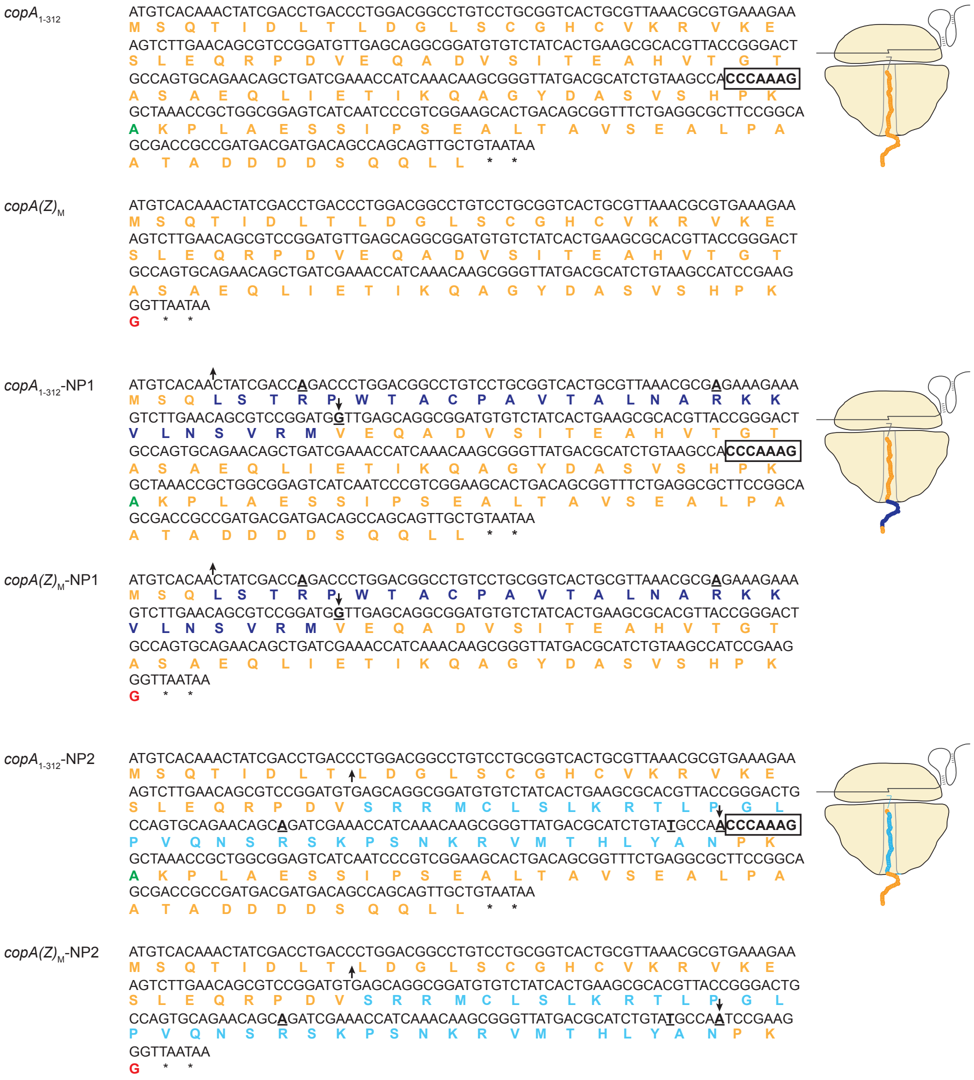


Figure S1. Generation of mutant nascent peptide templates, Related to Figure 4.
The nucleotide sequences of the DNA templates used for in vitro translation and the amino acid sequences of the proteins encoded in 0 frame. The *copA*$_{1\text{-}312}$ template carries the wt *copA* sequence except for insertion of two stop codons (UAA) after codon 104. The wt amino acid sequence (residues in orange) was changed in the *copA*$_{1\text{-}312}$-NP1 (amino acids shown in dark blue) and *copA*$_{1\text{-}312}$-NP2 (residues in light blue) templates by introducing compensatory indel mutations (indicated by the arrows). Additional mutations introduced to avoid the appearance of premature stop codons in the mutant constructs are indicated with bold and underlined characters. Notice that none of the changes in the templates disrupted the integrity of the CCCAAAG slippery sequence (boxed). The cartoons, which represent ribosomes positioned at the *copA* slippery sequence, illustrate the portion of the CopA nascent chain that has been altered. Also shown are the sequences of the marker templates *copA(Z)*$_M$, *copA(Z)*$_M$-NP1, and *copA(Z)*$_M$-NP2, in which the relevant CopA(Z) polypeptides, used as markers for the gel electrophoresis, are encoded in the 0 frame.

