GTGAGCCGTGCGGCGAATACGCAGGCGTTGTGGCGGGAAGCGCAGTGGCGGAATGTTACCGTGGTGGAGGATCTGGACTG  
CCATGACGCGCTGGCGCAAATGGCGCAATTATCGACAAGGTGGATAAAAATTTATCTGACTATCGATCTCGACGTATTGCC  
TGTCTGGGAAATGCCGGCCGTCTCCGCTCCCGCAGCGCTGGGCGTGCCGCTGATACAGGTTCTGCGTTTAATTGAGCCGG  
TTTGCCGCAGCGGAAAATTACAGGCGGCGGATCTGGTTGAGTTTAATCCACGCTTTGATGACGATGGCGCAGCGGCGCGC  
GTGGCGGCGCGGCTTGGCTGGCAAATCGCGCACTGGTGGCGTTAATCTGTCATCCGGAACACTATCCGCATAAGGAAG  
GCTTCACGCATGTATTCATCCCGCTCCCGTTCTGCGCCTGCGCCTTTTTACGAAACGGTGAAACAGGACATCTGTAAAAA  
AATAGCCGGCGGCGTCTGGCAGCCGCACGATCGCATTCCTCGGAAGCTGAACTGGTCGCCCAGTATGGCTTTAGCCGAA  
TGACCATCAACCGGGCGCTGCGTGAGCTGACGGATGAAGGGTGGCTGGTGCCTTTACAGGGCGTGGGAACCTTT

>18-Sbon-4

TGCCCATTTCAGCTAGCGTTTCGTCACTGGCGCAGTCTATGCGACGCGCAGAGCCGCGCGTTTCATTATGCCTGTTTCGG  
CGTGAGCCGTGCGGCGAATACGCAGGCGTTGTGGCGGGAAGCGCAGTGGCGGAATGTTACCGTGGTGGAGGATCTGGACT  
GCCATGACGCGCTGGCGCAAATGGCGCAATTATCGACAAGGTGGATAAAAATTTATCTGACTATCGATCTCGACGTATTGC  
CTGTCTGGGAAATGCCGGCCGTCTCCGCTCCCGCAGCGCTGGGCGTGCCGCTGATACAGGTTCTGCGTTTAATTGAGCCG  
GTTTGCCGCAGCGGAAAATTACAGGCGGCGGATCTGGTTGAGTTTAATCCACGCTTTGATGAAGATGGCGCAGCGGCGCG  
CGTGGCGGCGCGGCTTGGCTGGCAAATCGCGCACTGGTGGCGTTAATCTGTCATCCGGAACATTATCCGCATAAGGAA  
GGCTTCACGCATGTATTCATCCCGCTCCCGTTCTGCACCTGCGCCTTTTTACGAAACGGTGAAACAGGACATCTGTAAAA  
AAATAGCCGGCGGCGTCTGGCAGCCGCACGATCGCATTCCTCGGAAGCAGAACTGGTCGCCCAGTATGGCTTTAGCCGA  
ATGACCATCAATCGGGCGCTGCGTGAGCTGACGGATGAAGGGTGGCTGGTGCCTTTACAGGGCGTGGGAACCTTTGGGTGC  
CCGAAA

>18-Sbon-5

GTGGCTCCTCCGAGCTAGCGACGTCGTCACTGGCGCAGCTATGCGACGCGCAGAGCCGCGGGTTACATTATGCTTGTTTC  
GGCGTGAGCCGTGCGGCGAATACGCAGGCGTTGTGGCGGGAAGCGCAGTGGCGGAATGTTACCGTGGTGGAGGATCTGGA  
CTGCCATGACGCGCTGGCGCATATGACGCCATTATTGACAAGGTGGATAAAAATTTATCTGACTATCGATCTCGACGTATT  
GCCTGTCTGGGAAATGCCGGCCGTCTCCGCTCCCGCAGCGCTGGGCGTGCCGCTGATACAGGTTCTGCGTTTAATTGAGC  
CGGTTTGCCGCAGCGGAAAATTACAGGCGGCGGATCTGGTTGAATTTAATCCACGCTTTGATGAAGATGGCGCAGCGGCG  
CGCGTGGCGGCGCGGCTTGGCTGGCAAATCGCGCACTGGTGGCGTTAATCTGTCATCCGGAACATTATCCGCATAAGG

