Supporting Information

Kitahara et al. 10.1073/pnas.1213609109

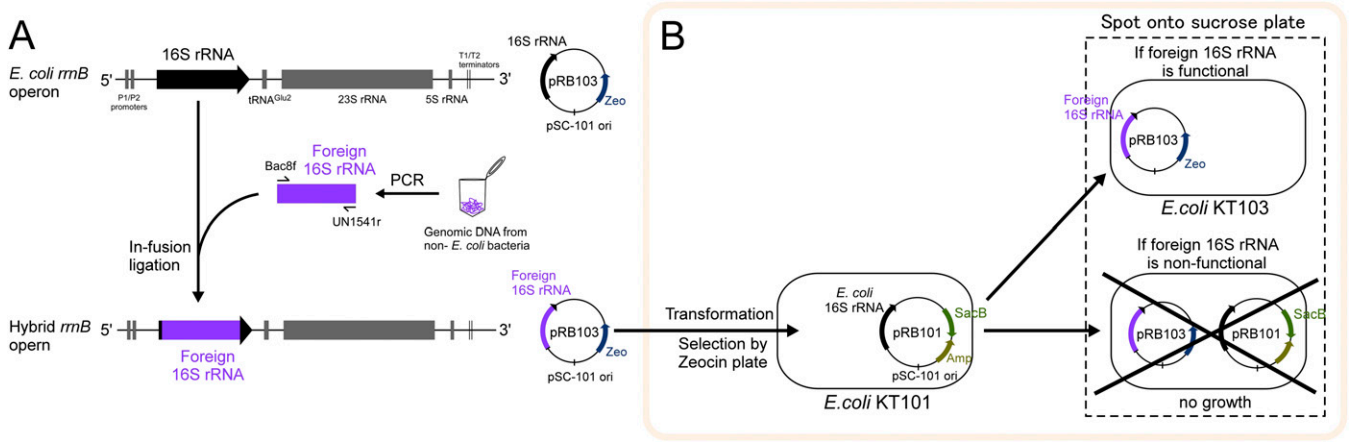

Fig. S1. Functionality test of metagenomically retrieved foreign 16S rRNA. (*A*) In-fusion cloning scheme of foreign 16S rRNA genes into an expression vector pRB103 containing the entire *rrnB* operon. The *Escherichia coli* 16S rRNA gene in pRB103 was substituted with foreign 16S rRNA genes amplified from the environmental DNA (metagenome). (*B*) A genetic method to test the functionality of foreign 16S rRNA genes. *E. coli* Δ7 strain KT101was used to screen for foreign 16S rRNA genes compatible with an *E. coli* genetic background.