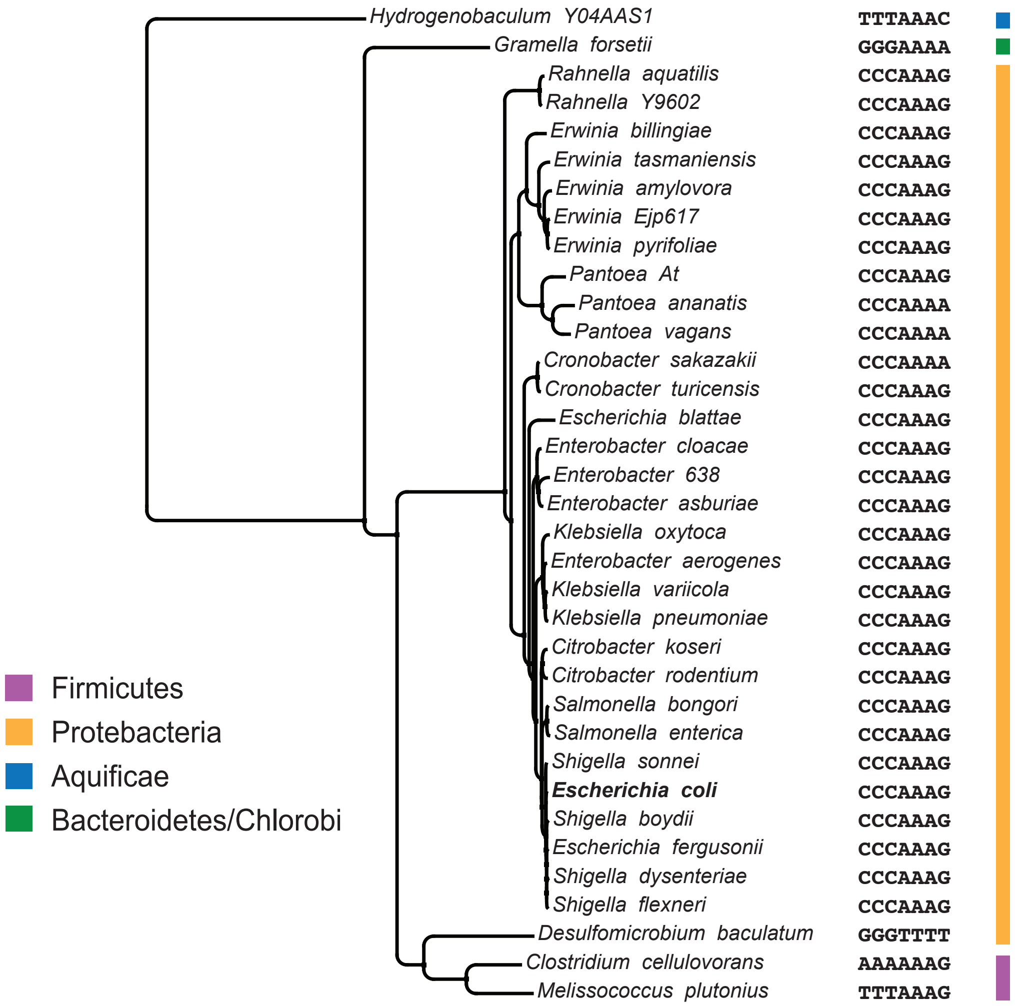
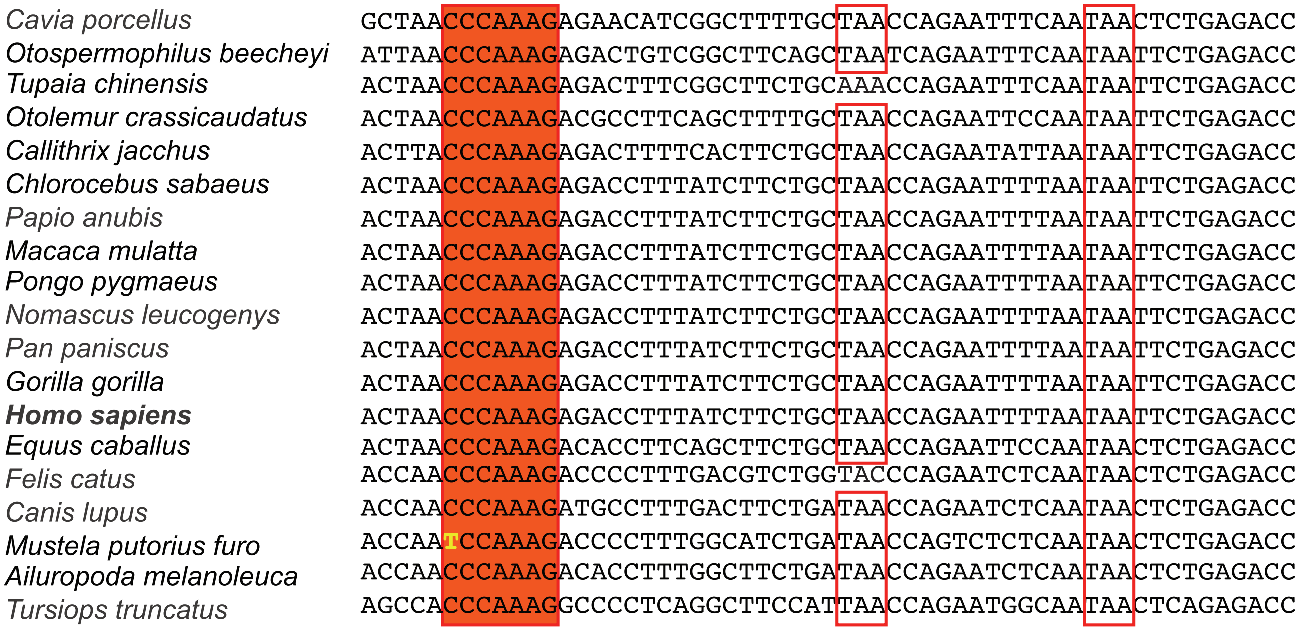