AAGGCTTCACGCATGTATTCATCCCGCTCCCGTTCTGCGCCTGCGCCTTTTACGAAACGGTGAAACAGGACATCTGTAA  
AAAAATAGCCGGCGGCGTCTGGCAGCCGCACGATCGCATTCCGTCGGAAGCTGAACTGGTCGCTCAGTATGGCTTTAGCC  
GAATGACCATCAACCGGGCGCTGCGTGAGCTGACGGATGAAGGGTGGCTGGTGCGTTTACAGGGCGTGGGAACCTTTGGT  
CGCCGAA

>18-Sbon-6

AAGCCATCGACTAGCCGTCTCGTCACTGCGCGCAGCTATGCTGACGCGCAGAGCCGCGCGTTTCATTATGCCTGTTTCGG  
CGTGAGCCGTGCGGCGAATACGCAGGCGTTGTGGCGGGAAGCGCAGTGGCGGAATGTTACCGTGGTGAAGATCTGGACT  
GCCGTGACGCGCTGGCGCAAATGACACACATTATCGACAAGGTGGATAAAATTTATCTGACTATCGATCTCGACGTATTG  
CCTGTCTGGGAAATGCCGGCCGTCTCCGCTCCCGCAGCGCTGGGCGTGCCGCTGATACAGGTTCTGCGTTTAATTGAGCC  
GGTTTGCCGCAGCGGAAAATTACAGGCGGCGGATCTGGTTGAGTTTAATCCACGCTTTGATGACGATGGCGCAGCGGCGC  
GCGTGGCGGCGCGGCTTGGCTGGCAAATCGCGCACTGGTGGCGTTAATCTGTCATCCGGAACACTATCCGCATAAGGA  
AGGCTTTACGCATGTATTCATCCCGCTCCCGTTCTGCGCCTGCGCCTTTTACGAAACGGTGAAACAGGACATCTGTAA  
AAAAATAGCCGGCGGCGTCTGGCAGCCGCACGATCGCATTCCGTCGGAAGCAGAACTGGTCGCCCAGTATGGCTTTAGCCG  
AATGACCATCAACCGGGCGCTGCGTGAGCTGACGGATGAAGGGTGGCTGGTGCGTTTACAGGGCGTGGGAACCTTTGTCTG  
CCCGAA

```

      10      20      30      40      50      60      70      80      90
18-Sbon-1  TCGTCACIG CCGCAG CTATGC GACGCGCAGAGC CGCGC GTTACATTATG CCTGG TTCGGCGT GAGCCGT GCGGCGAATACGCAGG
18-Sbon-2  .....CG...CT.....G...GC...T.....C.....
18-Sbon-3  .....G.....T.....T.....
18-Sbon-4  .....G...T.....T.....T.....
18-Sbon-5  .....G.....G...T.....
18-Sbon-6  .....CG.....T.....T.....T.....

      100     110     120     130     140     150     160     170     180
18-Sbon-1  CGTTGTGGCGGGAAGCGCAGTGGCGGAATGTTACCGTGGTGGAGGATCTGGACTGCCATGACGCGCTGGCGCAATATGACGCACATTATC
18-Sbon-2  .....T.....ATG.....
18-Sbon-3  .....G.....
18-Sbon-4  .....G.....
18-Sbon-5  .....T.....T.....
18-Sbon-6  .....A.....G.....A.....

      190     200     210     220     230     240     250     260     270
18-Sbon-1  GGCAGGTGGATAAATTTATCTGACTATCGATCTCGCGTATTGCCTGTCTGGGAAATGCCGGCGTCTCCGTCGCCGACGCGCTGGGC
18-Sbon-2  .....
18-Sbon-3  .....
18-Sbon-4  .....
18-Sbon-5  .....
18-Sbon-6  .....

      280     290     300     310     320     330     340     350     360
18-Sbon-1  GTGCCGCTGATACAGGTTCTGCGTTTAAITGAGCCGTTTGCCGCAGCGGAAATTTACAGCGCGCGGATCTGGTTGAATTTAATCCACGC
18-Sbon-2  .....G.....
18-Sbon-3  .....G.....
18-Sbon-4  .....G.....
18-Sbon-5  .....
18-Sbon-6  .....G.....

      370     380     390     400     410     420     430     440     450
18-Sbon-1  TTTGATGAAGATGGCGACGCGCGCGCTGGCGCGCGGCTTGGCTGGCAAAATCGCGCACTGGTGGCGTTAATCTGTCTATCCGGAATACA
18-Sbon-2  .....
18-Sbon-3  .....C.....
18-Sbon-4  .....
18-Sbon-5  .....
18-Sbon-6  .....C.....

      460     470     480     490     500     510     520     530     540
18-Sbon-1  TTATCCGCAATAGGAAGGCTTCACGCATGTATTCAATCCGCTCCCGTTCTGCACCTGCGCCTTTTACGAACGGTGAAACAGGAATCTCT
18-Sbon-2  C.C.....G.....
18-Sbon-3  C.....G.....
18-Sbon-4  .....G.....
18-Sbon-5  .....G.....
18-Sbon-6  C.....T.....G.....

      550     560     570     580     590     600     610     620     630
18-Sbon-1  GTAAAAAATAGCCGGCGGCGTCTGGCAGCCGCAGATCGCATTCCGTGGGAGCAGAACTGGTCCGCCAGTATGGCTTTAGCCGAATGA
18-Sbon-2  .....T.....T.....
18-Sbon-3  .....T.....
18-Sbon-4  .....
18-Sbon-5  .....T.....T.....
18-Sbon-6  .....

      640     650     660     670     680     690
18-Sbon-1  CCAATCAATCGGGCGCTGGGTGAGCTGACGGATGAAGGGTGGCTGGTGGCTTTACAGGGCGTGGGAATT
18-Sbon-2  .....C.....C.....
18-Sbon-3  .....C.....
18-Sbon-4  .....
18-Sbon-5  .....C.....C.....
18-Sbon-6  .....C.....

