

Supplementary Information

Firczuk et al. 2012

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Full mathematical model

$$\begin{aligned}
\frac{d[\text{eIF2_GDP}]}{dt} &= - (k_{1r1} \cdot [\text{eIF2_GDP}] \cdot [\text{eIF2B}] - k_{2r1} \cdot [\text{eIF2_GDP_eIF2B}]) \\
&\quad + k_{r18} \cdot [60\text{S}] \cdot [48\text{S_Ded1_eIF5B_GTP}] \cdot \text{mRNA_init_free} \\
\frac{d[\text{eIF2B}]}{dt} &= - (k_{1r1} \cdot [\text{eIF2_GDP}] \cdot [\text{eIF2B}] - k_{2r1} \cdot [\text{eIF2_GDP_eIF2B}]) \\
&\quad + (k_{1r2} \cdot [\text{eIF2_GDP_eIF2B}] - k_{2r2} \cdot [\text{eIF2_GTP}] \cdot [\text{eIF2B}]) \\
\frac{d[\text{eIF2_GDP_eIF2B}]}{dt} &= + (k_{1r1} \cdot [\text{eIF2_GDP}] \cdot [\text{eIF2B}] - k_{2r1} \cdot [\text{eIF2_GDP_eIF2B}]) \\
&\quad - (k_{1r2} \cdot [\text{eIF2_GDP_eIF2B}] - k_{2r2} \cdot [\text{eIF2_GTP}] \cdot [\text{eIF2B}]) \\
\frac{d[\text{eIF2_GTP}]}{dt} &= k_{1r2} \cdot [\text{eIF2_GDP_eIF2B}] - k_{2r2} \cdot [\text{eIF2_GTP}] \cdot [\text{eIF2B}] \\
&\quad - (k_{1r3} \cdot [\text{eIF2_GTP}] \cdot [\text{Met-tRNA}] - k_{2r3} \cdot [\text{eIF2_GTP_Met-tRNA}]) \\
\frac{d[\text{eIF2_GTP_Met-tRNA}]}{dt} &= k_{1r3} \cdot [\text{eIF2_GTP}] \cdot [\text{Met-tRNA}] \\
&\quad - k_{2r3} \cdot [\text{eIF2_GTP_Met-tRNA}] \\
&\quad - (k_{1r5} \cdot [\text{eIF2_GTP_Met-tRNA}] \cdot [\text{eIF3_eIF5}] \\
&\quad - k_{2r5} \cdot [\text{eIF3_eIF5_eIF2_GTP_Met-tRNA}]) \\
\frac{d[\text{eIF3}]}{dt} &= k_{r18} \cdot [60\text{S}] \cdot [48\text{S_Ded1_eIF5B_GTP}] \cdot \text{mRNA_init_free} \\
&\quad - (k_{1r4} \cdot [\text{eIF3}] \cdot [\text{eIF5}] - k_{2r4} \cdot [\text{eIF3_eIF5}]) \\
\frac{d[\text{eIF5}]}{dt} &= k_{r18} \cdot [60\text{S}] \cdot [48\text{S_Ded1_eIF5B_GTP}] \cdot \text{mRNA_init_free} \\
&\quad - (k_{1r4} \cdot [\text{eIF3}] \cdot [\text{eIF5}] - k_{2r4} \cdot [\text{eIF3_eIF5}]) \\
\frac{d[\text{eIF3_eIF5}]}{dt} &= k_{1r4} \cdot [\text{eIF3}] \cdot [\text{eIF5}] - k_{2r4} \cdot [\text{eIF3_eIF5}] \\
&\quad - (k_{1r5} \cdot [\text{eIF2_GTP_Met-tRNA}] \cdot [\text{eIF3_eIF5}] \\
&\quad - k_{2r5} \cdot [\text{eIF3_eIF5_eIF2_GTP_Met-tRNA}]) \\
\frac{d[\text{eIF3_eIF5_eIF2_GTP_Met-tRNA}]}{dt} &= k_{1r5} \cdot [\text{eIF2_GTP_Met-tRNA}] \cdot [\text{eIF3_eIF5}] \\
&\quad - k_{2r5} \cdot [\text{eIF3_eIF5_eIF2_GTP_Met-tRNA}] \\
&\quad - (k_{1r6} \cdot [\text{eIF1}] \cdot [\text{eIF3_eIF5_eIF2_GTP_Met-tRNA}] \\
&\quad - k_{2r6} \cdot [\text{eIF1_eIF3_eIF5_eIF2_GTP_Met-tRNA}]) \\
\frac{d[\text{eIF1}]}{dt} &= k_{r18} \cdot [60\text{S}] \cdot [48\text{S_Ded1_eIF5B_GTP}] \cdot \text{mRNA_init_free} \\
&\quad - (k_{1r6} \cdot [\text{eIF1}] \cdot [\text{eIF3_eIF5_eIF2_GTP_Met-tRNA}] \\
&\quad - k_{2r6} \cdot [\text{eIF1_eIF3_eIF5_eIF2_GTP_Met-tRNA}]) \\
\frac{d[\text{eIF1_eIF3_eIF5_eIF2_GTP_Met-tRNA}]}{dt} &= k_{1r6} \cdot [\text{eIF1}] \cdot [\text{eIF3_eIF5_eIF2_GTP_Met-tRNA}] \\
&\quad - k_{2r6} \cdot [\text{eIF1_eIF3_eIF5_eIF2_GTP_Met-tRNA}] \\
&\quad - k_{1r8} \cdot [\text{eIF1_eIF3_eIF5_eIF2_GTP_Met-tRNA}] \cdot [40\text{S_eIF1A}] \\
\frac{d[40\text{S}]}{dt} &= k_{1r33} \cdot [80\text{S_eRF1_eRF3_GTP}] - k_{1r7} \cdot [40\text{S}] \cdot [\text{eIF1A}] \\
\frac{d[\text{eIF1A}]}{dt} &= k_{r18} \cdot [60\text{S}] \cdot [48\text{S_Ded1_eIF5B_GTP}] \cdot \text{mRNA_init_free} \\
&\quad - k_{1r7} \cdot [40\text{S}] \cdot [\text{eIF1A}] \\
\frac{d[40\text{S_eIF1A}]}{dt} &= k_{1r7} \cdot [40\text{S}] \cdot [\text{eIF1A}] \\
&\quad - k_{1r8} \cdot [\text{eIF1_eIF3_eIF5_eIF2_GTP_Met-tRNA}] \cdot [40\text{S_eIF1A}]
\end{aligned}$$

$$\begin{aligned}
\frac{d[43S]}{dt} &= k_{1r8} \cdot [eIF1_eIF3_eIF5_eIF2_GTP_Met-tRNA] \cdot [40S_eIF1A] \\
&\quad - k_{1r14} \cdot [43S] \cdot [eIF4E_eIF4G_mRNA_Pab1_eIF4A_eIF4B] \\
\frac{d[eIF4E]}{dt} &= k_{r18} \cdot [60S] \cdot [48S_Ded1_eIF5B_GTP] \cdot mRNA_init_free \\
&\quad - (k_{1r9} \cdot [eIF4E] \cdot [eIF4G] - k_{2r9} \cdot [eIF4E_eIF4G]) \\
\frac{d[eIF4G]}{dt} &= k_{r18} \cdot [60S] \cdot [48S_Ded1_eIF5B_GTP] \cdot mRNA_init_free \\
&\quad - (k_{1r9} \cdot [eIF4E] \cdot [eIF4G] - k_{2r9} \cdot [eIF4E_eIF4G]) \\
\frac{d[eIF4E_eIF4G]}{dt} &= k_{1r9} \cdot [eIF4E] \cdot [eIF4G] - k_{2r9} \cdot [eIF4E_eIF4G] \\
&\quad - (k_{1r11} \cdot [eIF4E_eIF4G] \cdot [mRNA_Pab1] - k_{2r11} \cdot [eIF4E_eIF4G_mRNA_Pab1]) \\
\frac{d[mRNA_cap]}{dt} &= k_{r18} \cdot [60S] \cdot [48S_Ded1_eIF5B_GTP] \cdot mRNA_init_free \\
&\quad - (k_{1r10} \cdot [mRNA_cap] \cdot [Pab1] - k_{2r10} \cdot [mRNA_Pab1]) \\
\frac{d[Pab1]}{dt} &= k_{r18} \cdot [60S] \cdot [48S_Ded1_eIF5B_GTP] \cdot mRNA_init_free \\
&\quad - (k_{1r10} \cdot [mRNA_cap] \cdot [Pab1] - k_{2r10} \cdot [mRNA_Pab1]) \\
\frac{d[mRNA_Pab1]}{dt} &= k_{1r10} \cdot [mRNA_cap] \cdot [Pab1] - k_{2r10} \cdot [mRNA_Pab1] \\
&\quad - (k_{1r11} \cdot [eIF4E_eIF4G] \cdot [mRNA_Pab1] - k_{2r11} \cdot [eIF4E_eIF4G_mRNA_Pab1]) \\
\frac{d[eIF4E_eIF4G_mRNA_Pab1]}{dt} &= k_{1r11} \cdot [eIF4E_eIF4G] \cdot [mRNA_Pab1] - k_{2r11} \cdot [eIF4E_eIF4G_mRNA_Pab1] \\
&\quad - (k_{1r12} \cdot [eIF4A] \cdot [eIF4E_eIF4G_mRNA_Pab1] \\
&\quad - k_{2r12} \cdot [eIF4A_eIF4E_eIF4G_mRNA_Pab1]) \\
\frac{d[eIF4A]}{dt} &= k_{r18} \cdot [60S] \cdot [48S_Ded1_eIF5B_GTP] \cdot mRNA_init_free \\
&\quad - (k_{1r12} \cdot [eIF4A] \cdot [eIF4E_eIF4G_mRNA_Pab1] \\
\frac{d[eIF4A_eIF4E_eIF4G_mRNA_Pab1]}{dt} &= k_{1r12} \cdot [eIF4A] \cdot [eIF4E_eIF4G_mRNA_Pab1] \\
&\quad - k_{2r12} \cdot [eIF4A_eIF4E_eIF4G_mRNA_Pab1] \\
&\quad - (k_{1r13} \cdot [eIF4B] \cdot [eIF4A_eIF4E_eIF4G_mRNA_Pab1] \\
&\quad - k_{2r13} \cdot [eIF4E_eIF4G_mRNA_Pab1_eIF4A_eIF4B]) \\
\frac{d[eIF4B]}{dt} &= k_{r18} \cdot [60S] \cdot [48S_Ded1_eIF5B_GTP] \cdot mRNA_init_free \\
&\quad - (k_{1r13} \cdot [eIF4B] \cdot [eIF4A_eIF4E_eIF4G_mRNA_Pab1] \\
&\quad - k_{2r13} \cdot [eIF4E_eIF4G_mRNA_Pab1_eIF4A_eIF4B]) \\
\frac{d[eIF4E_eIF4G_mRNA_Pab1_eIF4A_eIF4B]}{dt} &= k_{1r13} \cdot [eIF4B] \cdot [eIF4A_eIF4E_eIF4G_mRNA_Pab1] \\
&\quad - k_{2r13} \cdot [eIF4E_eIF4G_mRNA_Pab1_eIF4A_eIF4B]) \\
&\quad - k_{1r14} \cdot [43S] \cdot [eIF4E_eIF4G_mRNA_Pab1_eIF4A_eIF4B] \\
\frac{d[48S]}{dt} &= k_{1r14} \cdot [43S] \cdot [eIF4E_eIF4G_mRNA_Pab1_eIF4A_eIF4B] \\
&\quad - (k_{1r15} \cdot [48S] \cdot [Ded1] - k_{2r15} \cdot [48S_Ded1]) \\
\frac{d[Ded1]}{dt} &= k_{r18} \cdot [60S] \cdot [48S_Ded1_eIF5B_GTP] \cdot mRNA_init_free \\
&\quad - (k_{1r15} \cdot [48S] \cdot [Ded1] - k_{2r15} \cdot [48S_Ded1]) \\
\frac{d[48S_Ded1]}{dt} &= k_{1r15} \cdot [48S] \cdot [Ded1] - k_{2r15} \cdot [48S_Ded1] \\
&\quad - (k_{1r17} \cdot [48S_Ded1] \cdot [eIF5B_GTP] - k_{2r17} \cdot [48S_Ded1_eIF5B_GTP])
\end{aligned}$$

$$\begin{aligned}
\frac{d[\text{eIF5B_GDP}]}{dt} &= k_{r18} \cdot [60\text{S}] \cdot [48\text{S_Ded1_eIF5B_GTP}] \cdot \text{mRNA_init_free} \\
&\quad - (k_{1r16} \cdot [\text{eIF5B_GDP}] - k_{2r16} \cdot [\text{eIF5B_GTP}]) \\
\frac{d[\text{eIF5B_GTP}]}{dt} &= k_{1r16} \cdot [\text{eIF5B_GDP}] - k_{2r16} \cdot [\text{eIF5B_GTP}] \\
&\quad - (k_{1r17} \cdot [48\text{S_Ded1}] \cdot [\text{eIF5B_GTP}] - k_{2r17} \cdot [48\text{S_Ded1_eIF5B_GTP}]) \\
\frac{d[48\text{S_Ded1_eIF5B_GTP}]}{dt} &= k_{1r17} \cdot [48\text{S_Ded1}] \cdot [\text{eIF5B_GTP}] - k_{2r17} \cdot [48\text{S_Ded1_eIF5B_GTP}] \\
&\quad - k_{r18} \cdot [60\text{S}] \cdot [48\text{S_Ded1_eIF5B_GTP}] \cdot \text{mRNA_init_free} \\
\frac{d[60\text{S}]}{dt} &= k_{1r33} \cdot [80\text{S_eRF1_eRF3_GTP}] \\
&\quad - k_{r18} \cdot [60\text{S}] \cdot [48\text{S_Ded1_eIF5B_GTP}] \cdot \text{mRNA_init_free} \\
\frac{d[\text{eEF1A_GDP}]}{dt} &= k_{23f} \cdot [80\text{S_aa-tRNA_eEF1A_GTP_1}] \\
&\quad + k_{23f} \cdot [80\text{S_aa-tRNA_eEF1A_GTP_2}] \\
&\quad + k_{23f} \cdot [80\text{S_aa-tRNA_eEF1A_GTP_3}] \\
&\quad + k_{23f} \cdot [80\text{S_aa-tRNA_eEF1A_GTP_4}] \\
&\quad + k_{23f} \cdot [80\text{S_aa-tRNA_eEF1A_GTP_5}] \\
&\quad + k_{23f} \cdot [80\text{S_aa-tRNA_eEF1A_GTP_6}] \\
&\quad + k_{23f} \cdot [80\text{S_aa-tRNA_eEF1A_GTP_7}] \\
&\quad + k_{23f} \cdot [80\text{S_aa-tRNA_eEF1A_GTP_8}] \\
&\quad + k_{23f} \cdot [80\text{S_aa-tRNA_eEF1A_GTP_9}] \\
&\quad + k_{23f} \cdot [80\text{S_aa-tRNA_eEF1A_GTP_10}] \\
&\quad + k_{23f} \cdot [80\text{S_aa-tRNA_eEF1A_GTP_11}] \\
&\quad + k_{23f} \cdot [80\text{S_aa-tRNA_eEF1A_GTP_12}] \\
&\quad + k_{23f} \cdot [80\text{S_aa-tRNA_eEF1A_GTP_13}] \\
&\quad + k_{23f} \cdot [80\text{S_aa-tRNA_eEF1A_GTP_14}] \\
&\quad + k_{23f} \cdot [80\text{S_aa-tRNA_eEF1A_GTP_15}] \\
&\quad + k_{23f} \cdot [80\text{S_aa-tRNA_eEF1A_GTP_16}] \\
&\quad + k_{23f} \cdot [80\text{S_aa-tRNA_eEF1A_GTP_17}] \\
&\quad + k_{23f} \cdot [80\text{S_aa-tRNA_eEF1A_GTP_18}] \\
&\quad + k_{23f} \cdot [80\text{S_aa-tRNA_eEF1A_GTP_19}] \\
&\quad - (k_{1r19} \cdot [\text{eEF1A_GDP}] \cdot [\text{eEF1B}] - k_{2r19} \cdot [\text{eEF1A_GDP_eEF1B}]) \\
\frac{d[\text{eEF1B}]}{dt} &= k_{1r20} \cdot [\text{eEF1A_GDP_eEF1B}] - k_{2r20} \cdot [\text{eEF1A_GTP}] \cdot [\text{eEF1B}] \\
&\quad - (k_{1r19} \cdot [\text{eEF1A_GDP}] \cdot [\text{eEF1B}] - k_{2r19} \cdot [\text{eEF1A_GDP_eEF1B}]) \\
\frac{d[\text{eEF1A_GDP_eEF1B}]}{dt} &= k_{1r19} \cdot [\text{eEF1A_GDP}] \cdot [\text{eEF1B}] - k_{2r19} \cdot [\text{eEF1A_GDP_eEF1B}] \\
&\quad - (k_{1r20} \cdot [\text{eEF1A_GDP_eEF1B}] - k_{2r20} \cdot [\text{eEF1A_GTP}] \cdot [\text{eEF1B}]) \\
\frac{d[\text{eEF1A_GTP}]}{dt} &= k_{1r20} \cdot [\text{eEF1A_GDP_eEF1B}] - k_{2r20} \cdot [\text{eEF1A_GTP}] \cdot [\text{eEF1B}] \\
&\quad - (k_{1r21} \cdot [\text{eEF1A_GTP}] \cdot [\text{aa-tRNA}] - k_{2r21} \cdot [\text{aa-tRNA_eEF1A_GTP}])
\end{aligned}$$

