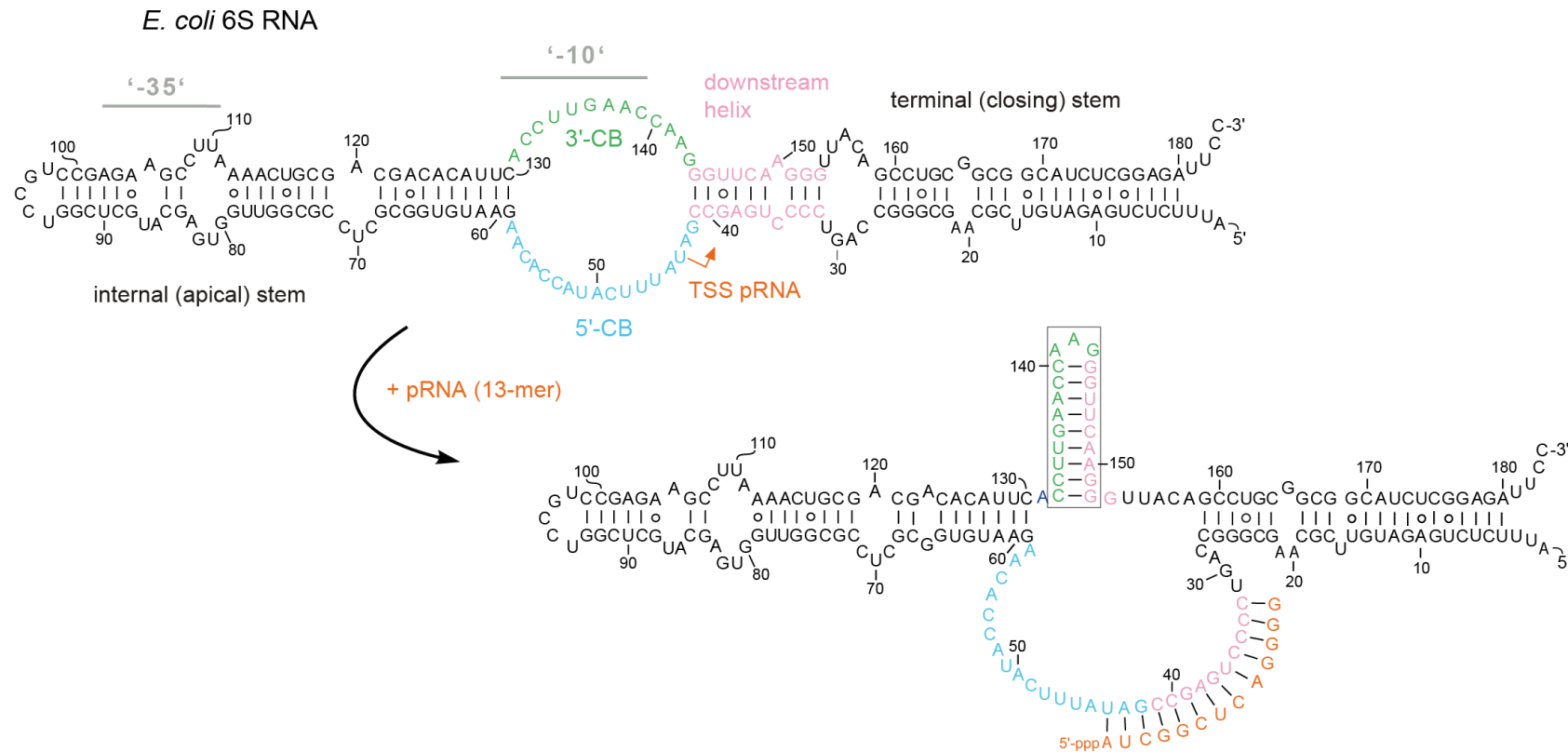


A



**Figure S1: (A) The pRNA-induced structural transition of *E. coli* 6S RNA and (B) sequence identity between *E. coli* 6S RNA and *B. subtilis* 6S-1 RNA. (A)** Adapted from [12,14]. For more details on abbreviations and color code, see Figure 1 of the main text. **(B) Top:** sequence identity between *E. coli* 6S RNA and *B. subtilis* 6S-1 RNA based on the 6S RNA seed alignment in the Rfam database (Rfam 14.7, RF00013; I. Kalvari et al., 2017, *Nucleic Acids Res.*, doi: 10.1093/nar/gkx1038); **bottom:** sequence identity predicted by ClustalW pairwise alignment (J.D. Thompson et al., 2002, *Curr. Protoc. Bioinformatics*; Chapter 2:Unit 2.3; doi: 10.1002/0471250953.bi0203s00).

## B

Sequence identity between between *E. coli* 6S RNA and *B. subtilis* 6S-1 RNA based on the Rfam 6S RNA seed alignment

```

Eco AUUUCUCUGAGAUGUUCGCAAGCGGGCCA GUCCCCUGAGCCGAUAUUAUACCAACAAGAAUGUGGCGCUCCGCGGUUGGUGAGCAUGCUCGG-----UCC
Bsu AAAGUCCUGAUGUGUUAGUUGUACACCUA-GUUU-UGA-CCGAACAUAUUUUUUGAUUUUGGAGCCCGCAUUUUUAAAUGGCGUACAUGCUCUUUUUCAUUC

Eco -GU--CCGAAGAGCCUUAACUCGCGACGACAUAUACCCUUG-AAACAAAGGUUCAAGGGU---UACAGCCUGCGGCGGCAU-CUCGGAGAUUCC 184 nt
Bsu GGUAAAGAGGACUUAACAAGAUUUAAAAAGAGGGCACCACCUCGUCAGAGCGGGUUCA-AAACAAAGGAAGCUGCAACGGCACUAUUGGGACUUUA 193 nt
  
