Table S1: Complete List of Model Parameters, Related to Figure 1 and Table 1

Para	Description	Value	References
R^t	Number of ribosomes	2×10^5	(von der Haar, 2008; Warner, 1999)
A^t	Number of mRNAs	6×10^4	(Zenklusen *et al.*, 2008)
T^t	Number of tRNAs	3.3×10^6	(Waldron & Lacroute, 1975)
T_n	Number of types of tRNAs	41	(Chan & Lowe, 2009)
T_j^t	Number of tRNAs of type j	$\sim 12,000 - 190,000$	(Chan & Lowe, 2009)
A_i	Number of mRNAs of gene i	$1 - 1254$	(Ingolia *et al.*, 2009)
p_i	Gene-specific initiation probability	$\sim 3.5 \times 10^{-6} - 0.115$	(Experimental Methods)
n	Number of genes	3795	(Ingolia *et al.*, 2009)
D_r	Diffusion coefficient of ribosomes	$3 \times 10^{-13}\text{m}^2/\text{s}$	(Politz *et al.*, 2003)
D_t	Diffusion coefficient of tRNAs	$8.42 \times 10^{-11}\text{m}^2/\text{s}$	(Werner, 2011)
C_r	Size of ribosome in codons	10	(Ingolia *et al.*, 2009)
s	tRNA competition coefficient	7.78×10^{-4}	(Experimental Methods)
V	Volume of the cell	4.2×10^{-17} m^3	(Jorgensen *et al.*, 2002)
R^b	Number of bound ribosomes		(Extended Experimental Procedure)
R^f	Number of free ribosomes		(Extended Experimental Procedure)
T_j^b	Number of bound tRNAs of type j		(Extended Experimental Procedure)
T_j^f	Number of free tRNAs of type j		(Extended Experimental Procedure)
ϵ_i	Total elongation rate of gene i		(Extended Experimental Procedure)
ρ_i	Initiation rate of gene i		(Extended Experimental Procedure)
L_i	Length of gene i in codons	$36 - 4910$	(Ingolia *et al.*, 2009)
$u_{j,i}$	Frequency of codon j in gene i		(Extended Experimental Procedure)
λ_r	Characteristic length of ribosomes	3×10^{-8} m	(Politz *et al.*, 2003)
λ_t	Characteristic length of tRNAs	1.5×10^{-8} m	(Nissen *et al.*, 1999)
τ_r	Characteristic time of ribosomes	5×10^{-4} s	(Extended Experimental Procedure)
τ_t	Characteristic time of tRNAs	4.45×10^{-7} s	(Extended Experimental Procedure)
N_r	Positions for ribosomes in volume V	1.56×10^6	(Extended Experimental Procedure)
N_t	Positions for tRNAs in volume V	1.24×10^7	(Extended Experimental Procedure)
t	Total simulation time	1,500 s	(Extended Experimental Procedure)
t_b	Burn-in simulation time	1,000 s	(Extended Experimental Procedure)
w	Wobble parameters	$w_{rr/yy} = 0.61$ $w_{ry/yr} = 0.64$	(Curran & Yarus, 1989; Lim & Curran, 2001)

Table S2. Markov States and Transition Rates, Related to Figure 1

Initiation	Gene #	mRNA # of gene			Initiation rate	Event probability	ΔState
	1	1			0	0	N/A
	1	2			0	0	N/A
	1	3			$\frac{R^f p_1}{\tau_r N_r}$	$\frac{R^f p_1}{\tau_r N_r(\rho^t + \epsilon^t)}$	$R^f \to R^f - 1$
	1	A_1			$\frac{R^f p_1}{\tau_r N_r}$	$\frac{R^f p_1}{\tau_r N_r(\rho^t + \epsilon^t)}$	$R^f \to R^f - 1$
	2	1			$\frac{R^f p_2}{\tau_r N_r}$	$\frac{R^f p_2}{\tau_r N_r(\rho^t + \epsilon^t)}$	$R^f \to R^f - 1$
	2	2			$\frac{R^f p_2}{\tau_r N_r}$	$\frac{R^f p_2}{\tau_r N_r(\rho^t + \epsilon^t)}$	$R^f \to R^f - 1$
	2	.	.	.	.	.	.
	2	A_2			0	0	N/A
	.	.	.	.	.	.	.
	n	.	.	.	.	.	.
	n	A_n			$\frac{R^f p_n}{\tau_r N_r}$	$\frac{R^f p_n}{\tau_r N_r(\rho^t + \epsilon^t)}$	$R^f \to R^f - 1$
				Total initiation rate	$\rho^t = \sum_{i=1}^{n} \frac{R^f f_i A_i p_i}{\tau_r N_r}$		
Elongation	Gene #	mRNA # of gene	Codon position	Ribosome bound	Elongation rate	Event probability	ΔState
	1	1	1	N	0	0	N/A
	1	1	2	Y	$\frac{T^f_{\phi(1,2)} w_{1,2} s}{\tau_t N_t}$	$\frac{T^f_{\phi(1,2)} w_{1,2} s}{\tau_t N_t(\rho^t + \epsilon^t)}$	Ribosome bound at codon 2 →N Ribosome bound at codon 3 →Y
	1	1	3	N	0	0	N/A
	1	1	.	.	.	.	.
	1	1	L_1	N	0	0	N/A
	1	2	1	Y	0	0	N/A
	1	2	.	.	.	.	.
	1	2	11	Y	$\frac{T^f_{\phi(1,11)} w_{1,11} s}{\tau_t N_t}$	$\frac{T^f_{\phi(1,11)} w_{1,11} s}{\tau_t N_t(\rho^t + \epsilon^t)}$	Ribosome bound at codon 11 →N Ribosome bound at codon 12 →Y
	1	2	.	.	.	.	.
	1	2	L_1	Y	$\frac{T^f_{\phi(1,L_1)} w_{1,L_1} s}{\tau_t N_t}$	$\frac{T^f_{\phi(1,L_1)} w_{1,L_1} s}{\tau_t N_t(\rho^t + \epsilon^t)}$	$R^f \to R^f + 1$
	1	.	.	.	.	.	.
	1	A_1	L_1	.	.	.	.
	2	.	.	.	.	.	.
	2	A_2	L_2	.	.	.	.
	.	.	.	.	.	.	.
	n	A_n	L_n	.	.	.	.
				Total elongation rate	$\epsilon^t = \sum_{j=1}^{61} \frac{R^b(j) T^f_{\phi(j)} w_j s}{\tau_t N_t}$		