$$\begin{aligned}
\frac{d[\text{eEF2_GTP}]}{dt} = & k1_{r24} \cdot [\text{eEF2_GDP}] - k2_{r24} \cdot [\text{eEF2_GTP}] \\
& - (k25f \cdot [\text{eEF2_GTP}] \cdot [\text{80S_aa-tRNA_14}] - k25b \cdot [\text{80S_aa-tRNA_eEF2_GTP_14}]) \\
& - (k25f \cdot [\text{eEF2_GTP}] \cdot [\text{80S_aa-tRNA_15}] - k25b \cdot [\text{80S_aa-tRNA_eEF2_GTP_15}]) \\
& - (k25f \cdot [\text{eEF2_GTP}] \cdot [\text{80S_aa-tRNA_16}] - k25b \cdot [\text{80S_aa-tRNA_eEF2_GTP_16}]) \\
& - (k25f \cdot [\text{eEF2_GTP}] \cdot [\text{80S_aa-tRNA_17}] - k25b \cdot [\text{80S_aa-tRNA_eEF2_GTP_17}]) \\
& - (k25f \cdot [\text{eEF2_GTP}] \cdot [\text{80S_aa-tRNA_18}] - k25b \cdot [\text{80S_aa-tRNA_eEF2_GTP_18}]) \\
& - (k25f \cdot [\text{eEF2_GTP}] \cdot [\text{80S_aa-tRNA_19}] - k25b \cdot [\text{80S_aa-tRNA_eEF2_GTP_19}]) \\
& - (k25f \cdot [\text{eEF2_GTP}] \cdot [\text{80S_aa-tRNA_1}] - k25b \cdot [\text{80S_aa-tRNA_eEF2_GTP_1}]) \\
& - (k25f \cdot [\text{eEF2_GTP}] \cdot [\text{80S_aa-tRNA_2}] - k25b \cdot [\text{80S_aa-tRNA_eEF2_GTP_2}]) \\
& - (k25f \cdot [\text{eEF2_GTP}] \cdot [\text{80S_aa-tRNA_3}] - k25b \cdot [\text{80S_aa-tRNA_eEF2_GTP_3}]) \\
& - (k25f \cdot [\text{eEF2_GTP}] \cdot [\text{80S_aa-tRNA_4}] - k25b \cdot [\text{80S_aa-tRNA_eEF2_GTP_4}]) \\
& - (k25f \cdot [\text{eEF2_GTP}] \cdot [\text{80S_aa-tRNA_5}] - k25b \cdot [\text{80S_aa-tRNA_eEF2_GTP_5}]) \\
& - (k25f \cdot [\text{eEF2_GTP}] \cdot [\text{80S_aa-tRNA_6}] - k25b \cdot [\text{80S_aa-tRNA_eEF2_GTP_6}]) \\
& - (k25f \cdot [\text{eEF2_GTP}] \cdot [\text{80S_aa-tRNA_7}] - k25b \cdot [\text{80S_aa-tRNA_eEF2_GTP_7}]) \\
& - (k25f \cdot [\text{eEF2_GTP}] \cdot [\text{80S_aa-tRNA_8}] - k25b \cdot [\text{80S_aa-tRNA_eEF2_GTP_8}]) \\
& - (k25f \cdot [\text{eEF2_GTP}] \cdot [\text{80S_aa-tRNA_9}] - k25b \cdot [\text{80S_aa-tRNA_eEF2_GTP_9}]) \\
& - (k25f \cdot [\text{eEF2_GTP}] \cdot [\text{80S_aa-tRNA_10}] - k25b \cdot [\text{80S_aa-tRNA_eEF2_GTP_10}]) \\
& - (k25f \cdot [\text{eEF2_GTP}] \cdot [\text{80S_aa-tRNA_11}] - k25b \cdot [\text{80S_aa-tRNA_eEF2_GTP_11}]) \\
& - (k25f \cdot [\text{eEF2_GTP}] \cdot [\text{80S_aa-tRNA_12}] - k25b \cdot [\text{80S_aa-tRNA_eEF2_GTP_12}]) \\
& - (k25f \cdot [\text{eEF2_GTP}] \cdot [\text{80S_aa-tRNA_13}] - k25b \cdot [\text{80S_aa-tRNA_eEF2_GTP_13}])
\end{aligned}$$

$$\begin{aligned}
\frac{d[\text{eEF3_GDP}]}{dt} = & k29f \cdot [\text{80S_tRNA_eEF3_GTP_2}] \\
& + k29f \cdot [\text{80S_tRNA_eEF3_GTP_3}] \\
& + k29f \cdot [\text{80S_tRNA_eEF3_GTP_4}] \\
& + k29f \cdot [\text{80S_tRNA_eEF3_GTP_5}] \\
& + k29f \cdot [\text{80S_tRNA_eEF3_GTP_6}] \\
& + k29f \cdot [\text{80S_tRNA_eEF3_GTP_7}] \\
& + k29f \cdot [\text{80S_tRNA_eEF3_GTP_8}] \\
& + k29f \cdot [\text{80S_tRNA_eEF3_GTP_9}] \\
& + k29f \cdot [\text{80S_tRNA_eEF3_GTP_10}] \\
& + k29f \cdot [\text{80S_tRNA_eEF3_GTP_11}] \\
& + k29f \cdot [\text{80S_tRNA_eEF3_GTP_12}] \\
& + k29f \cdot [\text{80S_tRNA_eEF3_GTP_13}] \\
& + k29f \cdot [\text{80S_tRNA_eEF3_GTP_14}] \\
& + k29f \cdot [\text{80S_tRNA_eEF3_GTP_15}] \\
& + k29f \cdot [\text{80S_tRNA_eEF3_GTP_16}] \\
& + k29f \cdot [\text{80S_tRNA_eEF3_GTP_17}] \\
& + k29f \cdot [\text{80S_tRNA_eEF3_GTP_18}] \\
& + k29f \cdot [\text{80S_tRNA_eEF3_GTP_19}] \\
& + k29f \cdot [\text{80S_tRNA_eEF3_GTP_20}] \\
& - (k1_{r27} \cdot [\text{eEF3_GDP}] - k2_{r27} \cdot [\text{eEF3_GTP}])
\end{aligned}$$

$$\begin{aligned}
\frac{d[\text{eEF3_GTP}]}{dt} &= k_{1r27} \cdot [\text{eEF3_GDP}] - k_{2r27} \cdot [\text{eEF3_GTP}] \\
&\quad - k_{28f} \cdot [\text{80S_tRNA_2}] \cdot [\text{eEF3_GTP}] \\
&\quad - k_{28f} \cdot [\text{80S_tRNA_3}] \cdot [\text{eEF3_GTP}] \\
&\quad - k_{28f} \cdot [\text{80S_tRNA_4}] \cdot [\text{eEF3_GTP}] \\
&\quad - k_{28f} \cdot [\text{80S_tRNA_5}] \cdot [\text{eEF3_GTP}] \\
&\quad - k_{28f} \cdot [\text{80S_tRNA_6}] \cdot [\text{eEF3_GTP}] \\
&\quad - k_{28f} \cdot [\text{80S_tRNA_7}] \cdot [\text{eEF3_GTP}] \\
&\quad - k_{28f} \cdot [\text{80S_tRNA_8}] \cdot [\text{eEF3_GTP}] \\
&\quad - k_{28f} \cdot [\text{80S_tRNA_9}] \cdot [\text{eEF3_GTP}] \\
&\quad - k_{28f} \cdot [\text{80S_tRNA_10}] \cdot [\text{eEF3_GTP}] \\
&\quad - k_{28f} \cdot [\text{80S_tRNA_11}] \cdot [\text{eEF3_GTP}] \\
&\quad - k_{28f} \cdot [\text{80S_tRNA_12}] \cdot [\text{eEF3_GTP}] \\
&\quad - k_{28f} \cdot [\text{80S_tRNA_13}] \cdot [\text{eEF3_GTP}] \\
&\quad - k_{28f} \cdot [\text{80S_tRNA_14}] \cdot [\text{eEF3_GTP}] \\
&\quad - k_{28f} \cdot [\text{80S_tRNA_15}] \cdot [\text{eEF3_GTP}] \\
&\quad - k_{28f} \cdot [\text{80S_tRNA_16}] \cdot [\text{eEF3_GTP}] \\
&\quad - k_{28f} \cdot [\text{80S_tRNA_17}] \cdot [\text{eEF3_GTP}] \\
&\quad - k_{28f} \cdot [\text{80S_tRNA_18}] \cdot [\text{eEF3_GTP}] \\
&\quad - k_{28f} \cdot [\text{80S_tRNA_19}] \cdot [\text{eEF3_GTP}] \\
&\quad - k_{28f} \cdot [\text{80S_tRNA_20}] \cdot [\text{eEF3_GTP}] \\
\frac{d[\text{80S_1}]}{dt} &= k_{r18} \cdot [\text{60S}] \cdot [\text{48S_Ded1_eIF5B_GTP}] \cdot \text{mRNA_init_free} \\
&\quad - (k_{22f} \cdot [\text{aa-tRNA_eEF1A_GTP}] \cdot [\text{80S_1}] - k_{22b} \cdot [\text{80S_aa-tRNA_eEF1A_GTP_1}]) \\
\frac{d[\text{80S_aa-tRNA_eEF1A_GTP_1}]}{dt} &= k_{22f} \cdot [\text{aa-tRNA_eEF1A_GTP}] \cdot [\text{80S_1}] - k_{22b} \cdot [\text{80S_aa-tRNA_eEF1A_GTP_1}] \\
&\quad - k_{23f} \cdot [\text{80S_aa-tRNA_eEF1A_GTP_1}] \\
\frac{d[\text{80S_aa-tRNA_1}]}{dt} &= k_{23f} \cdot [\text{80S_aa-tRNA_eEF1A_GTP_1}] \\
&\quad - (k_{25f} \cdot [\text{eEF2_GTP}] \cdot [\text{80S_aa-tRNA_1}] - k_{25b} \cdot [\text{80S_aa-tRNA_eEF2_GTP_1}]) \\
\frac{d[\text{80S_aa-tRNA_eEF2_GTP_1}]}{dt} &= k_{25f} \cdot [\text{eEF2_GTP}] \cdot [\text{80S_aa-tRNA_1}] - k_{25b} \cdot [\text{80S_aa-tRNA_eEF2_GTP_1}] \\
&\quad - k_{26f} \cdot [\text{80S_aa-tRNA_eEF2_GTP_1}] \cdot \frac{\text{mRNA_num1}}{\text{mRNA_den1}} \\
\frac{d[\text{80S_2}]}{dt} &= k_{29f} \cdot [\text{80S_tRNA_eEF3_GTP_2}] \\
&\quad - (k_{22f} \cdot [\text{aa-tRNA_eEF1A_GTP}] \cdot [\text{80S_2}] - k_{22b} \cdot [\text{80S_aa-tRNA_eEF1A_GTP_2}]) \\
\frac{d[\text{80S_aa-tRNA_eEF1A_GTP_2}]}{dt} &= k_{22f} \cdot [\text{aa-tRNA_eEF1A_GTP}] \cdot [\text{80S_2}] - k_{22b} \cdot [\text{80S_aa-tRNA_eEF1A_GTP_2}] \\
&\quad - k_{23f} \cdot [\text{80S_aa-tRNA_eEF1A_GTP_2}] \\
\frac{d[\text{80S_aa-tRNA_2}]}{dt} &= k_{23f} \cdot [\text{80S_aa-tRNA_eEF1A_GTP_2}] \\
&\quad - (k_{25f} \cdot [\text{eEF2_GTP}] \cdot [\text{80S_aa-tRNA_2}] - k_{25b} \cdot [\text{80S_aa-tRNA_eEF2_GTP_2}]) \\
\frac{d[\text{80S_aa-tRNA_eEF2_GTP_2}]}{dt} &= k_{25f} \cdot [\text{eEF2_GTP}] \cdot [\text{80S_aa-tRNA_2}] - k_{25b} \cdot [\text{80S_aa-tRNA_eEF2_GTP_2}] \\
&\quad - k_{26f} \cdot [\text{80S_aa-tRNA_eEF2_GTP_2}] \cdot \frac{\text{mRNA_num2}}{\text{mRNA_den2}} \\
\frac{d[\text{80S_tRNA_2}]}{dt} &= k_{26f} \cdot [\text{80S_aa-tRNA_eEF2_GTP_1}] \cdot \frac{\text{mRNA_num1}}{\text{mRNA_den1}} \\
&\quad - k_{28f} \cdot [\text{80S_tRNA_2}] \cdot [\text{eEF3_GTP}]
\end{aligned}$$

$$\begin{aligned}
\frac{d[80S_tRNA_eEF3_GTP_2]}{dt} &= k28f \cdot [80S_tRNA_2] \cdot [eEF3_GTP] - k29f \cdot [80S_tRNA_eEF3_GTP_2] \\
\frac{d[80S_3]}{dt} &= k29f \cdot [80S_tRNA_eEF3_GTP_3] \\
&\quad - (k22f \cdot [aa_tRNA_eEF1A_GTP] \cdot [80S_3] - k22b \cdot [80S_aa_tRNA_eEF1A_GTP_3]) \\
\frac{d[80S_aa_tRNA_eEF1A_GTP_3]}{dt} &= k22f \cdot [aa_tRNA_eEF1A_GTP] \cdot [80S_3] - k22b \cdot [80S_aa_tRNA_eEF1A_GTP_3] \\
&\quad - k23f \cdot [80S_aa_tRNA_eEF1A_GTP_3] \\
\frac{d[80S_aa_tRNA_3]}{dt} &= k23f \cdot [80S_aa_tRNA_eEF1A_GTP_3] \\
&\quad - (k25f \cdot [eEF2_GTP] \cdot [80S_aa_tRNA_3] - k25b \cdot [80S_aa_tRNA_eEF2_GTP_3]) \\
\frac{d[80S_aa_tRNA_eEF2_GTP_3]}{dt} &= k25f \cdot [eEF2_GTP] \cdot [80S_aa_tRNA_3] - k25b \cdot [80S_aa_tRNA_eEF2_GTP_3] \\
&\quad + k26f \cdot [80S_aa_tRNA_eEF2_GTP_3] \cdot \frac{mRNA_num3}{mRNA_den3} \\
\frac{d[80S_tRNA_3]}{dt} &= k26f \cdot [80S_aa_tRNA_eEF2_GTP_2] \cdot \frac{mRNA_num2}{mRNA_den2} \\
&\quad - k28f \cdot [80S_tRNA_3] \cdot [eEF3_GTP] \\
\frac{d[80S_tRNA_eEF3_GTP_3]}{dt} &= k28f \cdot [80S_tRNA_3] \cdot [eEF3_GTP] - k29f \cdot [80S_tRNA_eEF3_GTP_3] \\
\frac{d[80S_4]}{dt} &= k29f \cdot [80S_tRNA_eEF3_GTP_4] \\
&\quad - (k22f \cdot [aa_tRNA_eEF1A_GTP] \cdot [80S_4] - k22b \cdot [80S_aa_tRNA_eEF1A_GTP_4]) \\
\frac{d[80S_aa_tRNA_eEF1A_GTP_4]}{dt} &= k22f \cdot [aa_tRNA_eEF1A_GTP] \cdot [80S_4] - k22b \cdot [80S_aa_tRNA_eEF1A_GTP_4] \\
&\quad - (k23f \cdot [80S_aa_tRNA_eEF1A_GTP_4]) \\
\frac{d[80S_aa_tRNA_4]}{dt} &= k23f \cdot [80S_aa_tRNA_eEF1A_GTP_4] \\
&\quad - (k25f \cdot [eEF2_GTP] \cdot [80S_aa_tRNA_4] - k25b \cdot [80S_aa_tRNA_eEF2_GTP_4]) \\
\frac{d[80S_aa_tRNA_eEF2_GTP_4]}{dt} &= k25f \cdot [eEF2_GTP] \cdot [80S_aa_tRNA_4] - k25b \cdot [80S_aa_tRNA_eEF2_GTP_4] \\
&\quad - k26f \cdot [80S_aa_tRNA_eEF2_GTP_4] \cdot \frac{mRNA_num4}{mRNA_den4} \\
\frac{d[80S_tRNA_4]}{dt} &= k26f \cdot [80S_aa_tRNA_eEF2_GTP_3] \cdot \frac{mRNA_num3}{mRNA_den3} \\
&\quad - k28f \cdot [80S_tRNA_4] \cdot [eEF3_GTP] \\
\frac{d[80S_tRNA_eEF3_GTP_4]}{dt} &= k28f \cdot [80S_tRNA_4] \cdot [eEF3_GTP] - k29f \cdot [80S_tRNA_eEF3_GTP_4] \\
\frac{d[80S_5]}{dt} &= k29f \cdot [80S_tRNA_eEF3_GTP_5] \\
&\quad - (k22f \cdot [aa_tRNA_eEF1A_GTP] \cdot [80S_5] - k22b \cdot [80S_aa_tRNA_eEF1A_GTP_5]) \\
\frac{d[80S_aa_tRNA_eEF1A_GTP_5]}{dt} &= k22f \cdot [aa_tRNA_eEF1A_GTP] \cdot [80S_5] - k22b \cdot [80S_aa_tRNA_eEF1A_GTP_5] \\
&\quad - k23f \cdot [80S_aa_tRNA_eEF1A_GTP_5] \\
\frac{d[80S_aa_tRNA_5]}{dt} &= k23f \cdot [80S_aa_tRNA_eEF1A_GTP_5] \\
&\quad - (k25f \cdot [eEF2_GTP] \cdot [80S_aa_tRNA_5] - k25b \cdot [80S_aa_tRNA_eEF2_GTP_5]) \\
\frac{d[80S_aa_tRNA_eEF2_GTP_5]}{dt} &= k25f \cdot [eEF2_GTP] \cdot [80S_aa_tRNA_5] - k25b \cdot [80S_aa_tRNA_eEF2_GTP_5] \\
&\quad - k26f \cdot [80S_aa_tRNA_eEF2_GTP_5] \cdot \frac{mRNA_num5}{mRNA_den5}
\end{aligned}$$