```

The above alignment of gene, formimidoylglutamase (*hutG*) did not produce the all target sequences of *Salmonella*, where we did not find any suitable SNPs.

19-Sbon, Gene Name: Hypothetical ABC transporter ATP-binding (*yehX*)

|           |                     |
|-----------|---------------------|
| 19-Sbon-F | TCACGGCGGGTAAGAGGA  |
| 19-Sbon-R | ATGAGATTGCGCCAGGCCG |

>19-Sbon-1

CGCGGGCTGGTTCTCATGATAGATATCCGGTTCGTGCATCAGCGAGCAGGCCAGCGCCAGTCGCTGTTTAAAGCCCAGCG  
GCAGCGCATCGGTGGGATGCGACGCGATGCTTTTCAGACCAAACGCTTCACTCATGCGCTGAATTTTTTCATTTTGCGCG  
CGGCCCCGCAAACCGTAGACGCCGAGAAAAACGCAGGTTCTGCTCAACCGTCAGGTTGCCGTAAAGCGAAAATTTTTG  
CGCCATATAGCCCAGATGCTGACGGGCTTTGCCGGAGCTGACTTTCAGGTCCATATCCAGCACCAGCGCCTTGCCGGACG  
TCGGCACCAGCAGGCCGCACATCATTTTAAAGGTGGTTGATTTACCCGCGCCGTTCCGGCCGAGCAGGCCAAAAATCTCG  
CCGCGCTGTACGACGAAATTAACATGGTCCGTAGCCGCGAAATCGCCAAATTTTTTCGTGAGTTCCTGCGCTTCAATCAC  
CGTTTCGCCGGCAGTGCTTCAACCGTATGCAGGATTGAACCCAGCGGAGACTCCGAGGTTCCCGCTCCGCCAAGCAGAT  
CGATAAACGCATCTTCGAAGCGCGGCGGGTCTCATTGAGGGTGATTTCCGGCATCCCTTCGGCCTTGAAAAATTCTCAT  
A