```

*Eco*: *E. coli* 6S RNA (GenBank accession no. X01238.1); *Bsu*: *B. subtilis* 6S-1 RNA (GenBank accession no. AL009126.3, nt 2814682-2814490)

Identical nucleotides are marked by red letters / Alignment length: 197 nt / Sequence identity: 74 nt -->  $74/197 = 37.6\%$  --> average identity: ~ 38%

ClustalW (2.1) pairwise alignment of *E. coli* 6S RNA and *B. subtilis* 6S-1 RNA sequences

```

Eco AUUUCUCUGAGAUGUUCGCAAGCGGGCCAGUCCCCUGAGCCGAUAUUUCAUACCACAAGA
Bsu AAAGUCCUGAUGUGUUAGUUGUACACCUAGUU--UUGACCGAACAUUUUUUUGAUUUUGGG
      *      ****   **** *          *  ***      *** *  *  ****   *          *

Eco AUGUGGCGCUCCGCGGUUGGUGAGCAUGC-UCGGUCCGUCCG----AGAAGCCUAAAA-
Bsu AGCCCGCAUUUU-UAAAUGGCGUACAUGCCUCUUUUAUUCGGUAAAGAGGACUACAAG
      *      **   *          *** *  ***** **   *  *  *  **      *** *  **** **

Eco --CUGCGACGACACAUUCACCU-UGAACCAAGGGUUCAAGGGUAC--AGCCUGCGGCGG
Bsu AUUUAAAAGAGGGCACCCACCUGCUGAGAGCGGGUUCAAAACAAAGGAAAGCUGCAACGG
      *      *          **   *****   *      *****      *   *   ****   ***

Eco CAUCUCGGAGAUUCC- 184 nt
Bsu CACUAUUGGGACUUUA 193 nt
      **      *  ** *
  
```

Alignment length: 196 nt / Sequence identity: 88 nt -->  $88/196 = 44.9\%$  --> average identity: ~ 45%