$$\begin{aligned} \frac{d[80S_tRNA_5]}{dt} &= k26f \cdot [80S_aa-tRNA_eEF2_GTP_4] \cdot \frac{mRNA_num4}{mRNA_den4} \\ &\quad - k28f \cdot [80S_tRNA_5] \cdot [eEF3_GTP] \\ \frac{d[80S_tRNA_eEF3_GTP_5]}{dt} &= k28f \cdot [80S_tRNA_5] \cdot [eEF3_GTP] - k29f \cdot [80S_tRNA_eEF3_GTP_5] \\ \frac{d[80S_6]}{dt} &= k29f \cdot [80S_tRNA_eEF3_GTP_6] \\ &\quad - (k22f \cdot [aa-tRNA_eEF1A_GTP] \cdot [80S_6] - k22b \cdot [80S_aa-tRNA_eEF1A_GTP_6]) \\ \frac{d[80S_aa-tRNA_eEF1A_GTP_6]}{dt} &= k22f \cdot [aa-tRNA_eEF1A_GTP] \cdot [80S_6] - k22b \cdot [80S_aa-tRNA_eEF1A_GTP_6] \\ &\quad - k23f \cdot [80S_aa-tRNA_eEF1A_GTP_6] \\ \frac{d[80S_aa-tRNA_6]}{dt} &= k23f \cdot [80S_aa-tRNA_eEF1A_GTP_6] \\ &\quad - (k25f \cdot [eEF2_GTP] \cdot [80S_aa-tRNA_6] - k25b \cdot [80S_aa-tRNA_eEF2_GTP_6]) \\ \frac{d[80S_aa-tRNA_eEF2_GTP_6]}{dt} &= k25f \cdot [eEF2_GTP] \cdot [80S_aa-tRNA_6] - k25b \cdot [80S_aa-tRNA_eEF2_GTP_6] \\ &\quad - k26f \cdot [80S_aa-tRNA_eEF2_GTP_6] \\ \frac{d[80S_tRNA_6]}{dt} &= k26f \cdot [80S_aa-tRNA_eEF2_GTP_5] \cdot \frac{mRNA_num5}{mRNA_den5} \\ &\quad - k28f \cdot [80S_tRNA_6] \cdot [eEF3_GTP] \\ \frac{d[80S_tRNA_eEF3_GTP_6]}{dt} &= k28f \cdot [80S_tRNA_6] \cdot [eEF3_GTP] \\ &\quad - (k29f \cdot [80S_tRNA_eEF3_GTP_6]) \\ \frac{d[80S_7]}{dt} &= k29f \cdot [80S_tRNA_eEF3_GTP_7] \\ &\quad - (k22f \cdot [aa-tRNA_eEF1A_GTP] \cdot [80S_7] - k22b \cdot [80S_aa-tRNA_eEF1A_GTP_7]) \\ \frac{d[80S_aa-tRNA_eEF1A_GTP_7]}{dt} &= k22f \cdot [aa-tRNA_eEF1A_GTP] \cdot [80S_7] - k22b \cdot [80S_aa-tRNA_eEF1A_GTP_7] \\ &\quad - k23f \cdot [80S_aa-tRNA_eEF1A_GTP_7] \\ \frac{d[80S_aa-tRNA_7]}{dt} &= k23f \cdot [80S_aa-tRNA_eEF1A_GTP_7] \\ &\quad - (k25f \cdot [eEF2_GTP] \cdot [80S_aa-tRNA_7] - k25b \cdot [80S_aa-tRNA_eEF2_GTP_7]) \\ \frac{d[80S_aa-tRNA_eEF2_GTP_7]}{dt} &= k25f \cdot [eEF2_GTP] \cdot [80S_aa-tRNA_7] - k25b \cdot [80S_aa-tRNA_eEF2_GTP_7] \\ &\quad - k26f \cdot [80S_aa-tRNA_eEF2_GTP_7] \\ \frac{d[80S_tRNA_7]}{dt} &= k26f \cdot [80S_aa-tRNA_eEF2_GTP_6] - k28f \cdot [80S_tRNA_7] \cdot [eEF3_GTP] \\ \frac{d[80S_tRNA_eEF3_GTP_7]}{dt} &= k28f \cdot [80S_tRNA_7] \cdot [eEF3_GTP] - k29f \cdot [80S_tRNA_eEF3_GTP_7] \\ \frac{d[80S_8]}{dt} &= k29f \cdot [80S_tRNA_eEF3_GTP_8] \\ &\quad - (k22f \cdot [aa-tRNA_eEF1A_GTP] \cdot [80S_8] - k22b \cdot [80S_aa-tRNA_eEF1A_GTP_8]) \\ \frac{d[80S_aa-tRNA_eEF1A_GTP_8]}{dt} &= k22f \cdot [aa-tRNA_eEF1A_GTP] \cdot [80S_8] - k22b \cdot [80S_aa-tRNA_eEF1A_GTP_8] \\ &\quad - k23f \cdot [80S_aa-tRNA_eEF1A_GTP_8] \\ \frac{d[80S_aa-tRNA_8]}{dt} &= k23f \cdot [80S_aa-tRNA_eEF1A_GTP_8] \\ &\quad - (k25f \cdot [eEF2_GTP] \cdot [80S_aa-tRNA_8] - k25b \cdot [80S_aa-tRNA_eEF2_GTP_8]) \\ \frac{d[80S_aa-tRNA_eEF2_GTP_8]}{dt} &= k25f \cdot [eEF2_GTP] \cdot [80S_aa-tRNA_8] - k25b \cdot [80S_aa-tRNA_eEF2_GTP_8] \\ &\quad - k26f \cdot [80S_aa-tRNA_eEF2_GTP_8] \end{aligned}$$

$$\begin{aligned}
\frac{d[80S_tRNA_8]}{dt} &= k26f \cdot [80S_aa-tRNA_eEF2_GTP_7] - k28f \cdot [80S_tRNA_8] \cdot [eEF3_GTP] \\
\frac{d[80S_tRNA_eEF3_GTP_8]}{dt} &= k28f \cdot [80S_tRNA_8] \cdot [eEF3_GTP] - k29f \cdot [80S_tRNA_eEF3_GTP_8] \\
\frac{d[80S_9]}{dt} &= k29f \cdot [80S_tRNA_eEF3_GTP_9] \\
&\quad - (k22f \cdot [aa-tRNA_eEF1A_GTP] \cdot [80S_9] - k22b \cdot [80S_aa-tRNA_eEF1A_GTP_9]) \\
\frac{d[80S_aa-tRNA_eEF1A_GTP_9]}{dt} &= k22f \cdot [aa-tRNA_eEF1A_GTP] \cdot [80S_9] - k22b \cdot [80S_aa-tRNA_eEF1A_GTP_9] \\
&\quad - k23f \cdot [80S_aa-tRNA_eEF1A_GTP_9] \\
\frac{d[80S_aa-tRNA_9]}{dt} &= k23f \cdot [80S_aa-tRNA_eEF1A_GTP_9] \\
&\quad - (k25f \cdot [eEF2_GTP] \cdot [80S_aa-tRNA_9] - k25b \cdot [80S_aa-tRNA_eEF2_GTP_9]) \\
\frac{d[80S_aa-tRNA_eEF2_GTP_9]}{dt} &= k25f \cdot [eEF2_GTP] \cdot [80S_aa-tRNA_9] - k25b \cdot [80S_aa-tRNA_eEF2_GTP_9] \\
&\quad - k26f \cdot [80S_aa-tRNA_eEF2_GTP_9] \\
\frac{d[80S_tRNA_9]}{dt} &= k26f \cdot [80S_aa-tRNA_eEF2_GTP_8] - k28f \cdot [80S_tRNA_9] \cdot [eEF3_GTP] \\
\frac{d[80S_tRNA_eEF3_GTP_9]}{dt} &= k28f \cdot [80S_tRNA_9] \cdot [eEF3_GTP] - k29f \cdot [80S_tRNA_eEF3_GTP_9] \\
\frac{d[80S_10]}{dt} &= k29f \cdot [80S_tRNA_eEF3_GTP_10] \\
&\quad - (k22f \cdot [aa-tRNA_eEF1A_GTP] \cdot [80S_10] - k22b \cdot [80S_aa-tRNA_eEF1A_GTP_10]) \\
\frac{d[80S_aa-tRNA_eEF1A_GTP_10]}{dt} &= k22f \cdot [aa-tRNA_eEF1A_GTP] \cdot [80S_10] - k22b \cdot [80S_aa-tRNA_eEF1A_GTP_10] \\
&\quad - k23f \cdot [80S_aa-tRNA_eEF1A_GTP_10] \\
\frac{d[80S_aa-tRNA_10]}{dt} &= k23f \cdot [80S_aa-tRNA_eEF1A_GTP_10] \\
&\quad - (k25f \cdot [eEF2_GTP] \cdot [80S_aa-tRNA_10] - k25b \cdot [80S_aa-tRNA_eEF2_GTP_10]) \\
\frac{d[80S_aa-tRNA_eEF2_GTP_10]}{dt} &= k25f \cdot [eEF2_GTP] \cdot [80S_aa-tRNA_10] - k25b \cdot [80S_aa-tRNA_eEF2_GTP_10] \\
&\quad - k26f \cdot [80S_aa-tRNA_eEF2_GTP_10] \\
\frac{d[80S_tRNA_10]}{dt} &= k26f \cdot [80S_aa-tRNA_eEF2_GTP_9] - k28f \cdot [80S_tRNA_10] \cdot [eEF3_GTP] \\
\frac{d[80S_tRNA_eEF3_GTP_10]}{dt} &= k28f \cdot [80S_tRNA_10] \cdot [eEF3_GTP] - k29f \cdot [80S_tRNA_eEF3_GTP_10] \\
\frac{d[80S_11]}{dt} &= k29f \cdot [80S_tRNA_eEF3_GTP_11] \\
&\quad - (k22f \cdot [aa-tRNA_eEF1A_GTP] \cdot [80S_11] - k22b \cdot [80S_aa-tRNA_eEF1A_GTP_11]) \\
\frac{d[80S_aa-tRNA_eEF1A_GTP_11]}{dt} &= k22f \cdot [aa-tRNA_eEF1A_GTP] \cdot [80S_11] - k22b \cdot [80S_aa-tRNA_eEF1A_GTP_11] \\
&\quad - k23f \cdot [80S_aa-tRNA_eEF1A_GTP_11] \\
\frac{d[80S_aa-tRNA_11]}{dt} &= k23f \cdot [80S_aa-tRNA_eEF1A_GTP_11] \\
&\quad - (k25f \cdot [eEF2_GTP] \cdot [80S_aa-tRNA_11] - k25b \cdot [80S_aa-tRNA_eEF2_GTP_11]) \\
\frac{d[80S_aa-tRNA_eEF2_GTP_11]}{dt} &= k25f \cdot [eEF2_GTP] \cdot [80S_aa-tRNA_11] - k25b \cdot [80S_aa-tRNA_eEF2_GTP_11] \\
&\quad - k26f \cdot [80S_aa-tRNA_eEF2_GTP_11] \\
\frac{d[80S_tRNA_11]}{dt} &= k26f \cdot [80S_aa-tRNA_eEF2_GTP_10] - k28f \cdot [80S_tRNA_11] \cdot [eEF3_GTP]
\end{aligned}$$

$$\begin{aligned}
\frac{d[80S_tRNA_eEF3_GTP_11]}{dt} &= k28f \cdot [80S_tRNA_11] \cdot [eEF3_GTP] - k29f \cdot [80S_tRNA_eEF3_GTP_11] \\
\frac{d[80S_12]}{dt} &= k29f \cdot [80S_tRNA_eEF3_GTP_12] \\
&\quad - (k22f \cdot [aa_tRNA_eEF1A_GTP] \cdot [80S_12] - k22b \cdot [80S_aa_tRNA_eEF1A_GTP_12]) \\
\frac{d[80S_aa_tRNA_eEF1A_GTP_12]}{dt} &= k22f \cdot [aa_tRNA_eEF1A_GTP] \cdot [80S_12] - k22b \cdot [80S_aa_tRNA_eEF1A_GTP_12] \\
&\quad - k23f \cdot [80S_aa_tRNA_eEF1A_GTP_12] \\
\frac{d[80S_aa_tRNA_12]}{dt} &= k23f \cdot [80S_aa_tRNA_eEF1A_GTP_12] \\
&\quad - (k25f \cdot [eEF2_GTP] \cdot [80S_aa_tRNA_12] - k25b \cdot [80S_aa_tRNA_eEF2_GTP_12]) \\
\frac{d[80S_aa_tRNA_eEF2_GTP_12]}{dt} &= k25f \cdot [eEF2_GTP] \cdot [80S_aa_tRNA_12] - k25b \cdot [80S_aa_tRNA_eEF2_GTP_12] \\
&\quad - k26f \cdot [80S_aa_tRNA_eEF2_GTP_12] \\
\frac{d[80S_tRNA_12]}{dt} &= k26f \cdot [80S_aa_tRNA_eEF2_GTP_11] - k28f \cdot [80S_tRNA_12] \cdot [eEF3_GTP] \\
\frac{d[80S_tRNA_eEF3_GTP_12]}{dt} &= k28f \cdot [80S_tRNA_12] \cdot [eEF3_GTP] - k29f \cdot [80S_tRNA_eEF3_GTP_12] \\
\frac{d[80S_13]}{dt} &= k29f \cdot [80S_tRNA_eEF3_GTP_13] \\
&\quad - (k22f \cdot [aa_tRNA_eEF1A_GTP] \cdot [80S_13] - k22b \cdot [80S_aa_tRNA_eEF1A_GTP_13]) \\
\frac{d[80S_aa_tRNA_eEF1A_GTP_13]}{dt} &= k22f \cdot [aa_tRNA_eEF1A_GTP] \cdot [80S_13] - k22b \cdot [80S_aa_tRNA_eEF1A_GTP_13] \\
&\quad - k23f \cdot [80S_aa_tRNA_eEF1A_GTP_13] \\
\frac{d[80S_aa_tRNA_13]}{dt} &= k23f \cdot [80S_aa_tRNA_eEF1A_GTP_13] \\
&\quad - (k25f \cdot [eEF2_GTP] \cdot [80S_aa_tRNA_13] - k25b \cdot [80S_aa_tRNA_eEF2_GTP_13]) \\
\frac{d[80S_aa_tRNA_eEF2_GTP_13]}{dt} &= k25f \cdot [eEF2_GTP] \cdot [80S_aa_tRNA_13] - k25b \cdot [80S_aa_tRNA_eEF2_GTP_13] \\
&\quad - k26f \cdot [80S_aa_tRNA_eEF2_GTP_13] \\
\frac{d[80S_tRNA_13]}{dt} &= k26f \cdot [80S_aa_tRNA_eEF2_GTP_12] - k28f \cdot [80S_tRNA_13] \cdot [eEF3_GTP] \\
\frac{d[80S_tRNA_eEF3_GTP_13]}{dt} &= k28f \cdot [80S_tRNA_13] \cdot [eEF3_GTP] - k29f \cdot [80S_tRNA_eEF3_GTP_13] \\
\frac{d[80S_14]}{dt} &= k29f \cdot [80S_tRNA_eEF3_GTP_14] \\
&\quad - (k22f \cdot [aa_tRNA_eEF1A_GTP] \cdot [80S_14] - k22b \cdot [80S_aa_tRNA_eEF1A_GTP_14]) \\
\frac{d[80S_aa_tRNA_eEF1A_GTP_14]}{dt} &= k22f \cdot [aa_tRNA_eEF1A_GTP] \cdot [80S_14] - k22b \cdot [80S_aa_tRNA_eEF1A_GTP_14] \\
&\quad - k23f \cdot [80S_aa_tRNA_eEF1A_GTP_14] \\
\frac{d[80S_aa_tRNA_14]}{dt} &= k23f \cdot [80S_aa_tRNA_eEF1A_GTP_14] \\
&\quad - (k25f \cdot [eEF2_GTP] \cdot [80S_aa_tRNA_14] - k25b \cdot [80S_aa_tRNA_eEF2_GTP_14]) \\
\frac{d[80S_aa_tRNA_eEF2_GTP_14]}{dt} &= k25f \cdot [eEF2_GTP] \cdot [80S_aa_tRNA_14] - k25b \cdot [80S_aa_tRNA_eEF2_GTP_14] \\
&\quad - k26f \cdot [80S_aa_tRNA_eEF2_GTP_14] \\
\frac{d[80S_tRNA_14]}{dt} &= k26f \cdot [80S_aa_tRNA_eEF2_GTP_13] - k28f \cdot [80S_tRNA_14] \cdot [eEF3_GTP] \\
\frac{d[80S_tRNA_eEF3_GTP_14]}{dt} &= k28f \cdot [80S_tRNA_14] \cdot [eEF3_GTP] - k29f \cdot [80S_tRNA_eEF3_GTP_14]
\end{aligned}$$