>19-Sbon-2

GTCCGGGCATGGTTCTCAAGGCATATATATCCGGTTCGTGCATCAGCGAGCAGGCCAGCGCCAGTCGCTGTTTAAAGCCC  
AGCGGCAGCGCATCGGTGGGATGCGACGCGATGCTTTTCAGACCAAACGCTTCACTCATGCGCTGAATTTTTTCATTTTG  
CGCGCGCCCCGCAAACCGTAGACGCCGAGAAAAACGCAGGTTCTGCTCAACCGTCAGGTTGCCGTAAAGCGAAAATT  
TTTGCGCCATATAGCCCAGATGCTGACGGGCTTTGCCGGAGCTGACTTTCAGGTCCATATCCAGCACCAGCGCCTTGCCG  
GACGTCGGCACCAGCAGGCCGCACATCATTTTAAAGGTGGTTGATTTACCCGCGCCGTTCCGGCCGAGCAGGCCAAAAAT  
CTCGCCGCGTTGTACGACGAAATTAACATGGTCCGTGGCCGCGAAATCGCCAAATTTTTTCGTGAGTTCCTGCGCTTCAA  
TCACCGTTTCGCCGGCAGTGCTTCAACCGTATGCAGGATTGAACCCAGCGGAGACTCCGAGGTTCCCGCTCCGCCAAGC  
AGATCGATAAACGCATCTTCGAAGCGCGGCGGGTCTCATTGAGGGTGATTTCCGGCATTCCTTCGGCCTGCGAAATCTC  
AT

>19-Sbon-4

GAGGGGCATGGTCTCATGATATATATCCGGTTCGTGCATCAGCGAGCAGGCCAGCGCCAGTCGCTGTTTAAAGCCCAGCG  
GCAGCGCATCGGTGGGATGCGACGCGATGCTTTTCAGACCAAACGCTTCACTCATGCGCTGAATTTTTTCATTTTGCGCG  
CGGCCCCGCAAACCGTAGACGCCGAGAAAAACGCAGGTTCTGCTCAACCGTCAGGTTGCCGTAAAGCGAAAATTTTTG  
CGCCATATAGCCCAGATGCTGACGGGCTTTGCCGGAGCTGACTTTCAGGTCCATATCCAGCACCAGCGCCTTGCCGGACG  
TCGGCACCAGCAGGCCGCACATCATTTTAAAGGTGGTTGATTTACCCGCGCCGTTCCGGCCGAGCAGGCCAAAAATCTCG

CCGCGCTGTACGACGAAATTAACATGGTCCGTAGCCGCGAAATCGCCAAATTTTTTCGTAGTTCTGCGCTTCAATCAC  
 CGTTTCGCCGGCAGTGCCTTCAACCGTATGCAGGATTGAACCCAGCGGAGACTCCGAGGTTCCCGCTCCGCCAAGCAGAT  
 CGATAAACGCATCTTCGAAGCGCGGCGGGTCTCATTGAGGGTGATTTCCGGCATCCCTTCGGCCTGCGAAATCTCAT  
 >19-Sbon-5

GTGGGGCATGGTTATCACGATACATATCCGGTTCGTGCATCAGCGAGCAGGCCAGCGCCAGTCGCTGTTTTAAACCCAGC  
 GGCAGCGCATCGGTGGGATGCGACGCGATGCTTTTTAGACCAAATGCTTCACTCATGCGTGAATTTTTTCATTTTGC  
 GCGCCCCGCAAACCGTAGACGCCGAGAAAAACGCAGGTTCTGCTCAACCGTCAGGTTGCCGTAAAGCGAAAAATTTTT  
 GCGCCATATAGCCCAGATGCTGACGGGCTTTGCCGGAGCTGACTTTCAGGTCCATATCCAGCACCAGCGCCTTGCCGGAC  
 GTCGGCACCAGCAGGCCGCACATCATTTTAAAGGTGGTTGATTTACCCGCGCCGTTCCGGCCGAGCAGGCCAAAAATCTC  
 GCCGCGTTGTACGACGAAATTAACATGGTCCGTGGCCGCGAAATCGCCAAATTTTTTCGTAGTTCTGCGCTTCAATCA  
 CCGTTTCGCCGGCAGTGCCTTCAACCGTATGCAGGATTGAACCCAGCGGAGACTCCGAGGTTCCCGCTCCGCCAAGCAGA  
 TCGATAAACGCATCTTCGAACGCGGCGGGTCTCATTGAGGGTGATTTCCGGCATCCCTTCGGCCTGGCGAATCTAATG

A



*The above alignment of the gene, hypothetical ABC transporter ATP-binding (yehX) did not produce the all target sequences of Salmonella, where we did not find any suitable SNPs.*

21-Sbon, Gene Name: pyruvate formate-lyase 3-activating enzyme (*ybiY*)

