

Table S1.

		q1_{Δr} (count)	q2_{Δr}	q3_{Δr}	q4_{Δr}	χ² test P value (Bonferroni correction)
A. rare codons score	1	354	345	338	232	8.7e-07 (2.6e-06)
	0	409	397	398	494	0.0015 (0.0045)
	-1	483	503	509	519	0.71
	Binomial test on +1 and -1 charge score counts, P value (Bonferroni correction)	9.3e-06 (3.7e-05)	6.4e-08 (2.6e-07)	4.6e-09 (1.8e-08)	<2.2e-16 (8.8e-16)	-
B. rare pair score	1	60	73	49	25	2.5e-05 (7.5e-09)
	0	1074	1057	1084	1148	0.23
	-1	112	115	112	72	0.0063 (0.019)
	Binomial test on +1 and -1 tAI score counts, P value (Bonferroni correction)	9.0e-05 (0.00036)	0.0027 (0.011)	7.5e-07 (3.0e-06)	1.9e-06 (7.7e-06)	-

Table S1. Table 1 of the main text redone using rare codons which are defined to occur with genomic infrequency shows rare codons do not slow ribosomes. In the main text we investigate whether non-optimal codons, i.e. those with low tAI scores, might slow codons and find that they do not. To ensure that our finding that these ‘rare’ codons do not slow ribosomes does not simply hinge on our definition of ‘rare’, we have repeated the analysis using an alternative definition. Here, we define ‘rare’ codons according to their actual frequency in the genome as measured from our set of filtered genes. This rare set, of equal size to the rare tAI set, comprises the following codons: CGG, CGC, CGA, TGC, CCG, CTC, GGG, GCG, CGT, CCC, CAC, TGT, ACG, TCG, AGG. Quantiles of the difference in average ribosomal density between the two windows identified within a transcript are shown, with q1 representing the smallest differences and q4 the largest. A score of 1 indicates the putative retarding feature is more present within the more occluded intra-transcript window; -1, less present; 0, present in both windows in equal amounts. Rare (infrequent) codons and codon pairs tend to be found more in the less dense (faster translated) window. Similarly, the presence of rare pairs and rare codons decreases in the slowly-translated windows as the difference in degree of ribosomal slowing grows.