$$\begin{aligned}
\frac{d[80S_{15}]}{dt} &= k_{29f} \cdot [80S_tRNA_eEF3_GTP_{15}] \\
&\quad - (k_{22f} \cdot [aa-tRNA_eEF1A_GTP] \cdot [80S_{15}] - k_{22b} \cdot [80S_aa-tRNA_eEF1A_GTP_{15}]) \\
\frac{d[80S_aa-tRNA_eEF1A_GTP_{15}]}{dt} &= k_{22f} \cdot [aa-tRNA_eEF1A_GTP] \cdot [80S_{15}] - k_{22b} \cdot [80S_aa-tRNA_eEF1A_GTP_{15}] \\
&\quad - k_{23f} \cdot [80S_aa-tRNA_eEF1A_GTP_{15}] \\
\frac{d[80S_aa-tRNA_{15}]}{dt} &= k_{23f} \cdot [80S_aa-tRNA_eEF1A_GTP_{15}] \\
&\quad - (k_{25f} \cdot [eEF2_GTP] \cdot [80S_aa-tRNA_{15}] - k_{25b} \cdot [80S_aa-tRNA_eEF2_GTP_{15}]) \\
\frac{d[80S_aa-tRNA_eEF2_GTP_{15}]}{dt} &= k_{25f} \cdot [eEF2_GTP] \cdot [80S_aa-tRNA_{15}] - k_{25b} \cdot [80S_aa-tRNA_eEF2_GTP_{15}] \\
&\quad - k_{26f} \cdot [80S_aa-tRNA_eEF2_GTP_{15}] \\
\frac{d[80S_tRNA_{15}]}{dt} &= k_{26f} \cdot [80S_aa-tRNA_eEF2_GTP_{14}] - k_{28f} \cdot [80S_tRNA_{15}] \cdot [eEF3_GTP] \\
\frac{d[80S_tRNA_eEF3_GTP_{15}]}{dt} &= k_{28f} \cdot [80S_tRNA_{15}] \cdot [eEF3_GTP] - k_{29f} \cdot [80S_tRNA_eEF3_GTP_{15}] \\
\frac{d[80S_{16}]}{dt} &= k_{29f} \cdot [80S_tRNA_eEF3_GTP_{16}] \\
&\quad - (k_{22f} \cdot [aa-tRNA_eEF1A_GTP] \cdot [80S_{16}] - k_{22b} \cdot [80S_aa-tRNA_eEF1A_GTP_{16}]) \\
\frac{d[80S_aa-tRNA_eEF1A_GTP_{16}]}{dt} &= k_{22f} \cdot [aa-tRNA_eEF1A_GTP] \cdot [80S_{16}] - k_{22b} \cdot [80S_aa-tRNA_eEF1A_GTP_{16}] \\
&\quad - k_{23f} \cdot [80S_aa-tRNA_eEF1A_GTP_{16}] \\
\frac{d[80S_aa-tRNA_{16}]}{dt} &= k_{23f} \cdot [80S_aa-tRNA_eEF1A_GTP_{16}] \\
&\quad - (k_{25f} \cdot [eEF2_GTP] \cdot [80S_aa-tRNA_{16}] - k_{25b} \cdot [80S_aa-tRNA_eEF2_GTP_{16}]) \\
\frac{d[80S_aa-tRNA_eEF2_GTP_{16}]}{dt} &= k_{25f} \cdot [eEF2_GTP] \cdot [80S_aa-tRNA_{16}] - k_{25b} \cdot [80S_aa-tRNA_eEF2_GTP_{16}] \\
&\quad - k_{26f} \cdot [80S_aa-tRNA_eEF2_GTP_{16}] \\
\frac{d[80S_tRNA_{16}]}{dt} &= k_{26f} \cdot [80S_aa-tRNA_eEF2_GTP_{15}] - k_{28f} \cdot [80S_tRNA_{16}] \cdot [eEF3_GTP] \\
\frac{d[80S_tRNA_eEF3_GTP_{16}]}{dt} &= k_{28f} \cdot [80S_tRNA_{16}] \cdot [eEF3_GTP] - k_{29f} \cdot [80S_tRNA_eEF3_GTP_{16}] \\
\frac{d[80S_{17}]}{dt} &= k_{29f} \cdot [80S_tRNA_eEF3_GTP_{17}] \\
&\quad - (k_{22f} \cdot [aa-tRNA_eEF1A_GTP] \cdot [80S_{17}] - k_{22b} \cdot [80S_aa-tRNA_eEF1A_GTP_{17}]) \\
\frac{d[80S_aa-tRNA_eEF1A_GTP_{17}]}{dt} &= k_{22f} \cdot [aa-tRNA_eEF1A_GTP] \cdot [80S_{17}] - k_{22b} \cdot [80S_aa-tRNA_eEF1A_GTP_{17}] \\
&\quad - k_{23f} \cdot [80S_aa-tRNA_eEF1A_GTP_{17}] \\
\frac{d[80S_aa-tRNA_{17}]}{dt} &= k_{23f} \cdot [80S_aa-tRNA_eEF1A_GTP_{17}] \\
&\quad - (k_{25f} \cdot [eEF2_GTP] \cdot [80S_aa-tRNA_{17}] - k_{25b} \cdot [80S_aa-tRNA_eEF2_GTP_{17}]) \\
\frac{d[80S_aa-tRNA_eEF2_GTP_{17}]}{dt} &= k_{25f} \cdot [eEF2_GTP] \cdot [80S_aa-tRNA_{17}] - k_{25b} \cdot [80S_aa-tRNA_eEF2_GTP_{17}] \\
&\quad - k_{26f} \cdot [80S_aa-tRNA_eEF2_GTP_{17}] \\
\frac{d[80S_tRNA_{17}]}{dt} &= k_{26f} \cdot [80S_aa-tRNA_eEF2_GTP_{16}] - k_{28f} \cdot [80S_tRNA_{17}] \cdot [eEF3_GTP] \\
\frac{d[80S_tRNA_eEF3_GTP_{17}]}{dt} &= k_{28f} \cdot [80S_tRNA_{17}] \cdot [eEF3_GTP] - k_{29f} \cdot [80S_tRNA_eEF3_GTP_{17}] \\
\frac{d[80S_{18}]}{dt} &= k_{29f} \cdot [80S_tRNA_eEF3_GTP_{18}] \\
&\quad - (k_{22f} \cdot [aa-tRNA_eEF1A_GTP] \cdot [80S_{18}] - k_{22b} \cdot [80S_aa-tRNA_eEF1A_GTP_{18}])
\end{aligned}$$

$$\begin{aligned}
\frac{d[80S_aa-tRNA_eEF1A_GTP_18]}{dt} &= k22f \cdot [aa-tRNA_eEF1A_GTP] \cdot [80S_18] - k22b \cdot [80S_aa-tRNA_eEF1A_GTP_18] \\
&\quad - k23f \cdot [80S_aa-tRNA_eEF1A_GTP_18] \\
\frac{d[80S_aa-tRNA_18]}{dt} &= k23f \cdot [80S_aa-tRNA_eEF1A_GTP_18] \\
&\quad - (k25f \cdot [eEF2_GTP] \cdot [80S_aa-tRNA_18] - k25b \cdot [80S_aa-tRNA_eEF2_GTP_18]) \\
\frac{d[80S_aa-tRNA_eEF2_GTP_18]}{dt} &= k25f \cdot [eEF2_GTP] \cdot [80S_aa-tRNA_18] - k25b \cdot [80S_aa-tRNA_eEF2_GTP_18] \\
&\quad - k26f \cdot [80S_aa-tRNA_eEF2_GTP_18] \\
\frac{d[80S_tRNA_18]}{dt} &= k26f \cdot [80S_aa-tRNA_eEF2_GTP_17] - k28f \cdot [80S_tRNA_18] \cdot [eEF3_GTP] \\
\frac{d[80S_tRNA_eEF3_GTP_18]}{dt} &= k28f \cdot [80S_tRNA_18] \cdot [eEF3_GTP] - k29f \cdot [80S_tRNA_eEF3_GTP_18] \\
\frac{d[80S_19]}{dt} &= k29f \cdot [80S_tRNA_eEF3_GTP_19] \\
&\quad - (k22f \cdot [aa-tRNA_eEF1A_GTP] \cdot [80S_19] - k22b \cdot [80S_aa-tRNA_eEF1A_GTP_19]) \\
\frac{d[80S_aa-tRNA_eEF1A_GTP_19]}{dt} &= k22f \cdot [aa-tRNA_eEF1A_GTP] \cdot [80S_19] - k22b \cdot [80S_aa-tRNA_eEF1A_GTP_19] \\
&\quad - k23f \cdot [80S_aa-tRNA_eEF1A_GTP_19] \\
\frac{d[80S_aa-tRNA_19]}{dt} &= k23f \cdot [80S_aa-tRNA_eEF1A_GTP_19] \\
&\quad - (k25f \cdot [eEF2_GTP] \cdot [80S_aa-tRNA_19] - k25b \cdot [80S_aa-tRNA_eEF2_GTP_19]) \\
\frac{d[80S_aa-tRNA_eEF2_GTP_19]}{dt} &= k25f \cdot [eEF2_GTP] \cdot [80S_aa-tRNA_19] - k25b \cdot [80S_aa-tRNA_eEF2_GTP_19] \\
&\quad - k26f \cdot [80S_aa-tRNA_eEF2_GTP_19] \\
\frac{d[80S_tRNA_19]}{dt} &= k26f \cdot [80S_aa-tRNA_eEF2_GTP_18] - k28f \cdot [80S_tRNA_19] \cdot [eEF3_GTP] \\
\frac{d[80S_tRNA_eEF3_GTP_19]}{dt} &= k28f \cdot [80S_tRNA_19] \cdot [eEF3_GTP] - k29f \cdot [80S_tRNA_eEF3_GTP_19] \\
\frac{d[80S_20]}{dt} &= k29f \cdot [80S_tRNA_eEF3_GTP_20] - k1_{r32} \cdot [eRF1_eRF3_GTP] \cdot [80S_20] \\
\frac{d[80S_tRNA_20]}{dt} &= k26f \cdot [80S_aa-tRNA_eEF2_GTP_19] - k28f \cdot [80S_tRNA_20] \cdot [eEF3_GTP] \\
\frac{d[80S_tRNA_eEF3_GTP_20]}{dt} &= k28f \cdot [80S_tRNA_20] \cdot [eEF3_GTP] - k29f \cdot [80S_tRNA_eEF3_GTP_20] \\
\frac{d[eRF3_GDP]}{dt} &= k1_{r33} \cdot [80S_eRF1_eRF3_GTP] - (k1_{r30} \cdot [eRF3_GDP] - k2_{r30} \cdot [eRF3_GTP]) \\
\frac{d[eRF3_GTP]}{dt} &= k1_{r30} \cdot [eRF3_GDP] - k2_{r30} \cdot [eRF3_GTP] \\
&\quad - (k1_{r31} \cdot [eRF1] \cdot [eRF3_GTP] - k2_{r31} \cdot [eRF1_eRF3_GTP]) \\
\frac{d[eRF1]}{dt} &= k1_{r33} \cdot [80S_eRF1_eRF3_GTP] - (k1_{r31} \cdot [eRF1] \cdot [eRF3_GTP] - k2_{r31} \cdot [eRF1_eRF3_GTP]) \\
\frac{d[eRF1_eRF3_GTP]}{dt} &= k1_{r31} \cdot [eRF1] \cdot [eRF3_GTP] - k2_{r31} \cdot [eRF1_eRF3_GTP] \\
&\quad - k1_{r32} \cdot [eRF1_eRF3_GTP] \cdot [80S_20] \\
\frac{d[80S_eRF1_eRF3_GTP]}{dt} &= k1_{r32} \cdot [eRF1_eRF3_GTP] \cdot [80S_20] - k1_{r33} \cdot [80S_eRF1_eRF3_GTP]
\end{aligned}$$

$$\begin{aligned}
\text{mRNA_init_free} = & \text{mRNA_tot} - ([80\text{S}_1] + [80\text{S_aa-tRNA_eEF1A_GTP}_1] \\
& + [80\text{S_aa-tRNA}_1] + [80\text{S_aa-tRNA_eEF2_GTP}_1] + [80\text{S}_2] + [80\text{S_aa-tRNA_eEF1A_GTP}_2] \\
& + [80\text{S_aa-tRNA}_2] + [80\text{S_aa-tRNA_eEF2_GTP}_2] + [80\text{S_tRNA}_2] + [80\text{S_tRNA_eEF3_GTP}_2] \\
& + [80\text{S}_3] + [80\text{S_aa-tRNA_eEF1A_GTP}_3] + [80\text{S_aa-tRNA}_3] + [80\text{S_aa-tRNA_eEF2_GTP}_3] \\
& + [80\text{S_tRNA}_3] + [80\text{S_tRNA_eEF3_GTP}_3] + [80\text{S}_4] + [80\text{S_aa-tRNA_eEF1A_GTP}_4] \\
& + [80\text{S_aa-tRNA}_4] + [80\text{S_aa-tRNA_eEF2_GTP}_4] + [80\text{S_tRNA}_4] + [80\text{S_tRNA_eEF3_GTP}_4] \\
& + [80\text{S}_5] + [80\text{S_aa-tRNA_eEF1A_GTP}_5] + [80\text{S_aa-tRNA}_5] + [80\text{S_aa-tRNA_eEF2_GTP}_5] \\
& + [80\text{S_tRNA}_5] + [80\text{S_tRNA_eEF3_GTP}_5] + [80\text{S}_6] + [80\text{S_aa-tRNA_eEF1A_GTP}_6] \\
& + [80\text{S_aa-tRNA}_6] + [80\text{S_aa-tRNA_eEF2_GTP}_6] + [80\text{S_tRNA}_6] + [80\text{S_tRNA_eEF3_GTP}_6] \\
& + [80\text{S}_7] + [80\text{S_aa-tRNA_eEF1A_GTP}_7] + [80\text{S_aa-tRNA}_7] + [80\text{S_aa-tRNA_eEF2_GTP}_7] \\
& + [80\text{S_tRNA}_7] + [80\text{S_tRNA_eEF3_GTP}_7] + [80\text{S}_8] + [80\text{S_aa-tRNA_eEF1A_GTP}_8] \\
& + [80\text{S_aa-tRNA}_8] + [80\text{S_aa-tRNA_eEF2_GTP}_8] + [80\text{S_tRNA}_8] + [80\text{S_tRNA_eEF3_GTP}_8] \\
& + [80\text{S_tRNA}_9] + [80\text{S_tRNA_eEF3_GTP}_9] + [80\text{S}_{10}] + [80\text{S_aa-tRNA_eEF1A_GTP}_{10}] \\
& + [80\text{S_aa-tRNA}_{10}] + [80\text{S_aa-tRNA_eEF2_GTP}_{10}] + [80\text{S_tRNA}_{10}] + [80\text{S_tRNA_eEF3_GTP}_{10}] \\
& + [80\text{S}_{11}] + [80\text{S_aa-tRNA_eEF1A_GTP}_{11}] + [80\text{S_aa-tRNA}_{11}] + [80\text{S_aa-tRNA_eEF2_GTP}_{11}] \\
& + [80\text{S_tRNA}_{11}] + [80\text{S_tRNA_eEF3_GTP}_{11}] + [80\text{S}_{12}] + [80\text{S_aa-tRNA_eEF1A_GTP}_{12}] \\
& + [80\text{S_aa-tRNA}_{12}] + [80\text{S_aa-tRNA_eEF2_GTP}_{12}] + [80\text{S_tRNA}_{12}] + [80\text{S_tRNA_eEF3_GTP}_{12}] \\
& + [80\text{S}_{13}] + [80\text{S_aa-tRNA_eEF1A_GTP}_{13}] + [80\text{S_aa-tRNA}_{13}] + [80\text{S_aa-tRNA_eEF2_GTP}_{13}] \\
& + [80\text{S_tRNA}_{13}] + [80\text{S_tRNA_eEF3_GTP}_{13}] + [80\text{S}_{14}] + [80\text{S_aa-tRNA_eEF1A_GTP}_{14}] \\
& + [80\text{S_aa-tRNA}_{14}] + [80\text{S_aa-tRNA_eEF2_GTP}_{14}] + [80\text{S_tRNA}_{14}] + [80\text{S_tRNA_eEF3_GTP}_{14}] \\
& + [80\text{S}_{15}] + [80\text{S_aa-tRNA_eEF1A_GTP}_{15}] + [80\text{S_aa-tRNA}_{15}] + [80\text{S_aa-tRNA_eEF2_GTP}_{15}] \\
& + [80\text{S_tRNA}_{15}] + [80\text{S_tRNA_eEF3_GTP}_{15}])
\end{aligned}$$

Supplementary Table I. Strains used in this study

Strain Name	Strain collection number	Derived from:	Genotype (difference from a parental strain)	Source
WT	PTC41	W303	MAT α <i>ade2-1 ura3-1 leu2-3, 112 his3-11,15 can1-100</i>	M. Tuite, University of Kent
<i>tetO7RPS5</i>	PTC389	PTC41	<i>RPS5-PtetO7:KanMX</i>	This study
<i>tetO7SUI1</i>	PTC277	PTC41	<i>SUI1-PtetO7:KanMX</i>	This study
<i>tetO7TIF11</i>	PTC269	PTC41	<i>TIF11-PtetO7:KanMX</i>	This study
<i>tetO7SUI2</i>	PTC390	PTC41	<i>SUI2-PtetO7:KanMX</i>	This study
<i>tetO7CGD11</i>	PTC273	PTC41	<i>GCD11-PtetO7:KanMX</i>	This study
<i>tetO7GCD6</i>	PTC272	PTC41	<i>GCD6-PtetO7:KanMX</i>	This study
<i>tetO7GCD1</i>	PTC400	PTC41	<i>GCD1-PtetO7:KanMX</i>	This study
<i>tetO7RPG1-60</i>	PTC391	PTC41	<i>RPG1-60bp-PtetO7:KanMX</i>	This study
<i>tetO7NIP1-60</i>	PTC401	PTC41	<i>NIP1-60bp-PtetO7:KanMX</i>	This study
<i>tetO7HCRI</i>	PTC270	PTC41	<i>HCRI-PtetO7:KanMX</i>	This study
<i>TIF1Δ</i>	PTC392	PTC41	<i>TIF1Δ</i>	This study
<i>TIF2Δ</i>	PTC267	PTC41	<i>TIF2Δ</i>	This study
<i>tetO7TIF2 TIF1Δ</i>	PTC393	PTC392	<i>TIF2-PtetO7:KanMX</i>	This study
<i>tetO7TIF3</i>	PTC394	PTC41	<i>TIF3-PtetO7:KanMX</i>	This study
<i>tetO7CDC33</i>	PTC278	PTC41	<i>CDC33-PtetO7:KanMX</i>	This study
<i>TIF4632Δ</i>	PTC274	PTC41	<i>TIF4632Δ</i>	This study
<i>tetO7TIF4631 TIF4632Δ</i>	PTC276	PTC274	<i>TIF4631-PtetO7:KanMX</i>	This study
<i>tetO7TIF5</i>	PTC268	PTC41	<i>TIF5-PtetO7:KanMX</i>	This study
<i>tetO7FUN12</i>	PTC265	PTC41	<i>FUN12-PtetO7:KanMX</i>	This study
<i>TEF1Δ</i>	PTC402	PTC41	<i>TEF1Δ</i>	This study
<i>TEF2Δ</i>	PTC354	PTC41	<i>TEF2Δ</i>	This study
<i>tetO7TEF1 TEF2Δ</i>	PTC362	PTC354	<i>TEF1-PtetO7:KanMX</i>	This study
<i>tetO7TEF5</i>	PTC363	PTC41	<i>TEF5-PtetO7:KanMX</i>	This study
<i>EFT1Δ</i>	PTC403	PTC41	<i>EFT1Δ</i>	This study
<i>EFT2Δ</i>	PTC355	PTC41	<i>EFT2Δ</i>	This study
<i>tetO7EFT1 EFT2Δ</i>	PTC364	PTC355	<i>EFT1-PtetO7:KanMX</i>	This study
<i>tetO7YEF3</i>	PTC365	PTC41	<i>YEF3-PtetO7:KanMX</i>	This study
<i>tetO7SUP35</i>	PTC367	PTC41	<i>SUP35-PtetO7:KanMX</i>	This study
<i>tetO7SUP45</i>	PTC366	PTC41	<i>SUP45-PtetO7:KanMX</i>	This study
<i>tetO7DBP5</i>	PTC398	PTC41	<i>DBP5-PtetO7:KanMX</i>	This study
<i>tetO7DED1-30</i>	PTC397	PTC41	<i>DED1-30bp-PtetO7:KanMX</i>	This study
<i>tetO7HYP2</i>	PTC395	PTC41	<i>HYP2-PtetO7:KanMX</i>	This study
<i>tetO7PAB1</i>	PTC271	PTC41	<i>PAB1-PtetO7:KanMX</i>	This study
<i>competitor</i>	PTC404	PTC41	<i>lys2Δ:KanMX</i>	This study