Figure S2. The presence of the slippery sequence at the end of the MBD1-coding segment in the *copA* gene of a variety of bacterial species, Related to Figure 2

Phylogenetic tree of bacterial species whose *copA* genes contain an SS heptamer followed by a nearby -1 frame stop codon. The colored vertical bars indicate the phylum of each bacterial species. The criteria applied for the selection of the species included in the tree is described in STAR methods.

Figure S3. Conservation of the predicted mRNA pseudoknot that facilitates -1 PRF in the *copA* gene among different bacterial species, Related to Figure 3

The stems S1 and S2 of the predicted pseudoknot downstream from the slippery sequence (boxed) in the *copA* gene of different bacteria are indicated by green and blue arches, respectively. Note that the covariation of residues within the S1 and S2 sequences is consistent with the folding of mRNA into the pseudoknot structure.



Cavia porcellus	GCTAACCCAAAGAGAACATCGGCTTTTGCTAACCAGAATTTCAATAACTCTGAGACC
Otospermophilus beecheyi	ATTAACCCAAAGAGACTGTCGGCTTCAGCTAATCAGAATTTCAATAATTCTGAGACC
Tupaia chinensis	ACTAACCCAAAGAGACTTTCGGCTTCTGCAAACCAGAATTTCAATAATTCTGAGACC
Otolemur crassicaudatus	ACTAACCCAAAGACGCCTTCAGCTTTTGCTAACCAGAATTCCAATAATTCTGAGACC
Callithrix jacchus	ACTTACCCAAAGAGACTTTTCACTTCTGCTAACCAGAATATTAATAATTCTGAGACC
Chlorocebus sabaeus	ACTAACCCAAAGAGACCTTTATCTTCTGCTAACCAGAATTTTAATAATTCTGAGACC
Papio anubis	ACTAACCCAAAGAGACCTTTATCTTCTGCTAACCAGAATTTTAATAATTCTGAGACC
Macaca mulatta	ACTAACCCAAAGAGACCTTTATCTTCTGCTAACCAGAATTTTAATAATTCTGAGACC
Pongo pygmaeus	ACTAACCCAAAGAGACCTTTATCTTCTGCTAACCAGAATTTTAATAATTCTGAGACC
Nomascus leucogenys	ACTAACCCAAAGAGACCTTTATCTTCTGCTAACCAGAATTTTAATAATTCTGAGACC
Pan paniscus	ACTAACCCAAAGAGACCTTTATCTTCTGCTAACCAGAATTTTAATAATTCTGAGACC
Gorilla gorilla	ACTAACCCAAAGAGACCTTTATCTTCTGCTAACCAGAATTTTAATAATTCTGAGACC
Homo sapiens	ACTAACCCAAAGAGACCTTTATCTTCTGCTAACCAGAATTTTAATAATTCTGAGACC
Equus caballus	ACTAACCCAAAGACACCTTCAGCTTCTGCTAACCAGAATTCCAATAACTCTGAGACC
Felis catus	ACCAACCCAAAGACCCCTTTGACGTCTGGTACCCAGAATCTCAATAACTCTGAGACC
Canis lupus	ACCAACCCAAAGATGCCTTTGACTTCTGATAACCAGAATCTCAATAACTCTGAGACC
Mustela putorius furo	ACCAATCCAAAGACCCCTTTGGCATCTGATAACCAGTCTCTCAATAACTCTGAGACC
Ailuropoda melanoleuca	ACCAACCCAAAGACACCTTTGGCTTCTGATAACCAGAATCTCAATAACTCTGAGACC
Tursiops truncatus	AGCCACCCAAAGGCCCCTCAGGCTTCCATTAACCAGAATGGCAATAACTCAGAGACC

