



Figure S17. Figure 2 redone on the non-redundant footprint set. We wanted to confirm that the exclusion of footprints which map to two or more potential locations in the genome was not systematically biasing our estimates of ribosomal density. For this reason we replotted the average relative change in ribosomal density within a gene upon translation of rare codon clusters using our non-redundant footprint set (see the end of the Methods section), in effect only considering those locations in the genome to which footprints uniquely map. Considering solely these regions in the transcriptome to which footprints can only ever be mapped unambiguously still shows rare codons do not slow translation. **A)** All genes with rare codon clusters. **B)** Genes with rare codon clusters which have 0 or 1 positive charges coded for in the last 30 codon positions plotted. These plots represent the net effect of tAI on ribosomal density with the bulk of the effect of positive charge removed. **C)** Genes with rare codon clusters which have 2 or more positive charges in the last 30 codon positions plotted.