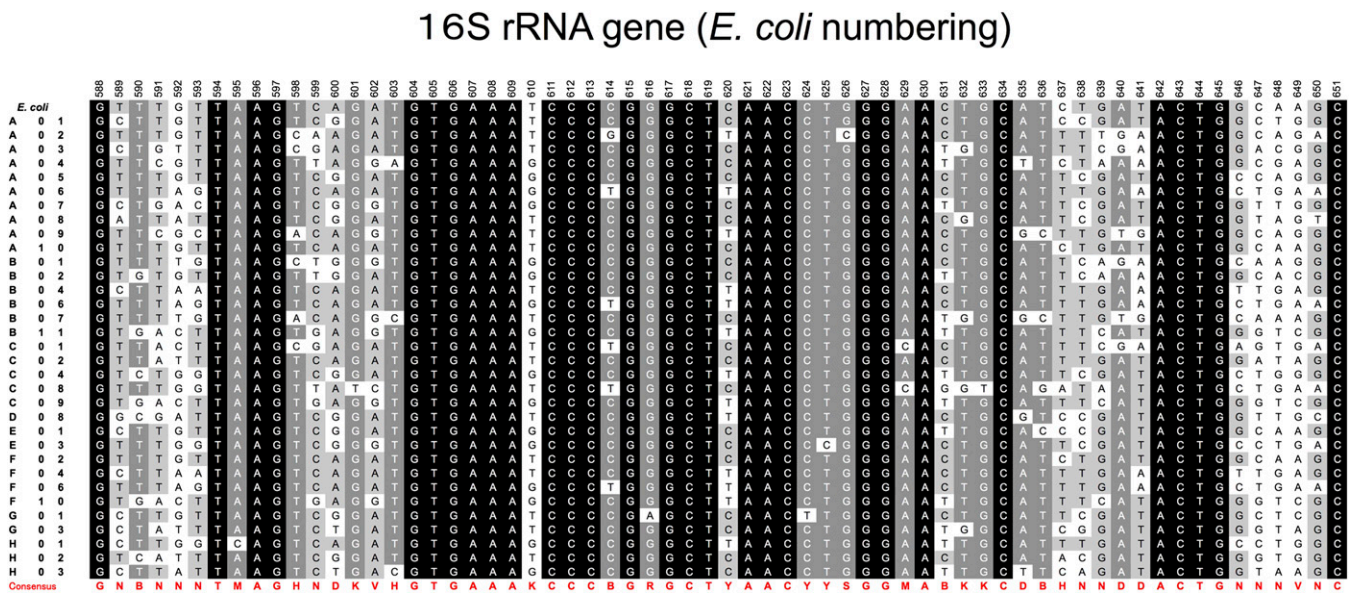

Fig. S2. Multiple alignment of the h21 region (G588–C651) of the 16S rRNA genes obtained from the environmental metagenome. The residues conserved in all of the sequences are shaded in black, those conserved in 80% of the sequences are in dark gray, and those conserved in 60% are in light gray. The consensus sequence is shown in red at the bottom of the alignment.

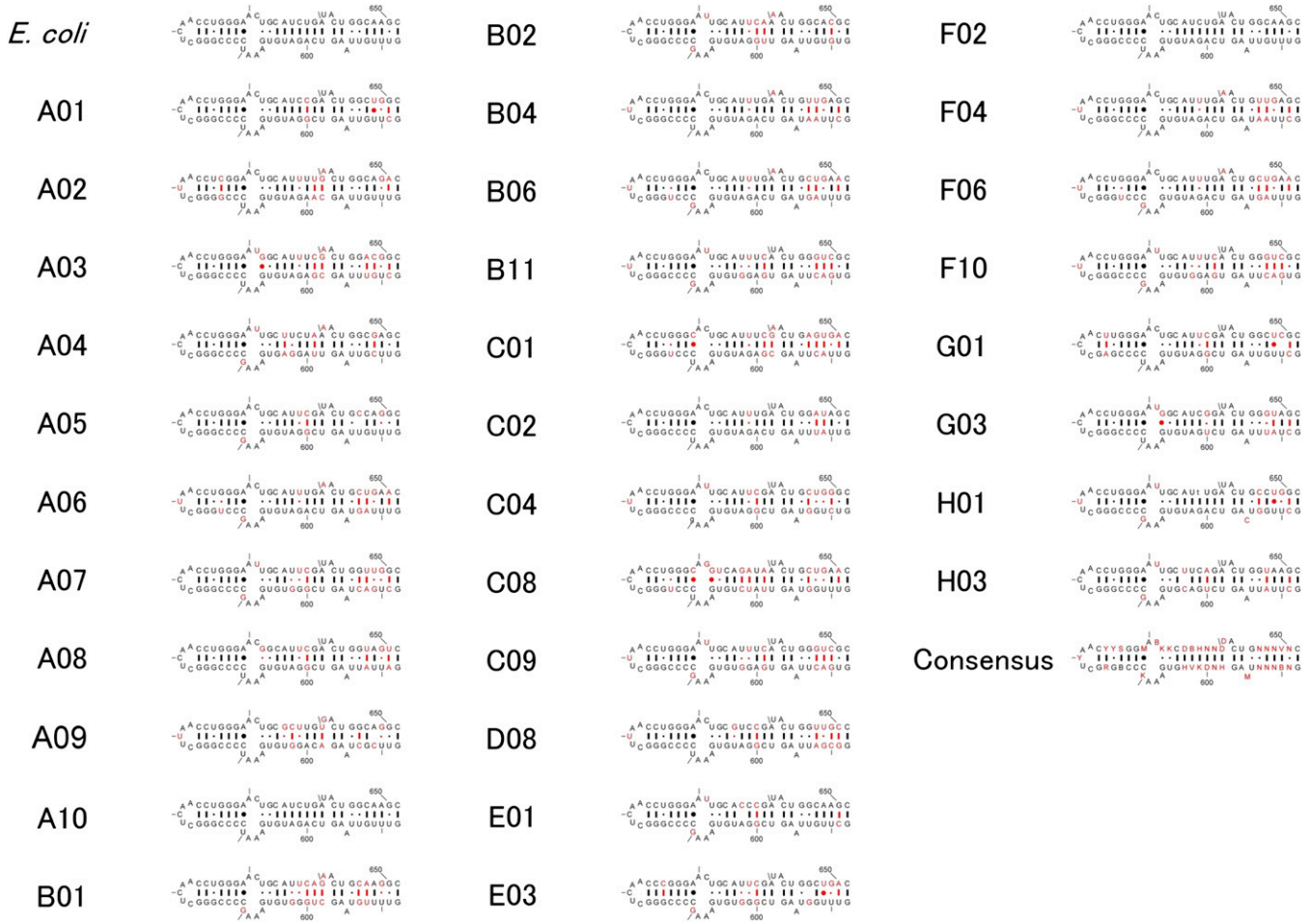

Fig. S3. Conserved nature of the secondary structure of h21 of the 16S rRNA obtained from the environmental metagenome.