Figure S4. Slippery sequence is found in in the *ATP7B* gene homologs of several eukaryotic species, Related to Figure 6

Sequence alignment of the *ATP7B* gene sequences in the vicinity of the slippery sequence (shaded red). The downstream stop codons in the -1 frame are boxed.

Table S1: Oligonucleotides used in this study, Related to the STAR Methods

	Sequence (5' to 3')	**Purpose**
1	ACGCATCTGTAAGCCATCCTAAGGCTAAACCGCTGG	Site directed mutagenesis for generation of p*copA*-mSS
2	TTATTAACCCTTCGGATGGCTTACAGATGCGTCATAAC	Reverse primer for *CopA(Z)*$_{\text{M}}$-NP1 and *CopA(Z)*$_{\text{M}}$
3	TTATTAACCCTTCGGATTGGCATACAGATGCGTCA	Reverse primer for *CopA(Z)*$_{\text{M}}$-NP2
4	CATGGATTCTTGACAATTAATCATCGGCTCGTATAATGTGTGGACTTAAGTATAAGGAGGAAAAAATATGTCACAA	Forward primer for *CopA(Z)*$_{\text{M}}$-NP1
5	CATGGATTCTTGACAATTAATCATCGGCTCGTATAATGTGTGGACTTAAGTATAAGGAGGAAAAAATATGTCACAAACTATC	Forward primer for all templates used in vitro
6	TTA TTA CAG CAA CTG CTG GCT G	Reverse primer for *copA*$_{1\text{-}312}$
7	TTA TTA GGT CGC TGC CGG	Reverse primer for *copA*$_{1\text{-}282}$
8	TTA TTA AGA AAC CGC TGT CAG TG	Reverse primer for *copA*$_{1\text{-}261}$
9	TTA TTA TTC CGA CGG GAT TGA TGA	Reverse primer for *copA*$_{1\text{-}243}$
10	TTA TTA CGC CAG CGG TTT AGC	Reverse primer for *copA*$_{1\text{-}222}$
11	TCACAAACTATCGACCTGACC	Forward primer for Fragment-1
12	GGCGCGTCCCATTCGCCATTCTCCGGTCGACTCTAGAGGATCCCACGAAACAGCACACTG	Reverse primer for Fragment-1
13	ATGTCTATTGCTGGTTTATTCGGTACCCGGGGATCGCGGCCGCTATCCGGCGGAGTACAG	Forward primer for Fragment-2
14	TTACAGATGCGTCATAACCCG	Reverse primer for Fragment-2
15	TTGAGCGAGTTCTCAAAAATGAACAAATGTCGACGTCACAAACTATCGACCTGACC	Forward primer for DLR1 and DLR1-NP2
16	GATGCGTCATAACCCGCTTG	Reverse primer for DLR1 and DLR1-NP2
17	ACCATCAAACAAGCGGGTTATGACGCATCTGTAAGCCACCCAAAGGCAAACCGCTGGCGG	Forward primer for DLR2
18	GCTTCCGACGGGATTGATGACTCCGCCAGCGGTTTGCCTTTGGGTGGCTTACAGATGCG	Reverse primer for DLR2
19	GCTGGCGGAGTCATCAATC	Forward primer for DLR3
20	CCTTTCTTTATGTTTTTGGCGTCTTCCATGAGCTCATCGTCATCGGCGGTCG	Reverse primer for DLR3
21	ACCATCAAACAAGCGGGTTATGACGCATCTGTAAGCCATCCTAAGGCAAACCGCTGGCGG	Forward primer for DLR2-mSS
22	GCTTCCGACGGGATTGATGACTCCGCCAGCGGTTTGCCTTAGGATGGCTTACAGATGCG	Reverse primer for DLR2-mSS
23	CCATCAAACAAGCGGGTTATGACGCATCTGTATGCCAACCCAAAGGCAAACCGCTGGCGG	Forward primer for DLR2-NP2
24	GCTTCCGACGGGATTGATGACTCCGCCAGCGGTTTGCCTTTGGGTTGGCATACAGATGCG	Reverse primer for DLR2-NP2
25	AATGTCGACGTCACAAACTATCGACCTGACC	Forward primer for DLR-C
26	CATGAGCTCATCGTCATCGGCGGTC	Reverse primer for DLR-C
27	CATCAAACAAGCGGGTTATGACGCATCTGTATGCCAATCCTAAGGCTAAACCGCTGGCGG	Forward primer for DLR2-NP2-C
28	CTTCCGACGGGATTGATGACTCCGCCAGCGGTTTAGCCTTAGGATTGGCATACAGATGCG	Reverse primer for DLR2-NP2-C
29	CCTTTCTTTATGTTTTTGGCGTCTTCCATGAGCTCATCGTCATCGGCGGTC	Reverse primer for DLR3-NP2-C

