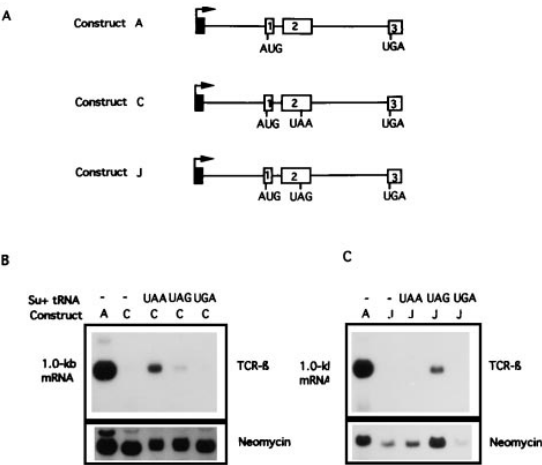
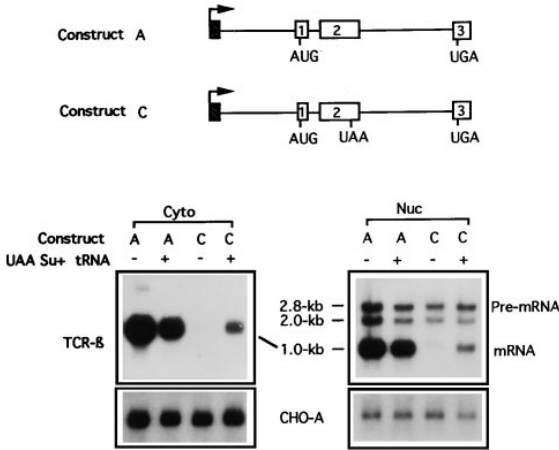


The images for Figs. 3 and 4 in Li et al. (March 17, 1997, 185:985–992) were mistakenly transposed. The figures, with their correct legends, appear below.



**Figure 3.** Specific suppressor tRNAs reverse nonsense-mediated regulation. (A) Constructs A and C are described in the Fig. 1 legend. Construct J contains a UAG nonsense codon in place of the UAA nonsense in construct C but is otherwise identical. (B and C) Northern blot analysis of total cellular RNA isolated from HeLa cells co-transfected with the constructs (4  $\mu$ g) shown in A, along with plasmids encoding UAA-, UAG-, and UGA-specific suppressor tRNAs (12  $\mu$ g). As with Fig. 1, neomycin mRNA levels were used as a measure of transfection efficiency, and similar loading of RNA in all lanes was demonstrated by methylene blue staining of 18S and 28S rRNA (data not shown), performed as described (42).



**Figure 4.** Suppressor tRNAs upregulate fully-spliced TCR- $\beta$  transcripts in the nuclear compartment. Northern blot analysis of nuclear and cytoplasmic RNA from HeLa cells transiently transfected with constructs A and C was isolated by method 2, as described in Materials and Methods. Hybridization with intron-specific probes demonstrated that the 2.8-kb pre-mRNA contains both the 0.8-kb  $\beta$ -actin intron (upstream of TCR- $\beta$  exon 1) and the 1.0-kb second TCR- $\beta$  intron, while the 2.0-kb pre-mRNA has spliced out the  $\beta$ -actin intron. The reason that the 2.0-kb pre-mRNA was highly expressed in the nuclei of the cells shown in this figure but not those in Fig. 2 is because the cells used for the latter figure were stably transfected. Methylene blue staining (42) of the blots showed that 32S and 45S rRNA precursors were present at high levels in the nuclear RNA and were absent in cytoplasmic RNA prepared at the same time (data not shown; see Wilkinson and MacLeod [40] and Wilkinson [43] for use of 32S and 45S rRNA precursors as a measure of nuclear RNA enrichment). Hybridization with the CHO-A housekeeping gene (28) probe demonstrated that 40-fold less CHO-A mature mRNA was present in the nuclear fraction than in the cytoplasmic fraction. This indicates that no more than 3% of the cytoplasmic RNA is contaminating the nuclear RNA. As with Fig. 1, neomycin mRNA levels were used as a measure of transfection efficiency (data not shown).