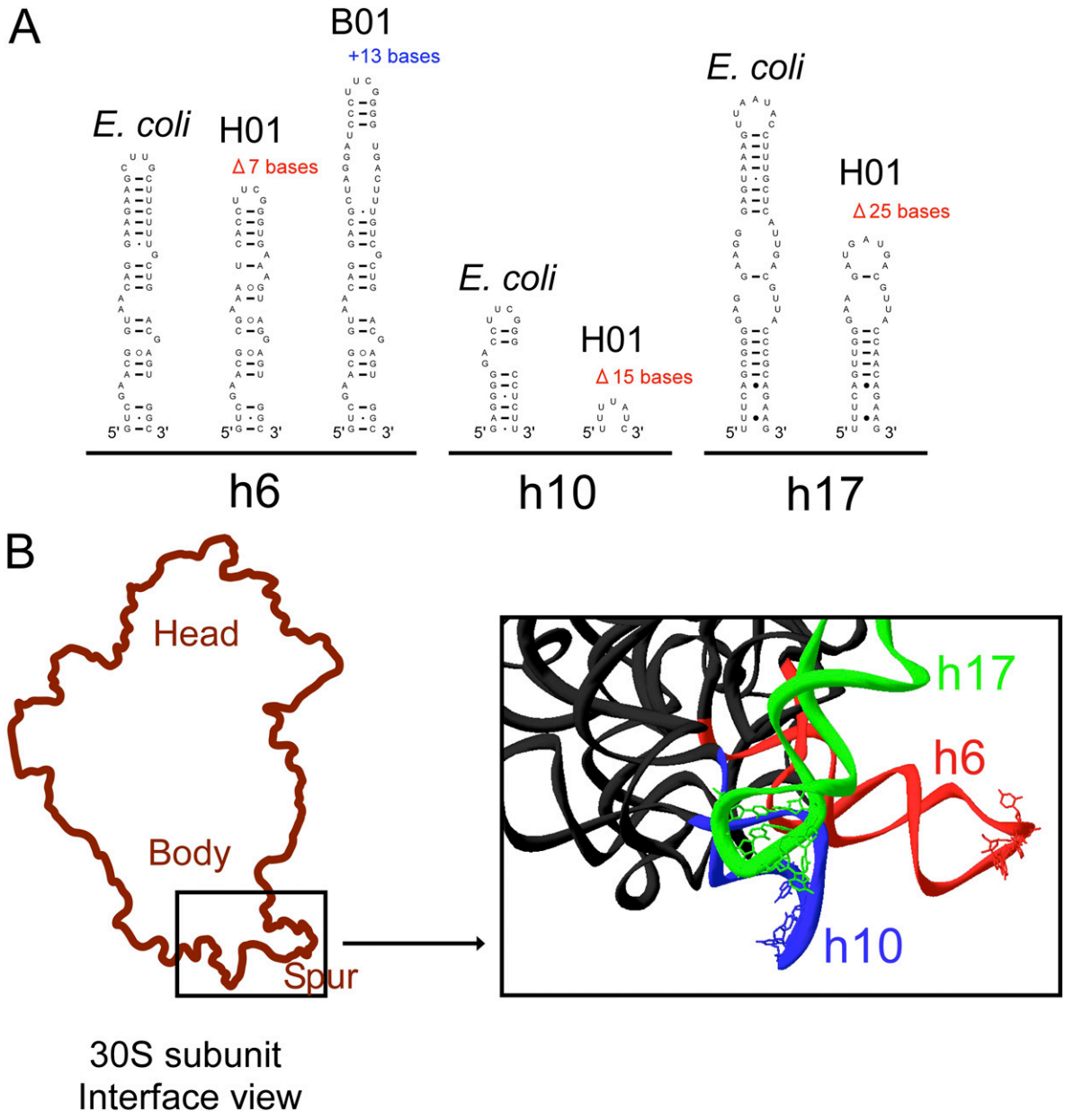

Fig. S4. Length polymorphism of RNA helices. (*A*) Comparison of secondary structures. The RNA h6, h10, and h17 of H01 are shorter than those of *E. coli* by 7, 15, and 25 bases, respectively. h6 of B01 is elongated by 13 bases. (*B*) Positions of h6, h10, and h17 in the crystal structure of the *E. coli* ribosome.