30	CATGGATTCTTGACAATTAATCATCGGCTCGTATAATGTGTGGACTTAAGTATAAGGAGGAAAAAATATGTCACAACTATCGACCAGACCCTGGACGGCCTGTCCTGCGGTCACTGCGTTAAACGCGAGAAAGAAAGTCTTGAACAGCGTCCGGATGGTTGAGCAGGCGGATGTGTCTATCACTGAAGCGCACGTTACCGGGACTGCCAGTGCAGAACAGCTGATCGAAACCATCAAACAAGCGGGTTATGACGCATCTGTAAGCCACCCAAAGGCTAAACCGCTGGCGGAGTCATCAATCCCGTCGGAAGCACTGACAGCGGTTTCTGAGGCGCTTCCGGCAGCGACCGCCGATGACGATGACAGCCAGCAGTTGCTGTAATAA	*copA*-gBlock for *copA*$_{1\text{-}312}$-NP1
31	CATGGATTCTTGACAATTAATCATCGGCTCGTATAATGTGTGGACTTAAGTATAAGGAGGAAAAAATATGTCACAAACTATCGACCTGACCCTGGACGGCCTGTCCTGCGGTCACTGCGTTAAACGCGTGAAAGAAAGTCTTGAACAGCGTCCGGATGTGAGCAGGCGGATGTGTCTATCACTGAAGCGCACGTTACCGGGACTGCCAGTGCAGAACAGCAGATCGAAACCATCAAACAAGCGGGTTATGACGCATCTGTATGCCAACCCAAAGGCTAAACCGCTGGCGGAGTCATCAATCCCGTCGGAAGCACTGACAGCGGTTTCTGAGGCGCTTCCGGCAGCGACCGCCGATGACGATGACAGCCAGCAGTTGCTGTAATAA	*copA*-gBlock for *copA*$_{1\text{-}312}$-NP2
32	TTCGTTGAGCGAGTTCTCAAAAATGAACAAATGTCGACCCCAAAGGACCTTTATCTTCT GCTAACCAGAATTTTAATAATTCTGAGACCTTGGGGCACCAAGGAAGCCATGTGGTCACC CTCCAACTGAGAATAGATGGAATGCACGGATCCCCCGGGGAGCTCATGGAAGACGCC	*ATP7B*-WT gBlock
33	TTCGTTGAGCGAGTTCTCAAAAATGAATAAATGTCGACCCCAAAGGACCTTTATCTTCT GCTAACCAGAATTTTAATAATTCTGAGACCTTGGGGCACCAAGGAAGCCATGTGGTCACC CTCCAACTGAGAATAGATGGAATGCACGGATCCCCCGGGGAGCTCATGGAAGACGCC	*ATP7B*-PTC Control gBlock
34	GTTGAGCGAGTTCTCAAAAATGAACAAATGTCGACCCCAAAGGACCTTTATCTTCTGCTAACCAGAATTTTAATAATTCTGAGACCTTGGGGCACCAAGGAAGCCATGTGGTCACCCTCCAACTGAGAATAGATGGAATGCACGGATCCCCCGGGGAGCTCATGGAAGACTAAGCCAAAAACATAAAGAAAGGCCCGGCGCCATTCTATCCTCTAGAGGATGGAACCGCTGG	*ATP7B*-OOF Control gBlock