**16-Sbon-F**

**CTGCTTAAACGGCGCGTC**

**16-Sbon-R**

**TGGTGCGGCATGATCCTG**

>21-Sbon-3

CGGGGGTTGCTGTCTGCAGATGTATGGCGGTCTATAACCGGGATGTAGTGAAAGTACCTAAAGGCTACCACCCGAGTTGC  
CACCATCGCGGGTTACGATAACTACTATCTGAACGTGATGGCCGGCCCCGCTACGAAAATGGCGTTTCACCTGGGAAGAGA  
ACCACGCGTGGATTAACCTACCAGACTACCCGCGATAACACTTCGTTGAGTGGTACTTTGCCAGCCGTCCTCTGCGGCTG  
GCTTTTTTATTCAACTCTGCGCCACACACGCTCATAAGATCGCTATCCGCCTTCTCTTAAATTATTTCCCTGTTTTGTAT  
ATAGCGTATTTACGGCACGGCCTCCACCAGGAATACGCAATAAAATAATGATGCAGAAGAAGACTTACCCTATTTGCCGA  
TATTATTATGGATCAAGTAGTTACGTAGAGGTGGTAAACACTGGGGAGGTTTCAACAGGTATATCCTGTGCGCACTCGT  
GGAGGGAGTAAAGGTTGTGTAACCAGCGGAGAATATCTCTGGATATTCTCCGCTAATATTGGAGAGGTATCAGGCTATTA  
CATCGCGACGTTTCCCCTGAATTTACGCAGCTTGTTCTCGGCCAGCCGTTCAATTTCTGTTAGCGGCACCCCTTTTGT  
TCCGGCACATAACGAGAAATAAGACATAGCAGACCAATTAAAGACGACAAAAATCCACATCGAGAAAGCGCCCGGAAG  
GTCTCCTGCAGCCAGGCGTTATCATTTATGACCGGGAACAACAGTGAGATGAGGAAGTTGGCTATCCACATCAGGCTCAC  
CGCCCAGCCCCATTCCCAAACCTTTTTATCTTTTTTCAGGGAAAACCTTCAGAATCAGTACCCATGCG

>21-Sbon-4

TTGGCAGCATCTGCAGATGTATGGCGGTCTATAACCGGGATGTAGTGAAAGTACCTAAGGGCTACCACCCGGTTGCCACC  
ATCGCGGGTTACGATAACTACTATCTGAACGTGATGGCCGGCCCCGCTACGAAAATGGCGTTTCACCTGGGAAGAGAACCA  
CGCGTGGATTAACCTACCAGACTACCCGCGATAACACTTCGTTGAGTGGTACTTTGCCAGCCGTCCTCTGCGGCTGGCTT  
TTTTATTCAACTCTGCGCCACACACGCTCATAAGATCGCTATCCGCCTTCTCTTAAATTATTTCCCTGTTTTGTATATAG  
CGTATTTACGGCACGGCCCCCACCAGGAATACGCAATAAAATAATGATGCAGAAGAAGACTTACCCTATTTGCCGATATT  
ATTATGGATCAATTAGTTACGTAGAGGTGGTAAACACTGGGGAGGTTTCAACAGGTATATCCTGTGCGCACTCGCTGGA  
GGGAGTAAAGGTTGTGTAACCAGCGGAGAATATCTCTGGATATTCTCCGCTAATATTGGAGAGGTATCAGGCTATTACAT  
CGCGACGTTTCCCCTGAATTTACGCAGCTTGTTCTCGGCCAGCCGTTCAATTTCTGTTAGCGGCACCCCTTTTGTTC  
GGCACATAACGAGAAATAAGACATAGCAGACCAATTAAAGACGACAAAAATCCACATCGAGAAAGCGCCCGGAAGGT  
CTCCTGCAGCCAGGCGTTATCATTTATGACCGGGAACAACAGTGAGATGAGGAAGTTGGCTATCCACATCAGACTCACCG  
CCAGCCCCATCCCAAACCTTTTTATCTTTTCAGGGAAAACCTCAGAAATCAGTACCCATGCGGCCAACGCTCCAGCTGA  
CGGCAACAGCAGCATAAAAAACAGGGATGCCGAAGATGGGTATTGTAGCCTGTATCGTGGGTCGTACAAAGCCGTAAT  
GACGCGATCAACAGGCCAGAGATTGTATCCGATGGTACCGAGTTTTTCATAAATGCGGATATAGCGGTCATCAGCGGTGGA

[illegible]