Supplementary Table II. Plasmids constructed in this study

Plasmid Name	Plasmid collection number	Description:
<i>pTRPEX</i>	pJM798	<i>GPF</i> promoter in <i>YCp33-Supex2</i> substituted with <i>TEF1</i> promoter
<i>pTEFEX</i>	pJM815	<i>GPF</i> promoter in <i>YCp33-Supex2</i> substituted with <i>TRP1</i> promoter
<i>pTRPEX SUI1</i>	pJM790	<i>SUI1</i> gene under control of <i>TRP1</i> promoter
<i>pLEUEX SUI1</i>	pJM860	<i>SUI1</i> gene under control of truncated <i>LEU4</i> promoter
<i>pPGKEX SUI1</i>	pJM866	<i>SUI1</i> gene under control of truncated <i>PGK1</i> promoter
<i>pTEFEX SUI1</i>	pJM832	<i>SUI1</i> gene under control of <i>TEF1</i> promoter
<i>pTEFEX TIF11</i>	pJM822	<i>TIF11</i> gene under control of <i>TEF1</i> promoter
<i>pTRPEX TIF11</i>	pJM810	<i>TIF11</i> gene under control of <i>TRP1</i> promoter
<i>pTRPEX SUI2</i>	pJM804	<i>SUI2</i> gene under control of <i>TRP1</i> promoter
<i>pLEUEX SUI2</i>	pJM862	<i>SUI2</i> gene under control of truncated <i>LEU4</i> promoter
<i>pPGKEX SUI2</i>	pJM867	<i>SUI2</i> gene under control of truncated <i>PGK1</i> promoter
<i>pTEFEX GCD1</i>	pJM901	<i>GCD1</i> gene under control of <i>TEF1</i> promoter
<i>pTRPEX GCD1</i>	pJM902	<i>GCD1</i> gene under control of <i>TRP1</i> promoter
<i>pTEFEX GCD6</i>	pJM826	<i>GCD6</i> gene under control of <i>TEF1</i> promoter
<i>pTRPEX GCD6</i>	pJM808	<i>GCD6</i> gene under control of <i>TRP1</i> promoter
<i>pTEFEX RPG1</i>	pJM827	<i>RPG1</i> gene under control of <i>TEF1</i> promoter
<i>pPGKEX RPG1</i>	pJM869	<i>RPG1</i> gene under control of truncated <i>PGK1</i> promoter
<i>pTRPEX RPG1</i>	pJM809	<i>RPG1</i> gene under control of <i>TRP1</i> promoter
<i>pTEFEX NIP1</i>	pJM880	<i>NIP1</i> gene under control of <i>TEF1</i> promoter
<i>pTRPEX NIP1</i>	pJM881	<i>NIP1</i> gene under control of <i>TRP1</i> promoter
<i>pTEFEX HCR1</i>	pJM824	<i>HCR1</i> gene under control of <i>TEF1</i> promoter
<i>pTEFEX TIF1</i>	pJM817	<i>TIF1</i> gene under control of <i>TEF1</i> promoter
<i>pTRPEX TIF1</i>	pJM813	<i>TIF1</i> gene under control of <i>TRP1</i> promoter
<i>pTEFEX TIF3</i>	pJM825	<i>TIF3</i> gene under control of <i>TEF1</i> promoter
<i>pTRPEX TIF3</i>	pJM806	<i>TIF3</i> gene under control of <i>TRP1</i> promoter
<i>pTEFEX CDC33</i>	pJM882	<i>CDC33</i> gene under control of <i>TEF1</i> promoter
<i>pTRPEX CDC33</i>	pJM883	<i>CDC33</i> gene under control of <i>TRP1</i> promoter
<i>pTEFEX TIF4631</i>	pJM884	<i>TIF4631</i> gene under control of <i>TEF1</i> promoter
<i>pTRPEX TIF4631</i>	pJM885	<i>TIF4631</i> gene under control of <i>TRP1</i> promoter
<i>pTEFEX TIF5</i>	pJM820	<i>TIF5</i> gene under control of <i>TEF1</i> promoter
<i>pTRPEX TIF5</i>	pJM807	<i>TIF5</i> gene under control of <i>TRP1</i> promoter
<i>pTEFEX FUN12</i>	pJM821	<i>FUN12</i> gene under control of <i>TEF1</i> promoter
<i>pTRPEX FUN12</i>	pJM886	<i>FUN12</i> gene under control of <i>TRP1</i> promoter
<i>pTEFEX DED1</i>	pJM816	<i>DED1</i> gene under control of <i>TEF1</i> promoter
<i>pTRPEX DED1</i>	pJM799	<i>DED1</i> gene under control of <i>TRP1</i> promoter
<i>pLEUEX DED1</i>	pJM887	<i>DED1</i> gene under control of truncated <i>LEU4</i> promoter
<i>pPGKEX DED1</i>	pJM888	<i>DED1</i> gene under control of truncated <i>PGK1</i> promoter
<i>pTEFEX PAB1</i>	pJM823	<i>PAB1</i> gene under control of <i>TEF1</i> promoter
<i>pTRPEX PAB1</i>	pJM889	<i>PAB1</i> gene under control of <i>TRP1</i> promoter
<i>pTEFEX TEF1</i>	pJM890	<i>TEF1</i> gene under control of <i>TEF1</i> promoter
<i>pTEF5EX TEF1</i>	pJM913	<i>TEF1</i> gene under control of <i>TEF5</i> promoter
<i>pTEFEX TEF5</i>	pJM891	<i>TEF5</i> gene under control of <i>TEF1</i> promoter
<i>pTEFEX YEF3</i>	pJM892	<i>YEF3</i> gene under control of <i>TEF1</i> promoter

<i>pTRPEX SUP45</i>	pJM805	<i>SUP45</i> gene under control of <i>TRP1</i> promoter
<i>pTEFEX SUP35</i>	pJM893	<i>SUP35</i> gene under control of <i>TEF1</i> promoter
<i>pTEFEX HYP2</i>	pJM894	<i>HYP2</i> gene under control of <i>TEF1</i> promoter
<i>pTRPEX HYP2</i>	pJM895	<i>HYP2</i> gene under control of <i>TRP1</i> promoter
<i>pTEFEX DBP5</i>	pJM896	<i>DBP5</i> gene under control of <i>TEF1</i> promoter
<i>pTRPEX DBP5</i>	pJM897	<i>DBP5</i> gene under control of <i>TRP1</i> promoter
<i>pTRPEX RPS5</i>	pJM802	<i>RPS5</i> gene under control of <i>TRP1</i> promoter
<i>pTRPEX-HIS3L2-LucF</i>	pJM898	<i>Firefly</i> luciferase gene with L2 mRNA leader sequence under control of <i>TRP1</i> promoter
<i>pDCDEX L0-LucR</i>	pJM899	<i>Renilla</i> luciferase gene with L0 mRNA leader sequence under control of <i>DCD1</i> promoter
<i>pDLV L2-LucF L0-LucR</i>	pJM900	Scanning competence assay vector containing two luciferase genes – <i>Renilla</i> and <i>Firefly</i> – preceded by leader sequences (L0 and L2, respectively)

Supplementary Table III. Interactions of translation machinery components

Translation Factor	Reported direct interactions	Source
eIF1	eIF2, eIF3, eIF4G, eIF5, R,	Asano <i>et al.</i> , 2000; He <i>et al.</i> , 2003; Singh <i>et al.</i> , 2004; Passmore <i>et al.</i> , 2007; Reibarkh <i>et al.</i> , 2008 ;
eIF1A	eIF2, eIF3, eIF5B, R,	Fekete <i>et al.</i> , 2007; Fringer <i>et al.</i> , 2007; Olsen <i>et al.</i> , 2003; Passmore <i>et al.</i> , 2007; Zheng <i>et al.</i> , 2011;
eIF2	eIF1, eIF1A, eIF2B, eIF3, eIF5, R, mRNA, Met-tRNA _i ^{Met}	Assano <i>et al.</i> , 1999; Bushman <i>et al.</i> , 1993; Kimball 1999; Laurino <i>et al.</i> , 1999; Mohammad-Qureshi <i>et al.</i> , 2007; Olsen <i>et al.</i> , 2003; Singh <i>et al.</i> , 2004; Valasek <i>et al.</i> , 2002;
eIF2B	eIF2,	Bushman <i>et al.</i> , 1993; Mohammad-Qureshi <i>et al.</i> , 2007;
eIF3	eIF1, eIF1A, eIF2, eIF4B, eIF5, R,	Asano <i>et al.</i> , 2000; Valasek <i>et al.</i> , 2002; Valasek <i>et al.</i> , 2003; Vornloche <i>et al.</i> , 1999; Olsen <i>et al.</i> , 2003;
eIF4A	eIF4G, mRNA,	Dominguez <i>et al.</i> , 1999; Marsden <i>et al.</i> , 2006; Neff and Sachs 1999; Rogers <i>et al.</i> , 1999; Schütz <i>et al.</i> , 2008;
eIF4B	eIF3, mRNA,	Altmann <i>et al.</i> , 1995; Marsden <i>et al.</i> , 2006; Vornloche <i>et al.</i> , 1999;
eIF4E	eIF4G, mRNA,	Altmann <i>et al.</i> , 1997; Mader <i>et al.</i> , 1995; Kiraga-Motoszko <i>et al.</i> , 2011;
eIF4G	eIF1, eIF4A, eIF4E, eIF5, Ded1, Pab1, mRNA,	Altmann <i>et al.</i> , 1997; Berset <i>et al.</i> , 2003; Dominguez <i>et al.</i> , 1999; Goyer <i>et al.</i> , 1993; He <i>et al.</i> , 2003; Hilliker <i>et al.</i> , 2011; Mader <i>et al.</i> , 1995; Neff and Sachs 1999; Schütz <i>et al.</i> , 2008; Tarun and Sachs 1996; Wells <i>et al.</i> , 1998;
eIF5	eIF1, eIF2, eIF3, eIF4G, R,	Assano <i>et al.</i> , 1999; Asano <i>et al.</i> , 2000; He <i>et al.</i> , 2003; Phan <i>et al.</i> , 1998; Reibarkh <i>et al.</i> , 2008; Singh <i>et al.</i> , 2004; Valasek <i>et al.</i> , 2003;
eIF5B	eIF1A, R,	Fringer <i>et al.</i> , 2007; Olsen <i>et al.</i> , 2003; Zheng <i>et al.</i> , 2011;
eEF1A	eEF1B, eEF3, R,	Anand <i>et al.</i> , 2006; Chakraborty and Triana-Alonso 1998; Kovalchuk <i>et al.</i> , 1998; Pedersen <i>et al.</i> , 2001; Pittman <i>et al.</i> , 2009;
eEF1B	eEF1A,	Pedersen <i>et al.</i> , 2001; Pittman <i>et al.</i> , 2009;
eEF2	Hyp2, R,	Nilsson <i>et al.</i> , 2007; Spahn <i>et al.</i> , 2004; Zanelli <i>et al.</i> , 2006;
eEF3	eEF1A, R,	Anand <i>et al.</i> , 2006; Andersen <i>et al.</i> , 2006; Chakraborty and Triana-Alonso 1998; Dasmahapatra and Chakraborty 1981; Kovalchuk <i>et al.</i> , 1998; Skogerson and Wakatama 1976; Triana-Alonso <i>et al.</i> , 1995;
eRF1	Dbp5, eRF3, R,	Eurwilaichitr <i>et al.</i> , 1999; Frolova <i>et al.</i> , 2000; Gross <i>et al.</i> , 2007; Kobayashi <i>et al.</i> , 2004;
eRF3	eRF1, Pab1,	Eurwilaichitr <i>et al.</i> , 1999; Hosoda <i>et al.</i> , 2003; Kobayashi <i>et al.</i> , 2004;
Dbp5	eRF1, mRNA,	Estruch and Cole 2003; Gross <i>et al.</i> , 2007;
Ded1	eIF4G, mRNA,	Chuang <i>et al.</i> , 1997; Iost <i>et al.</i> , 1999; Hilliker <i>et al.</i> , 2011; Marsden <i>et al.</i> , 2006;
Hyp2	eEF2, R,	Jao <i>et al.</i> , 2006; Zanelli <i>et al.</i> , 2006;
Pab1	eIF4G, eRF3, mRNA,	Hosoda <i>et al.</i> , 2003; Kobayashi <i>et al.</i> , 2004; Tarun and Sachs 1996; Wells <i>et al.</i> , 1998;

R – ribosome

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Quantified protein	Ribo3 Q-peptides
P40512 CSN11_YEAST	ISHEVVQDDSFSLLR YFDCCTK
P02994 EF1A_YEAST	IGGIGTVPVGR SHINVVVIGHVDVSGK
P16521 EF3A_YEAST	IVVEYIAAIGADLIDER LVLAAGTWQRPHLIVLDEPTNYLDR
P14741 eI2BA_YEAST	IAEIGVDFIADDDIILVHGYSR NLHLYGDWENCK
P32502 eI2BB_YEAST	LSPLYPFVDEK TFTVLVTEGFNNTK
P09032 eI2BG_YEAST	GSNLAPFTQPDFPFQTQNK LSNCYIEGHYVVEPK
P53235 eIF2A_YEAST	TSQDIELFQSYPTFEQSNTNSK WNPLGNAILCLAITDFDSSNK
P06103 eIF3B_YEAST	DFSFAPEGVK YLVTFSTEPIIVEEDNEFSPFTK
P32497 eIF3C_YEAST	DQLDSADYVDNLIDGLSTILSK VVEVLQSVIAELEIPAK
Q04067 eIF3G_YEAST	GLAFVTFSSVEAEQALR GSPAGPSAVTAR
P40217 eIF3I_YEAST	EFIILGGGQEAQK YETDCPLNTAVITPLK
P05453 ERF3_YEAST	FVAQIAIVELK VIAVLETEAPVCVETYQDYPQLGR
Q12099 FAL1_YEAST	GIYSYGFEAPSSIQSR HGCQAVSGTPGR
P34167 IF4B_YEAST	EDAPDLDWGAAR GGGADVWSSAR
P39936 IF4F2_YEAST	AQPISDIYEFAYPENVERPDIK WEDDGETLK
P38431 IF5_YEAST	GGGLSISDIAQGK NPETEIITK
P25637 YIH1_YEAST	HINSTAR WFGGAHIGPDR

Quantified protein	Ribo4 Q-peptides
P32324 EF2_YEAST	AEQLYEGPADDANCIAIK FSVSPVVQVAVEVK
P12754 eI2BD_YEAST	DASNEEDSNSK VITEFGALPPSSVPVILR
P32501 eI2BE_YEAST	CLLPLANVPLIEYTFLEFLAK TIEPAAFVLDK
P38249 eIF3A_YEAST	LATLPAPLDLSAWDIEK SGNNLVDLSDADTLQR
P12385 ERF1_YEAST	GLILAGSADFK VAEVAVQNFITNDK
P38912 IF1A_YEAST	DFQDDQCDVVHK VEASCFDGNK
P20459 IF2A_YEAST	AVTATEDAELQALLESK LSIIDETVWEGIEPPSK
P09064 IF2B_YEAST	EGTPSANSSIQQEVGLPYSELLSR TIFSNIQDIAEK
P32481 IF2G_YEAST	FAVPGGLIGVGTK GTIADGAPIVPISAQLK
P39730 IF2P_YEAST	GVVVQASTLGSLEALLDFLK IQLELAEQGLNSELYFQNK
P10081 IF4A_YEAST	GIDVQQVSLVINYDLPANK GVFGYGFEEPSAIQQR
P07260 IF4E_YEAST	GADIDELWLR NDVRPEWEDEANAK
P39935 IF4F1_YEAST	DATPIEDVFSFNYPEGIEGPDIK SDEAEAEVEAEAGDAGTK
P19211 IF5A1_YEAST	LEDLSPSTHNLEVPFVK VHLVTLDIFTGK
P23301 IF5A2_YEAST	APEGELGDSLQTAFDEGK VHLVAIDIFTGK
Q12522 IF6_YEAST	GLLVPTQTDDQELQHLR TQFENSNEIGVFSK
P32911 SUI1_YEAST	SFDPFADTGDDETATSNIYHIR TLTTVQGVPEEYDLK
Q03690 TIF31_YEAST	GGDEAAIAASNQDLK SVDELLFIEGDSSNSK

