Quantitative analysis of *in vivo* ribosomal events at UGA and UAG stop codons

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The publishers wish to apologise for the omission of the Figure 2 legend in the above paper. This figure with its accompanying legend is printed below.

**Figure 2.** (A) SDS–PAGE gel analysis of the +1 frameshift protein products. Efficiency of +1 frameshift at the context CCCUGG as compared to CUUUGG, in the presence and absence of SD-like upstream sequences. Ratios of frameshift event versus termination (or drop-off) shown in Table 2 correspond to protein bands in (A). Lanes 1 and 10 show protein products from a control plasmid (pSMT-244) where the relative position of the three protein bands (termination = 2A'; frameshift = 2A'S and readthrough = 3A') are compared to those from constructs without a stop codon (lanes 4–9; 11–16). Lanes 2 and 3 have products from a control plasmid with only a stop codon (pSM11 and pSM27; ref. 28) and no frameshifting or SD-like sequence upstream. Lanes 4–9 show the products from plasmids pSMT-206, -207, -247, -248, -253 and -254 respectively and the same order is maintained for lanes 11–16. Protein A' bands corresponding to 2A' can be visualized under assay condition of both normal and limiting amounts of tryptophan. (B) SDS–PAGE gel analysis of the protein products representing the three translation events at a stop codon. The three protein products as seen on an SDS–PAGE gel from plasmids described in Table 3A and B. Lanes 2 and 3 show the influence of suppressor tRNA *serU*(Su1), RF-1 mutant (*prfA1*) and different -2 amino acid in the nascent peptide on UAGA decoding, as compared to the wild-type strain. Also, lanes 2 and 7 show the peptide influence on UAGA decoding. Lanes 4 and 5 show the influence of mutant RF-2 (*prfB2*) on UGA decoding. Lanes 6 and 7 show the influence of mutant RF-1 (*prfA1*) in a suppressor tRNA *tyrT*(Su3) background. Lanes 8, 9 and 10 show the influence of an upstream SD-like sequence on UGA decoding in wild-type (Su–) and suppressor (Su9) strains.