A precise definition of the state space for our Markov model of translation. The table describes the state of the cell and all possible transitions to other states, along with their associated rates. The first column gives the gene number, which ranges from1 to *n* = 3,795 in our model. The second column indicates the mRNA number of each gene *i*, which ranges from 1 to A_i. The third column indicates the codon position in a given mRNA molecule of gene *i*, which ranges from 1 to L_i. The fourth column indicates whether or not a ribosome is currently bound at each codon position in each mRNA of each gene. In the example illustrated here, the current state features a ribosome bound at gene 1 – mRNA 1 – codon 2, at gene 1 – mRNA 2 – codon 1, at gene 1 – mRNA 2 – codon 11, etc. The fifth column gives the initiation rate of each mRNA molecule, which depends upon the current number of free ribosomes, the characteristic time of a ribosome, the number of positions a ribosome can occupy in the cell, and the gene-specific initiation probability p_i. Furthermore, a gene cannot be initiated if any ribosome is bound within its first 10 codons. The fifth column also indicates the elongation rate of each codon in each mRNA, which depends upon the number of free cognate tRNAs, the wobble parameter, the tRNA competition coefficient *s*, the characteristic time of a tRNA, and the number of position a tRNA can occupy in the cell. Furthermore, elongation at a codon is not possible if another ribosome is bound to the same mRNA molecule within the subsequent 10 codons. The last column indicates the change in state that would be caused by the associated initiation or elongation event. For instance, upon an initiation event, the number of free ribosomes in the cell, R^f decreases by 1. Alternatively, if the ribosome bound at gene 1 – mRNA 1 – codon 2 undergoes elongation, then it frees the ribosome bound at position 2 and adds a ribosome bound at position 3. Finally, if the ribosome bound at gene 1 – mRNA 2 – codon L_1 undergoes elongation, then this leads to termination of translation and increases the number of free ribosomes in the cell, R^f, by 1.

Table S3. List of Ribosomal Genes Used for Estimating RSCU, Related to Figure 2

YBL027W
YBL072C
YBL087C
YBL092W
YBR031W
YBR048W
YBR084CA
YBR181C
YBR189W
YBR191W
YCR031C
YDL061C
YDL075W
YDL081C
YDL082W
YDL083C
YDL130W
YDL136W
YDL184C
YDL191W
YDR012W
YDR025W
YDR064W
YDR382W
YDR418W
YDR447C
YDR450W
YDR471W
YDR500C
YEL054C
YER056CA
YER074W
YER102W
YER117W
YER131W
YFL034CA
YFR031CA
YGL030W
YGL031C
YGL076C
YGL103W
YGL123W
YGL135W
YGL147C
YGL189C
YGR027C
YGR034W
YGR085C
YGR118W
YGR148C
YGR214W
YHL001W
YHL015W
YHL033C
YHR010W
YHR021C
YHR141C
YHR203C
YIL018W
YIL052C
YIL069C
YIL133C
YIL148W
YJL136C
YJL177W
YJL189W
YJL190C
YJL191W
YJR094WA
YJR123W
YJR145C
YKL006W
YKL156W
YKL180W
YKR057W
YKR094C
YLL045C
YLR029C
YLR048W
YLR061W
YLR075W
YLR167W
YLR185W
YLR264W
YLR287CA
YLR325C
YLR333C
YLR340W
YLR344W
YLR367W
YLR388W
YLR406C
YLR441C
YLR448W
YML024W
YML026C
YML063W
YML073C
YMR121C
YMR142C
YMR143W
YMR194W
YMR230W
YMR242C
YNL067W
YNL069C
YNL096C
YNL162W
YNL178W
YNL301C
YNL302C
YOL039W
YOL040C
YOL120C
YOL121C
YOL127W
YOR063W
YOR096W
YOR167C
YOR182C
YOR234C
YOR293W
YOR312C
YOR369C
YPL079W
YPL081W
YPL090C
YPL131W
YPL143W
YPL198W
YPL220W
YPR043W
YPR102C
YPR132W