Quantified protein	Ribo1 Q-peptides
P02994 EF1A_YEAST	IGGIGTVPVGR SHINVVVIGHVDSGK
P14741 eI2BA_YEAST	GIPVTLIVDSAVGAVIDK VFGAEGVAESGGIINLVGTYSVGVLAHNAR
P32502 eI2BB_YEAST	QVAIQGIK TPVFAVAGLYK
P06103 eIF3B_YEAST	NINDNNDVSASLK IFDVQPEDASDDFTTIEEIVEEVLEETK
P40217 eIF3I_YEAST	NPGSINIYEIER VQGHFGPLNTVAISPQGTSYASGGEDGFIR
P05453 ERF3_YEAST	ISESTHNTNNANVTSADALIK DQGTTIAIGK
Q12099 FAL1_YEAST	GIYSYGFEAPSSIQSR DLQALILSPTR
P39936 IF4F2_YEAST	YTYGPTFLQFK EAPKPTGEANEVVIDGK
P38431 IF5_YEAST	GGGLSISDIAQ GK LQDVLDFGINK
P32324 EF2_YEAST	TDGNSFLINLIDSPGHVDFSEVTAALR AYLPVNESFGFTGELR
P32501 eI2BE_YEAST	LQAVVLTDSYETR HIYAYLTDEYAVR
P12385 ERF1_YEAST	LSVLSAITSTQQK NFGATLEFITDK
P38912 IF1A_YEAST	NQGELPENAK EEGQEYAQITK
P39730 IF2P_YEAST	VISLEINHQPVQEVK IFNADVIYHLDFSFTAYQEK
P07260 IF4E_YEAST	GADIDELWLR TVLSDSAHFDVK
P39935 IF4F1_YEAST	DATPIEDVFSFNYPEGIEGPDIK ADAEWVQSTASK
P19211 IF5A1_YEAST	LEDLSPSTHNLEVPFVK VHLVTLIDFTGK
P23301 IF5A2_YEAST	APEGELGDSLQTA FDEGK VHLVAIDIFTGK

Quantified protein	Ribo2 Q-peptides
P40512 CSN11_YEAST	IGHLLSINYGEK LQFSYLSSTLGIDLEDIK
P16521 EF3A_YEAST	VGNVGEDDAIPEVSHAGDVSTTLQVVNELLK TVYVEHDIDGTHSDTSVLDFVFESEGVGK
P09032 eI2BG_YEAST	GSNLAPFTQPDFPFQ TQNK EISVVAPVDEIELIESGLTSFLSLR
P53235 eIF2A_YEAST	VSLTTGPVHDF TWSPTSR LSDVYDLHFSPAGNYLSTWER
P32497 eIF3C_YEAST	DQLDSADYVDNLIDGLSTILSK ISLNSSNNASADER
Q04067 eIF3G_YEAST	LGEEVELR GSPAGPSAVTAR
P34167 IF4B_YEAST	SGGFGGSFGGR GAQFGKPPQTK
P25637 YIH1_YEAST	QEDGSIIIVK QDGSAA TYQSDDDGETAAGSR
P12754 eI2BD_YEAST	VLTELLHNAISLK VITEFGALPPSSVPVILR
P38249 eIF3A_YEAST	LATLPAPLDLSAWDIEK TAGGSSPATPATPATPTPSSGPK
P20459 IF2A_YEAST	GIEQLESAIEK LVAAPLYVLTQALDK
P09064 IF2B_YEAST	EGTPSANSSIQEVGLPYSELLSR TIFSNIQDIAEK
P32481 IF2G_YEAST	YNIDAVNEFIVK EFEEGGLPEQPLNPDFSK
P10081 IF4A_YEAST	TGTF SIAALQR GVFYGFEEPSAIQQR
Q12522 IF6_YEAST	GLLVPTQTTDQELQHLR LQDAQPESISGNLR
P32911 SUI1_YEAST	SDFPFADTGDDETATS NYIHIR TLTTVQGVPEEYDLK
Q03690 TIF31_YEAST	ELDSQIVHYEQNLK FVEPTTFLSLSDLTIIPR

Supplementary Table IV QconCAT peptides

The proteins to be quantitated were distributed over four QconCATs (Ribo1 - Ribo4), with two peptides per protein. A stringent set of rules were followed to select the most 'quantotypic' peptides from each protein. The Ribo1/Ribo2 peptides were generated first, with the Ribo3/Ribo4 peptides synthesised later using a modified set of rules with the aim of increasing the number of successful Q-peptides per protein. Note that some of the peptide sequences did not correspond to proteins studied in this work.

Supplementary Table Va - Transition list for QconCAT 'Ribo 3'. Using data independent acquisition on a Waters Synapt G2 mass spectrometer, transition lists were created. These provide information on the precursor retention time ('prec retT') as well as the product ion fragment number ('frag str') and mass/charge ('product m_z'). Acquisitions to optimise the collision energy ('ColE') and cone voltage ('ConeV') for each peptide were performed prior to quantification runs. For each peptide, in both heavy (QconCAT) and light (yeast analyte), two transitions were acquired. Peptide modification carbamidomethyl cysteine displayed as CAM+C.

Ribo3_2	P25637	13C+KR(16)	WFGGAHIGPDR_heavy	24.12	2	609.800	y10	516.760		2	1	25	40
Ribo3_2	P25637	13C+KR(16)	WFGGAHIGPDR_light	24.12	2	606.800	y5	557.300		1	1	28	40
Ribo3_2	P25637	13C+KR(16)	WFGGAHIGPDR_light	24.12	2	606.800	y10	513.760		2	1	25	40
Ribo3_2	P14741	CAM+C(11);13C+KR(12)	NLHLYGDWENCK_heavy	24.79	3	518.909	y4	556.250	900	1	1	15	25
Ribo3_2	P14741	CAM+C(11);13C+KR(12)	NLHLYGDWENCK_heavy	24.79	3	518.909	y8	1077.442	693	1	1	18	25
Ribo3_2	P14741	CAM+C(11);13C+KR(12)	NLHLYGDWENCK_light	24.79	3	516.909	y4	550.250	900	1	1	15	25
Ribo3_2	P14741	CAM+C(11);13C+KR(12)	NLHLYGDWENCK_light	24.79	3	516.909	y8	1071.442	693	1	1	18	25
Ribo3_2	P06103	13C+KR(10)	DFSFAPEGVK_heavy	26.08	2	551.780	y8	840.454	9125	1	1	19	25
Ribo3_2	P06103	13C+KR(10)	DFSFAPEGVK_heavy	26.08	2	551.780	y7	753.427	3379	1	1	19	25
Ribo3_2	P06103	13C+KR(10)	DFSFAPEGVK_light	26.08	2	548.780	y8	834.454	9125	1	1	19	25
Ribo3_2	P06103	13C+KR(10)	DFSFAPEGVK_light	26.08	2	548.780	y7	747.427	3379	1	1	19	25
Ribo3_2	P40512	13C+KR(15)	ISHEVVQDDSFLLR_heavy	26.33	3	584.308	y6	728.440	3832	1	1	21	25
Ribo3_2	P40512	13C+KR(15)	ISHEVVQDDSFLLR_heavy	26.33	3	584.308	y5	641.408	2090	1	1	21	25
Ribo3_2	P40512	13C+KR(15)	ISHEVVQDDSFLLR_light	26.33	3	582.308	y6	722.440	3832	1	1	21	25
Ribo3_2	P40512	13C+KR(15)	ISHEVVQDDSFLLR_light	26.33	3	582.308	y5	635.408	2090	1	1	21	25
Ribo3_2	P53235	13C+KR(22)	TSQDIELFQSYPTFEQSNTNSK_heavy	28.16	2	1285.604	y11	1258.601	2309	1	1	41	35
Ribo3_2	P53235	13C+KR(22)	TSQDIELFQSYPTFEQSNTNSK_heavy	28.16	2	1285.604	y13	1508.692	193	1	1	41	35
Ribo3_2	P53235	13C+KR(22)	TSQDIELFQSYPTFEQSNTNSK_light	28.16	2	1282.604	y11	1252.601	2309	1	1	41	35
Ribo3_2	P53235	13C+KR(22)	TSQDIELFQSYPTFEQSNTNSK_light	28.16	2	1282.604	y13	1502.692	193	1	1	41	35
Ribo3_2	P39936	13C+KR(18);13C+KR(22)	AQPISDIYEFAYPENVERPDIK_heavy	28.75	3	869.444	y20	1204.114	55402	2	2	27	35
Ribo3_2	P39936	13C+KR(18);13C+KR(22)	AQPISDIYEFAYPENVERPDIK_heavy	28.75	3	869.444	y10	1208.670	4316	1	2	34	35
Ribo3_2	P39936	13C+KR(18);13C+KR(22)	AQPISDIYEFAYPENVERPDIK_light	28.75	3	865.444	y20	1198.114	55402	2	2	27	35
Ribo3_2	P39936	13C+KR(18);13C+KR(22)	AQPISDIYEFAYPENVERPDIK_light	28.75	3	865.444	y10	1196.670	4316	1	2	34	35
Ribo3_2	P09032	13C+KR(19)	GSNLAPFTQPDFPFQTNK_heavy	29.30	2	1072.031	y14	850.918	5223	2	1	34	35
Ribo3_2	P09032	13C+KR(19)	GSNLAPFTQPDFPFQTNK_heavy	29.30	2	1072.031	y11	1355.667	464	1	1	34	35
Ribo3_2	P09032	13C+KR(19)	GSNLAPFTQPDFPFQTNK_light	29.30	2	1069.031	y14	847.918	5223	2	1	34	35
Ribo3_2	P09032	13C+KR(19)	GSNLAPFTQPDFPFQTNK_light	29.30	2	1069.031	y11	1349.667	464	1	1	34	35
Ribo3_2	P05453	13C+KR(11)	FVAQIAIVELK_heavy	29.55	2	618.886	y6	678.447	1062	1	1	22	25
Ribo3_2	P05453	13C+KR(11)	FVAQIAIVELK_heavy	29.55	2	618.886	y7	791.533	964	1	1	22	35
Ribo3_2	P05453	13C+KR(11)	FVAQIAIVELK_light	29.55	2	615.886	y6	672.447	1062	1	1	22	25
Ribo3_2	P05453	13C+KR(11)	FVAQIAIVELK_light	29.55	2	615.886	y7	785.533	964	1	1	22	35
Ribo3_2	P05453	CAM+C(12);13C+KR(24)	VIAVLETEAPVCVETYQDYPQLGR_heavy	29.75	3	919.468	y5	576.355	2143	1	1	32	35
Ribo3_2	P05453	CAM+C(12);13C+KR(24)	VIAVLETEAPVCVETYQDYPQLGR_heavy	29.75	3	919.468	y6	739.420	1000	1	1	34	35
Ribo3_2	P05453	CAM+C(12);13C+KR(24)	VIAVLETEAPVCVETYQDYPQLGR_light	29.75	3	917.468	y5	570.355	2143	1	1	32	35
Ribo3_2	P05453	CAM+C(12);13C+KR(24)	VIAVLETEAPVCVETYQDYPQLGR_light	29.75	3	917.468	y6	733.420	1000	1	1	34	35
Ribo3_2	P32497	13C+KR(17)	VVEVLQSVIAELEIPAK_heavy	35.94	3	615.034	y3	321.223	1733	1	1	26	25
Ribo3_2	P32497	13C+KR(17)	VVEVLQSVIAELEIPAK_heavy	35.94	3	615.034	y8	876.516	1396	1	1	19	25
Ribo3_2	P32497	13C+KR(17)	VVEVLQSVIAELEIPAK_light	35.94	3	613.034	y3	315.223	1733	1	1	26	25
Ribo3_2	P32497	13C+KR(17)	VVEVLQSVIAELEIPAK_light	35.94	3	613.034	y8	870.516	1396	1	1	19	25
Ribo3_2	P32497	13C+KR(22)	DQLDSADYVDNLIDGLSTILSK_heavy	39.15	2	1201.107	y10	1052.629	1298	1	1	41	40
Ribo3_2	P32497	13C+KR(22)	DQLDSADYVDNLIDGLSTILSK_heavy	39.15	2	1201.107	y6	654.411	942	1	1	43	35
Ribo3_2	P32497	13C+KR(22)	DQLDSADYVDNLIDGLSTILSK_light	39.15	2	1198.107	y10	1046.629	1298	1	1	41	40
Ribo3_2	P32497	13C+KR(22)	DQLDSADYVDNLIDGLSTILSK_light	39.15	2	1198.107	y6	648.411	942	1	1	43	35

Supplementary Table Vb - Transition list for QconCAT 'Ribo 4'. Using data independent acquisition on a Waters Synapt G2 mass spectrometer, transition lists were created. These provide information on the precursor retention time ('precursor retT') as well as the product ion fragment number ('fragment str') and mass/charge ('product m_'z). Acquisitions to optimise the collision energy ('ColE') and cone voltage ('ConeV') for each peptide were performed prior to quantification runs. For each peptide, in both heavy (QconCAT) and light (yeast analyte), two transitions were acquired.

Ribo4_2	P12385	13C+KR(11)	GLILAGSADFK_light	26.55	2	546.319	y7	695.355	1929	1	1	19	25
Ribo4_2	P32501	13C+KR(11)	TIEPAAFVLDK_heavy	27.76	2	605.344	y8	866.509	5544	1	1	21	30
Ribo4_2	P32501	13C+KR(11)	TIEPAAFVLDK_heavy	27.76	2	605.344	y9	995.552	4501	1	1	18	30
Ribo4_2	P32501	13C+KR(11)	TIEPAAFVLDK_light	27.76	2	602.344	y8	860.509	5544	1	1	21	30
Ribo4_2	P32501	13C+KR(11)	TIEPAAFVLDK_light	27.76	2	602.344	y9	989.552	4501	1	1	18	30
Ribo4_2	P07260	13C+KR(10)	GADIDELWLR_heavy	29.58	2	597.318	y6	837.459	8700	1	1	21	25
Ribo4_2	P07260	13C+KR(10)	GADIDELWLR_heavy	29.58	2	597.318	y5	722.430	2217	1	1	25	25
Ribo4_2	P07260	13C+KR(10)	GADIDELWLR_light	29.58	2	594.318	y6	831.459	8700	1	1	21	25
Ribo4_2	P07260	13C+KR(10)	GADIDELWLR_light	29.58	2	594.318	y5	716.430	2217	1	1	25	25
Ribo4_2	P39730	13C+KR(19)	IQLELAEQGLNSELYFQNK_heavy	29.70	2	1122.085	y11	1318.670		1	1	36	35
Ribo4_2	P39730	13C+KR(19)	IQLELAEQGLNSELYFQNK_heavy	29.70	2	1122.085	y12	1446.730		1	1	39	35
Ribo4_2	P39730	13C+KR(19)	IQLELAEQGLNSELYFQNK_light	29.70	2	1119.085	y11	1312.670		1	1	36	35
Ribo4_2	P39730	13C+KR(19)	IQLELAEQGLNSELYFQNK_light	29.70	2	1119.085	y12	1440.730		1	1	39	35
Ribo4_2	P10081	13C+KR(19)	GIDVQVSLVINYPANK_heavy	30.14	2	1046.574	y4	435.267	440	1	1	43	30
Ribo4_2	P10081	13C+KR(19)	GIDVQVSLVINYPANK_heavy	30.14	2	1046.574	y5	548.348	61	1	1	43	40
Ribo4_2	P10081	13C+KR(19)	GIDVQVSLVINYPANK_light	30.14	2	1043.574	y4	429.267	440	1	1	43	30
Ribo4_2	P10081	13C+KR(19)	GIDVQVSLVINYPANK_light	30.14	2	1043.574	y5	542.348	61	1	1	43	40
Ribo4_2	Q03690	13C+KR(17)	SVDELLTFIEGDSSNSK_heavy	32.54	2	923.956	y10	1089.520	1823	1	1	32	30
Ribo4_2	Q03690	13C+KR(17)	SVDELLTFIEGDSSNSK_heavy	32.54	2	923.956	y7	700.322	1778	1	1	32	40
Ribo4_2	Q03690	13C+KR(17)	SVDELLTFIEGDSSNSK_light	32.54	2	920.956	y10	1083.520	1823	1	1	32	30
Ribo4_2	Q03690	13C+KR(17)	SVDELLTFIEGDSSNSK_light	32.54	2	920.956	y7	694.322	1778	1	1	32	40
Ribo4_2	P39935	13C+KR(23)	DATPIEDVFSFNYPEGIEGPDIK_heavy	33.35	2	1280.117	y10	1060.567	1369	1	1	44	40
Ribo4_2	P39935	13C+KR(23)	DATPIEDVFSFNYPEGIEGPDIK_heavy	33.35	2	1280.117	y12	1337.639	949	1	1	41	40
Ribo4_2	P39935	13C+KR(23)	DATPIEDVFSFNYPEGIEGPDIK_light	33.35	2	1277.117	y10	1054.567	1369	1	1	44	40
Ribo4_2	P39935	13C+KR(23)	DATPIEDVFSFNYPEGIEGPDIK_light	33.35	2	1277.117	y12	1331.639	949	1	1	41	40
Ribo4_2	P39730	13C+KR(20)	GVVVQASTLGSLEALLDFLK_heavy	39.13	2	1033.597	y13	1425.830		1	1	38	35
Ribo4_2	P39730	13C+KR(20)	GVVVQASTLGSLEALLDFLK_heavy	39.13	2	1033.597	y14	1512.860		1	1	36	35
Ribo4_2	P39730	13C+KR(20)	GVVVQASTLGSLEALLDFLK_light	39.13	2	1030.597	y13	1419.830		1	1	38	35
Ribo4_2	P39730	13C+KR(20)	GVVVQASTLGSLEALLDFLK_light	39.13	2	1030.597	y14	1506.860		1	1	36	35

