

Figure S2: Simulated translation of all yeast mRNAs in wild-type tRNA concentrations, and with the concentration of each of the yeast tRNA types depleted by 75% in turn. This approach yielded 41 sets of transcriptome-wide simulations.

Each graph illustrates a scatter plot of the translation rate J of each mRNA in the two conditions, derived using the stochastic model of translation as described (Materials and Methods). Where the points lie along the $x=y$ axis, translation of those mRNAs is unaffected by depletion of the tRNA named in that graph's title. Where points lie to the right of the $x=y$ axis, the rate of translation J of that mRNA has been reduced in the tRNA depletion condition, when compared to translation in a wild-type tRNA milieu.



























