Table 2. Summary of data sets and variables used as an input of the model.

Input data	*E.coli*	*S.cerevisiae*	*H.sapiens*
Cell line	K12 MG1655	BY4741	HeLa
Temperature	37°C	30°C	37°C
Medium	MOPS	YEPD	–
Global parameters			
Transcriptome size	1,500 [15,35]	36,000 [36]	700,000*
Ribosomes/cell	20,000 [15]	200,000 [37]	9,500,000 [38]
Average cell volume	1e-18 m^3 [29]	42e-18 m^3 [39]	2425e-18 m^3 [40]
Parameters required to calculate mean codon elongation times			
tRNA decoding	[29]	[41]	[42]
tRNA abundances	[43]	[9]	[42]
tRNAs/cell	71,000 [43]	2,800,000 [9]	60,000,000*
Data sets			
Coding sequences	NCBI	SGD	UCSC
mRNA abundances	[11]	[44]	[45]
mRNA lifetime	[46] (M9 medium)	[10]	[47]
Ribosome footprints	[34]	[44]	[45]

Details on data parsing and calculations may be found in the main text. Cell lines and growth conditions (temperature and medium) denote those used in the ribosome profiling experiments. The numbers marked by an asterix were taken from the RNA Tools and Calculators section at the Invitrogen Website (www.invitrogen.com, accessed April 2013). The coding sequences were downloaded from the following databases: NCBI (www.ncbi.nlm.nih.gov.ftp, accessed May 2012), SGD (www.yeastgenome.org, accessed June 2009), and UCSC (http://genome.ucsc.edu, accessed July 2012).
doi:10.1371/journal.pone.0073943.t002