Translation Factor	Entry name	Acc	Biological replicates	Average (cpc)	unique peptides	Abundance (cpc)	SEM		
Initiation factor eIF1	SUI1_YEAST	P32911	Log_1	32,520	2	eIF2 average: 34,000	2,000		
			Log_2	37,345	2				
			Log_3	30,792	2				
Initiation factor eIF1A	IF1A_YEAST	P38912	Log_1	48,266	1	eIF1A average: 57,000	5,500		
			Log_2	67,203	1				
			Log_3	56,132	1				
Initiation factor eIF2 α	IF2A_YEAST	P20459	Log_1	6,133	1	eIF2 complex average of β and γ : 29,000	2,100		
			Log_2	8,215	1				
			Log_3	8,306	1				
Initiation factor eIF2 β	IF2B_YEAST	P09064	Log_1	20,690	1				
			Log_2	32,910	1				
			Log_3	27,986	1				
Initiation factor eIF2 γ	IF2G_YEAST	P32481	Log_1	32,844	3				
			Log_2	27,657	3				
			Log_3	31,588	3				
Initiation factor eIF2 $\beta\alpha$	eI2BA_YEAST	P14741	Q-peptides not suitable for quantification			eIF2B complex average of β to ϵ : 5,600	150		
Initiation factor eIF2 $\beta\beta$	eI2BB_YEAST	P32502	Log_1	5,394	2				
			Log_2	6,199	2				
			Log_3	5,521	2				
Initiation factor eIF2 $\beta\delta$	eI2BD_YEAST	P12754	Log_1	4,079	1				
			Log_2	5,267	1				
			Log_3	5,257	1				
Initiation factor eIF2 $\beta\epsilon$	eI2BE_YEAST	P32501	Log_1	5,057	3				
			Log_2	6,049	3				
			Log_3	6,010	3				
Initiation factor eIF2 $\beta\gamma$	eI2BG_YEAST	P09032	Log_1	6,042	3				
			Log_2	6,533	3				
			Log_3	6,035	3				
Initiation factor eIF3a	eIF3A_YEAST	P38249	Log_1	22,254	2	eIF3 complex average of a to g: 23,000	1,200		
			Log_2	31,602	2				
			Log_3	28,704	2				
Initiation factor eIF3b	eIF3B_YEAST	P06103	Log_1	22,199	2				
			Log_2	19,081	3				
			Log_3	20,626	3				
Initiation factor eIF3c	eIF3C_YEAST	P32497	Log_1	21,041	1				
			Log_2	17,807	1				
			Log_3	24,582	1				
Initiation factor eIF3g	eIF3G_YEAST	Q04067	Log_1	20,827	3				
			Log_2	26,496	3				
			Log_3	19,430	3				
Initiation factor	eIF3I_YEAST	P40217	Log_1	14,669	4				

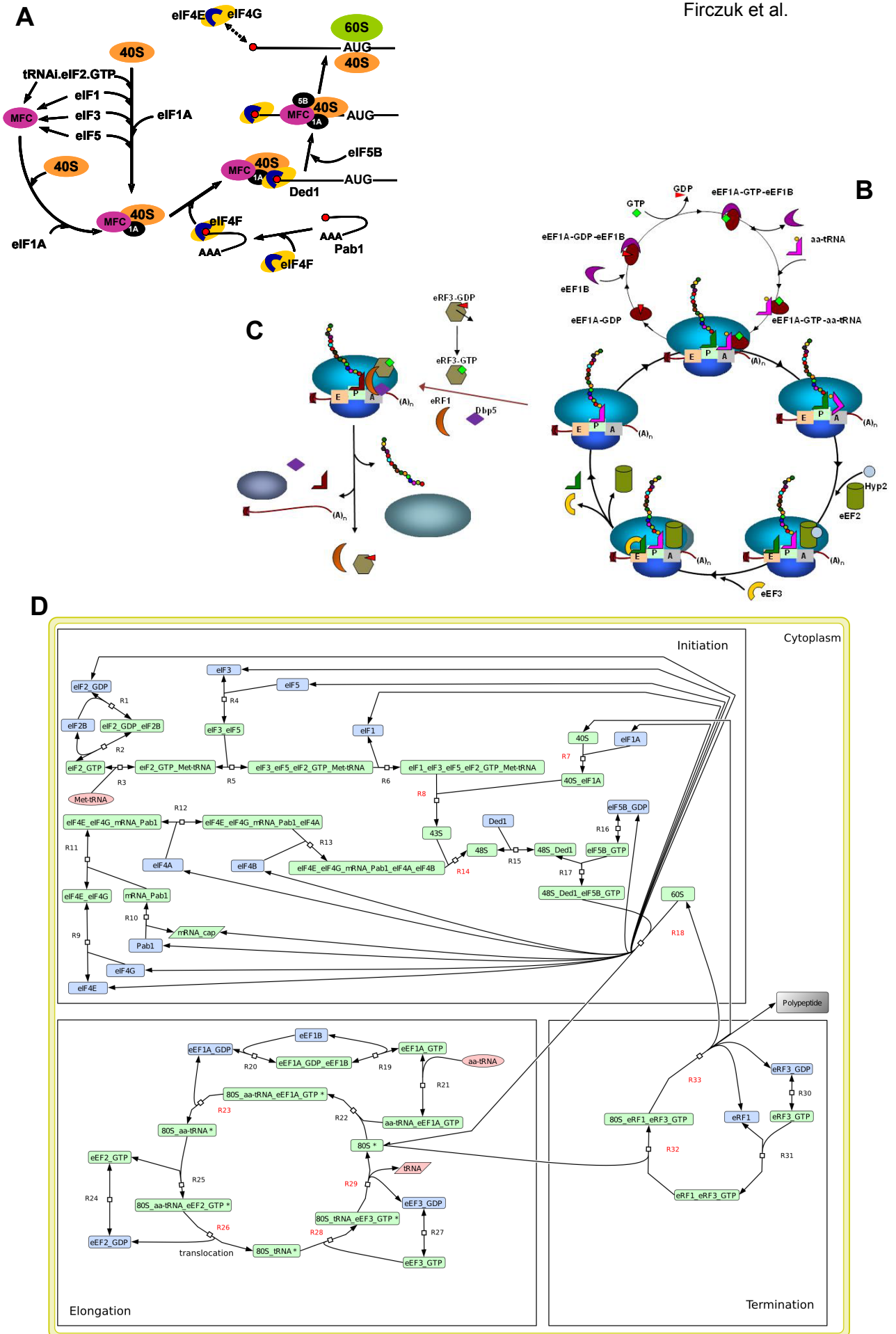
eIF3i			Log_2	17,205	4		
			Log_3	15,814	4		
Initiation factor eIF4A	IF4A_YEAST	P10081	Log_1	216,063	2	eIF4A average: 240,000	16,000
			Log_2	269,617	2		
			Log_3	234,767	3		
Initiation factor eIF4B	IF4B_YEAST	P34167	Log_1	27,655	3	eIF4B average: 28,000	1,400
			Log_2	30,976	3		
			Log_3	26,395	2		
Initiation factor eIF4E	IF4E_YEAST	P07260	Log_1	69,749	3	eIF4E average: 80,000	5,700
			Log_2	90,794	3		
			Log_3	80,292	3		
Initiation factor eIF4G2	IF4F2_YEAST	P39936	Log_1	2,338	2	total eIF4G = 22,000	2,700
			Log_2	1,975	2		
			Log_3	2,092	1		
Initiation factor eIF4G1	IF4F1_YEAST	P39935	Log_1	15,095	2		
			Log_2	24,323	2		
			Log_3	20,416	2		
Initiation factor eIF5	IF5_YEAST	P38431	Log_1	18,246	2	eIF5 average: 20,000	2,000
			Log_2	24,357	2		
			Log_3	18,358	2		
Hyp2	IF5A2_YEAST	P23301	Log_1	454,271	1	Hyp2 average: 410,000	64,000
			Log_2	526,435	1		
			Log_3	444,213	1		
Initiation factor eIF5B	IF2P_YEAST	P39730	Log_1	6,066	1	eIF5B average: 4,800	900
			Log_2	3,119	1		
			Log_3	5,135	1		
Elongation factor eEF1A	EF1A_YEAST	P02994	Log_1	1,036,757	1	eEF1A average: 1,000,000	32,000
			Log_2	1,102,238	1		
			Log_3	991,534	1		
Elongation factor eEF1B	EF1B_YEAST	P32471	Label free quantification (MS ^E)			79,000	1,000
Elongation factor eEF2	EF2_YEAST	P32324	Log_1	141,480	2	eEF2 average: 140,000	3,900
			Log_2	148,778	2		
			Log_3	135,308	2		
Elongation factor eEF3	EF3A_YEAST	P16521	Label free quantification (MS ^E)			110,000	3,500
Termination factor eRF1	ERF1_YEAST	P12385	Log_1	23,081	2	eRF1 average: 22,000	1,700
			Log_2	19,244	1		
			Log_3	24,881	2		
Termination factor eRF3	ERF3_YEAST	P05453	Log_1	14,935	1	eRF3 average: 14,000	400
			Log_2	13,893	1		
			Log_3	13,738	1		
Dbp5	DBP5_YEAST	P20449	Label free quantification (MS ^E)			15,000	800
Ded1	DED1_YEAST	P06634	Label free quantification (MS ^E)			28,000	500

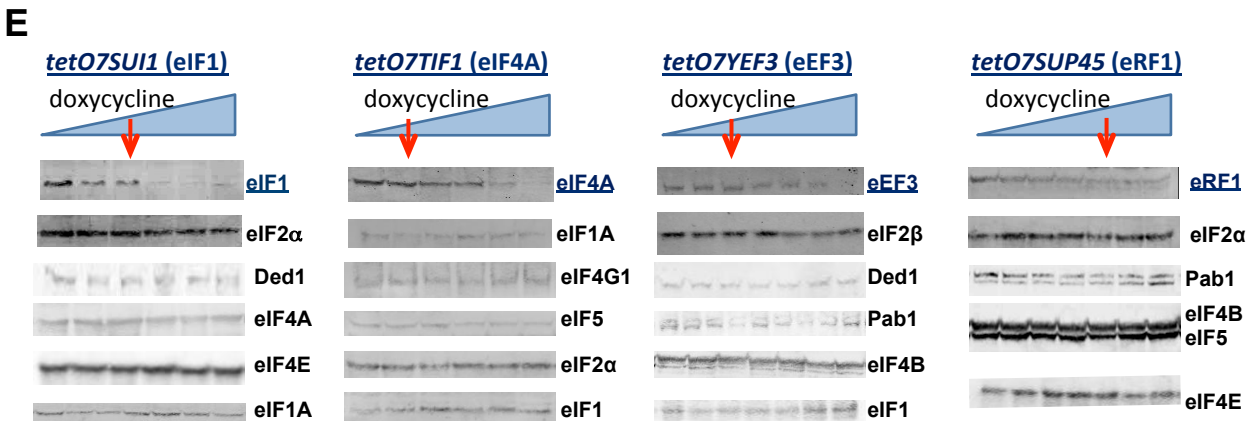
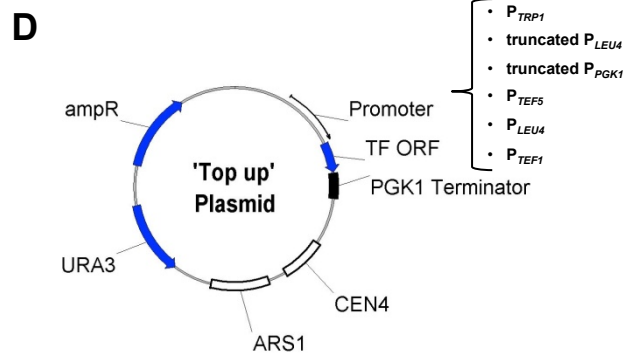
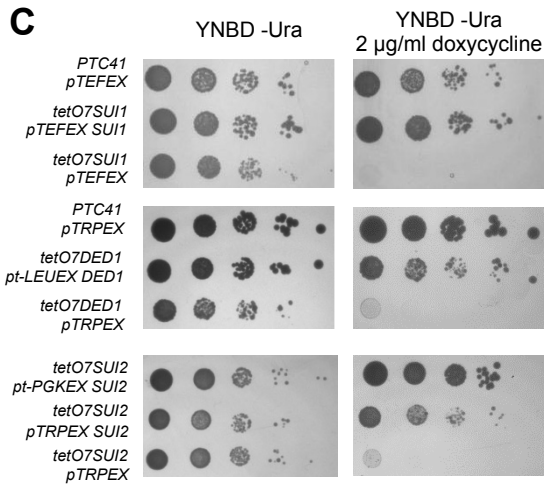
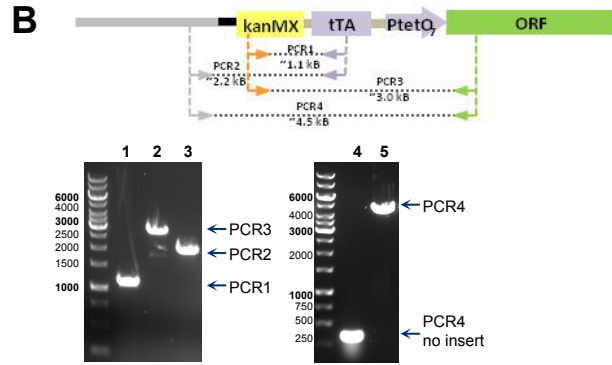
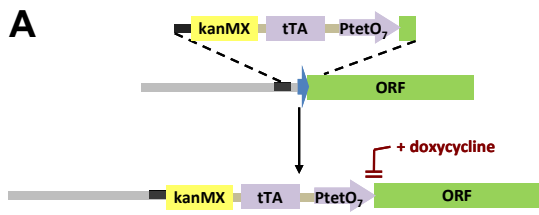
Pab1	PABP_YEAST	P04147	Label free quantification (MS ^E)	44,000	1,700
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Supplementary Table VI

Abundance values for translation factors

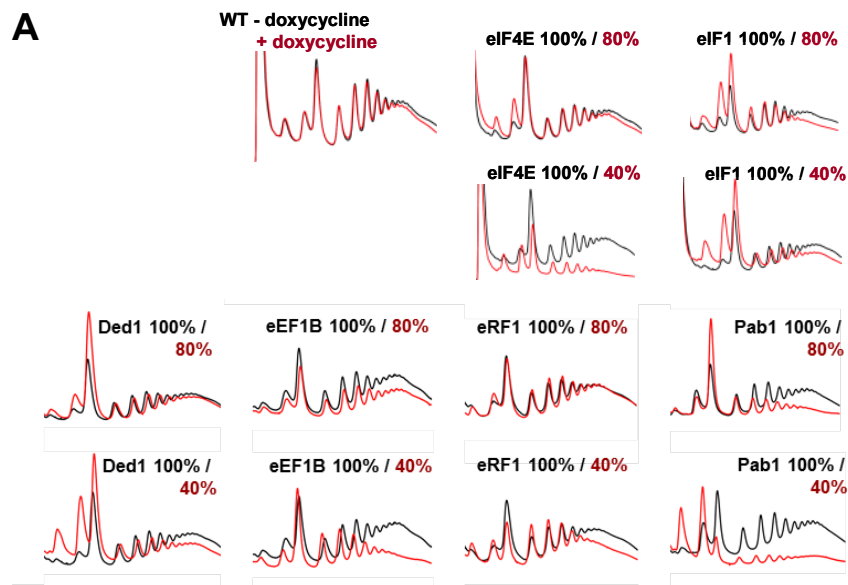
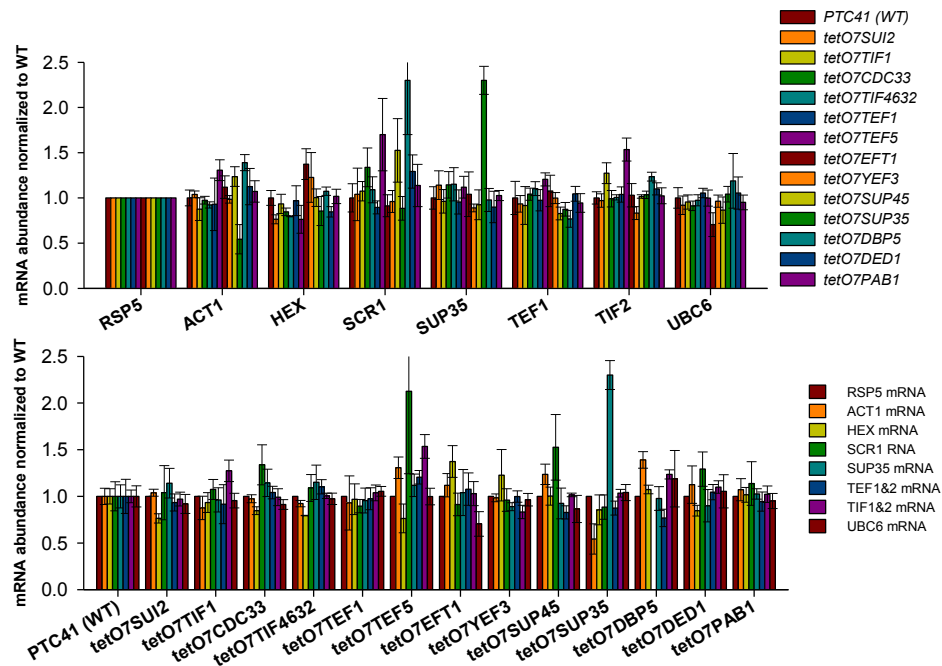
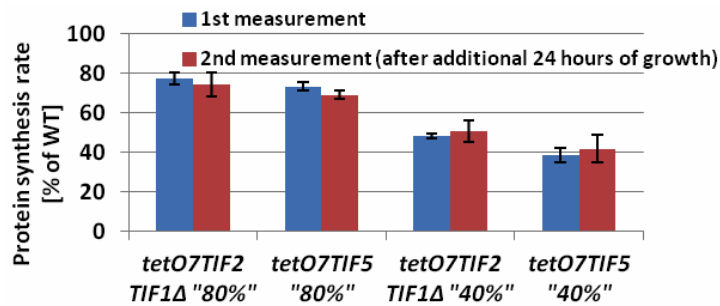
Summary of the proteins quantitated and the quantitation method used. Proteins of interest in three biological replicates of exponentially growing yeast (Log₁ to ₃) were quantitated using QconCAT Q-peptides, selected to represent each protein. Individual abundance values (in copies per cell, cpc) for the biological replicates contain data from multiple analyses, in some instances using two different MS platforms (Waters Xevo triple quadrupole and Thermo LTQ-Orbitrap Velos) for the number of Q-peptides stated (see Supplementary Figure VII for correlation between the two MS instruments used). Errors define biological not technical variance (see Supplementary Figure VII for technical variation). Label-free quantitation data were obtained from data-independent MSE acquisition on a Waters Synapt G2, using four biological replicates of comparable yeast (data provided by P. Brownridge).



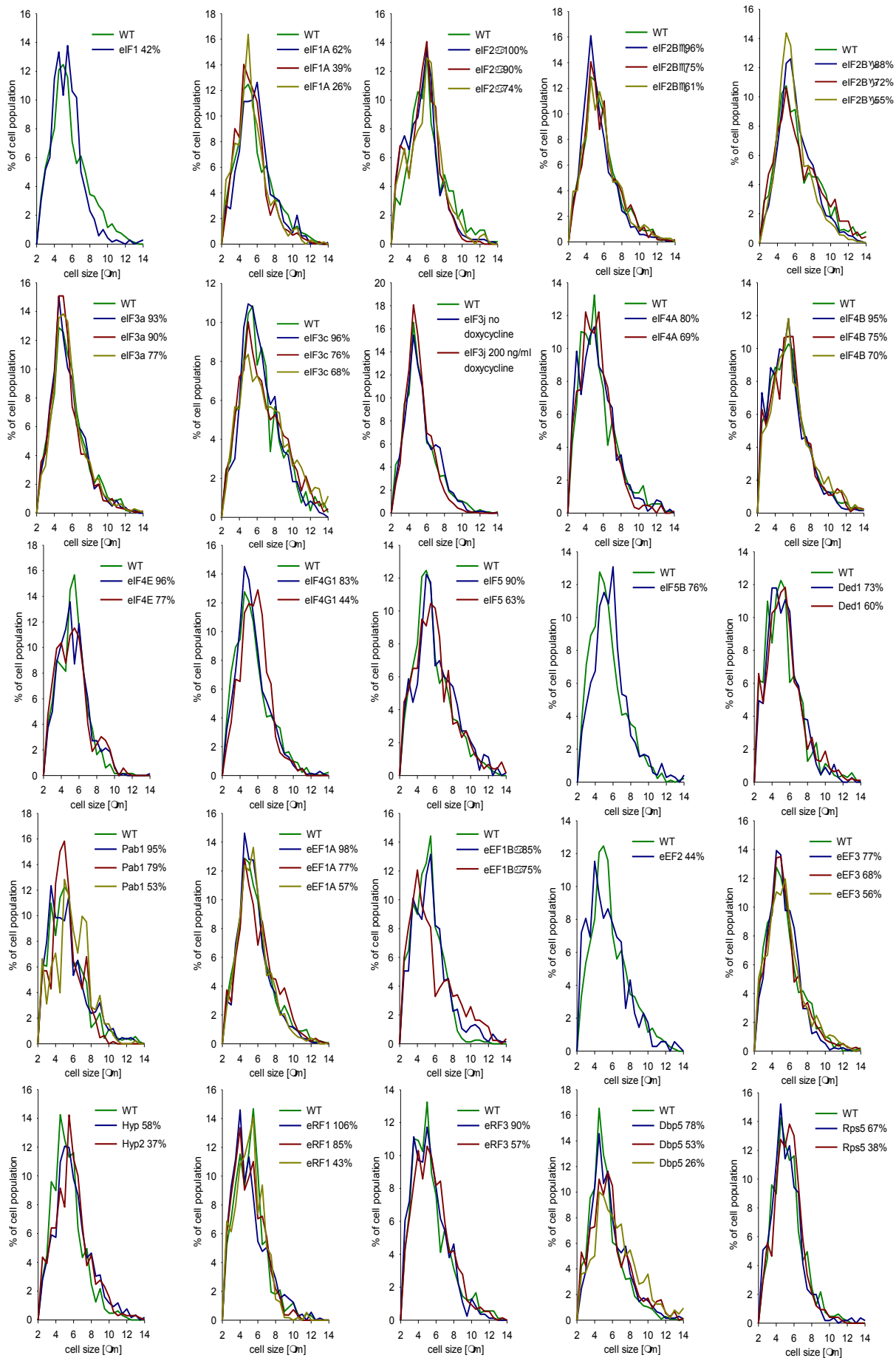


F

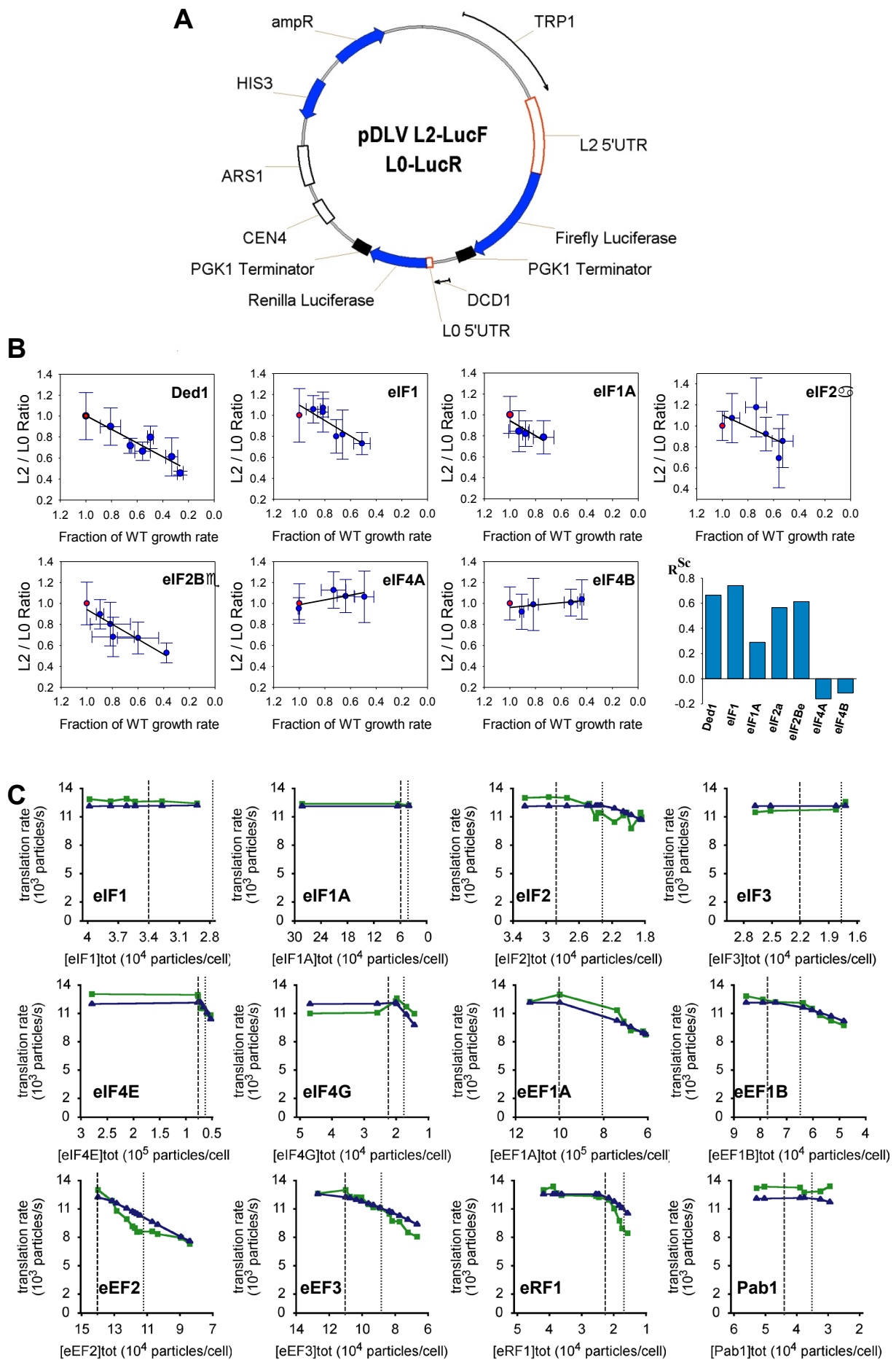
		Relative abundance (% of WT)									
		eIF2 α	eIF4A	eIF4E	eIF4G1	eEF1A	eEF1B	eEF2	eEF3	eRF1	Dbp5
Factor under tetO7 control	eIF2 α	54	102	98	101	104	102	103	94	105	90
	eIF4A	109	62	103	105	104	98	101	101	99	97
	eIF4E	106	101	48	94	103	107	100	100	104	92
	eIF4G1	102	100	104	63	98	99	98	104	98	101
	eEF1A	110	104	102	102	71	102	106	106	103	96
	eEF1B	109	101	108	106	101	30	113	104	96	102
	eEF2	100	101	105	102	106	81	29	101	106	107
	eEF3	100	99	103	97	98	92	115	68	109	101
	eRF1	104	99	99	101	98	98	102	104	57	101
	Dbp5	101	95	103	99	102	91	91	104	95	37

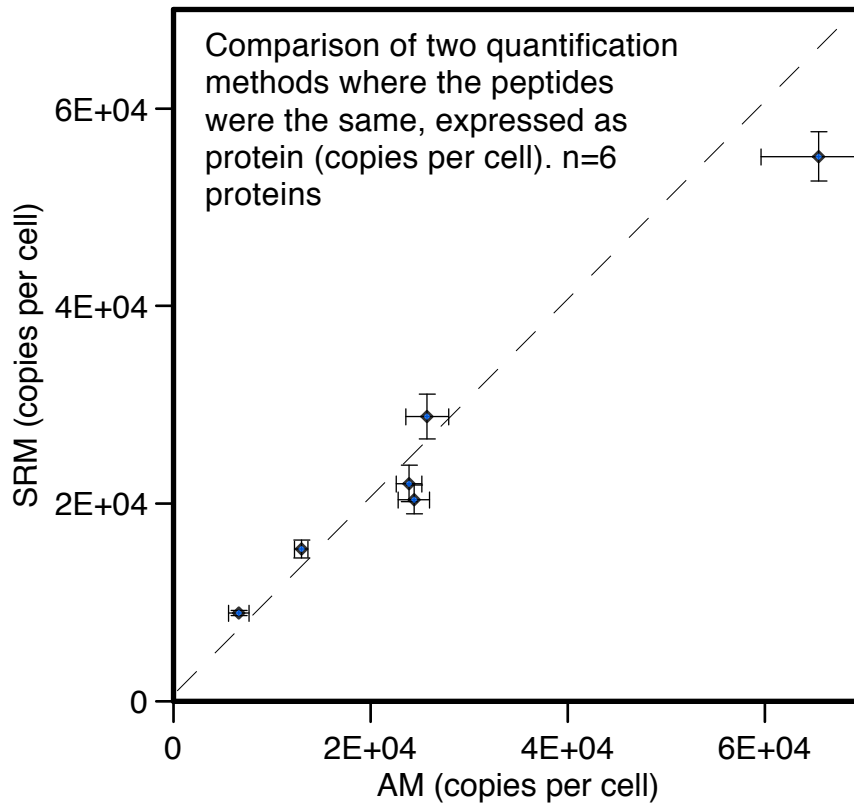
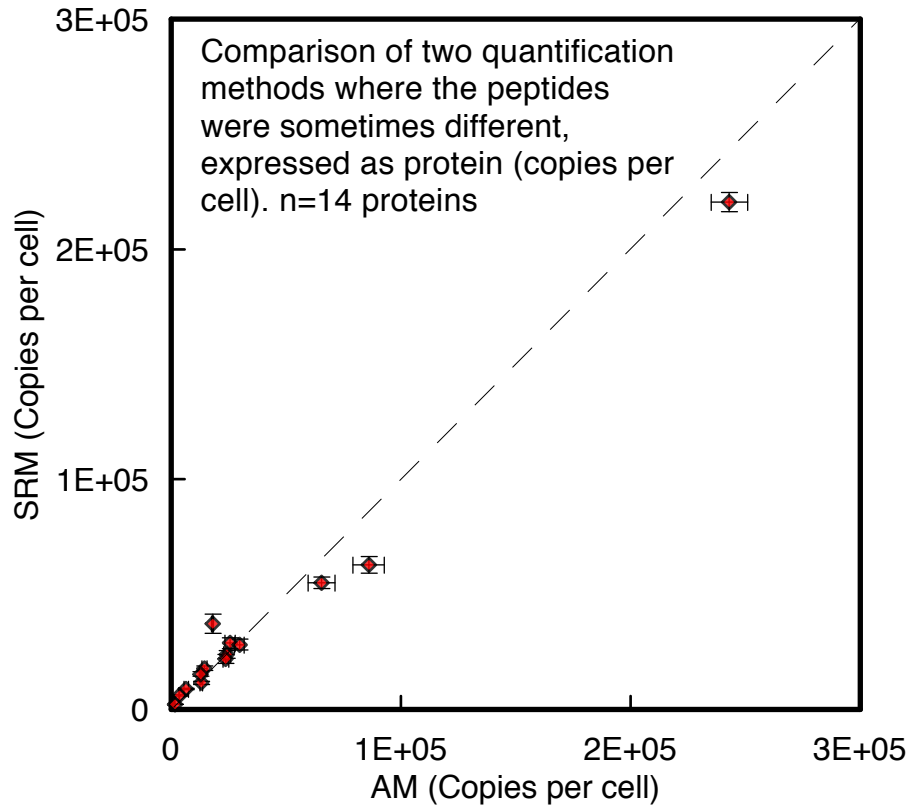
A**B****C**

Supplementary Figure 3
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Supplementary Figure 4
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Supplementary Figure 1. Schematic representation of the initiation (*A*), elongation (*B*) and termination (*C*) phases of translation. Panel *D* shows the overall reaction scheme used in the computational model. In order to keep the demand for computational capacity to a reasonable level, it was assumed that elongation cycled through a twenty-codon open reading frame. The full set of model equations are given elsewhere in the Supplementary Information section.

Supplementary Figure 2. Construction and analysis of *tet07* chromosomal integration strains. (A) Scheme for integration of the *tet07* regulatory cassette 5' of each translation factor gene. (B) Illustration of the method for PCR validation of the chromosomal integrations. The schematic diagram indicates which PCR products are expected from a successful integration experiment, while the stained agarose gels confirm that the expected bands are indeed generated from total genomic DNA, in this case from the *tet07 SUI1* strain. (C) Complementation of *tet07* phenotypes was used to confirm correct integration into the chromosome. Three examples are shown: in each case the slow-growth phenotype in the *tet07* strain was fully complemented by transformation using a plasmid bearing the corresponding gene transcribed from a constitutive promoter – this was one of the 'top-up' plasmids referred to in the main text and illustrated in panel D. No complementation was observed if an empty 'top-up' plasmid was used. (D) Six different promoters were used in the respective versions of the 'top-up' plasmid – these were engineered to provide a wide spread of transcription rates. (E) Examples of doxycycline titrations of the intracellular abundance of translation factors under the control of the *tet07* regulatory system. The Western blots reveal how the intracellular abundance of each translation factor encoded by its corresponding *tet07* regulatory system (underlined) was suppressed to varying degrees in response to the presence of different amounts of doxycycline. The vertical red arrows indicate at which point global protein synthesis was nearest to being 80% of the physiological rate. Other factor levels in each strain (i.e. those not under the control of the *tet07* regulatory system) were not detectably affected by the presence of doxycycline. Quantitation was normalized against hexokinase. (F) Table showing the relative abundance of translation factors in ten different *tet07* strains (those manifesting $R_1' > 0$) as determined by calibrated Western blotting. In all cases, data are shown for experiments where the protein synthesis rate had been suppressed to below 80% of the physiological level.

Supplementary Figure 3. Rate control data for the translation factors. (A) Sucrose density-gradient analysis reveals changes in the ribosome loading distributions on yeast mRNA. These examples include a wild-type control (lacking any chromosomal *tet07* construct; without doxycycline and plus 8 μ g ml⁻¹ doxycycline, i.e. higher than used with any of the *tet07* strains), and data for the *tet07CDC33* (eIF4E), *tet07SUI1* (eIF1), *tet07DED1* (Ded1), *tet07TEF5* (eEF1B), *tet07SUP45* (eRF1), and *tet07PAB1* (Pab1) strains (Table S1). (B) Intracellular mRNA abundance data [ordered along the X-axis according to mRNA species (top) and strain (bottom)] as estimated using RT-qPCR and expressed as a fraction of *RPS5* mRNA, averaged for at least 4 biological replicates and, for ease of comparison, normalized against the wild-type level. The error bars represent standard deviations. In the *tet07SUP35* strain, transcription of *SUP35* is higher than in the wild-type strain. (C) Comparison of suppression of protein synthesis in the strains *tet07TIF2* (eIF4A) and *tet07TIF5* (eIF5) after incubation with doxycycline for the period used in experimental work described in this paper and also after an additional 24 hours. The degree of inhibition is stably maintained and there is no sign of any compensatory mutations. This is consistent with our finding that up-regulation of the activity of individual factors does not generally lead to increases in global translation.

Supplementary Figure 4. Analysis of cell-size distributions. Histograms of cell size – each plot shows the distribution of cell diameters across a population of cells from each strain at the stated concentrations of doxycycline. Labelling of the colour-coded plots indicates to what degree the growth of each cell population was inhibited (as a percentage of the wild-type growth rate).

Supplementary Figure 5. Determination of the scanning ratio for the translation factors. (A) The scanning ratio assay plasmid. This contains two independent promoters (P_{TRP1} and P_{DCD1}) of comparable strength coupled to a short (L0; 65 nucleotides) and a long (L2; 1240 nucleotides) 5'UTR (Berthelot et al. 2004). Expression from the two promoter/5'UTR combinations was measured via the activities of the firefly and renilla luciferase reporters, respectively. (B) Plots of the L2/L0 ratio versus growth rate. The bar graph summarizes the R^{Sc} values for those factors where R^{Sc} is not zero. While most *tet07* strains showed no change in the L2/L0 ratio as a function of modulation of intracellular factor abundance, five strains manifested a positive dependence of this ratio on factor abundance. Most other strains showed a slope of zero (data not shown), and a small number manifested a small negative value for R^{Sc} (two examples are shown here: eIF4A and eIF4B). The negative slopes were small relative to the error estimates, and we therefore counted these results and the zero slope results as 'no change' (see Table 1). Since negative values for R^{Sc} would indicate a lack of enhancement of scanning by the factor under study, this mode of categorization is consistent with our procedure for identifying factors that stabilize scanning on longer 5'UTRs. The red point, set at 1.0 in each case, is the ratio observed for the wild type strain in which the addition of doxycycline does not affect the abundance of any of the translation factors. (C) Outputs from the computational model. The *in silico* translation machinery manifests properties that closely resemble those of the *in vivo* system. Here we see the relationship between global protein synthesis rate and the intracellular abundance of each factor. Each plot features the experimental data (green; rate of global protein synthesis vs molecules of translation factor per cell) compared to the predicted relationship from the model (blue). The vertical lines indicate the points on the x-axis (intracellular abundance in molecules per cell) at the 100% physiological level (dashed) and at the 80% level (dotted).

Berthelot K, Muldoon M, Rajkowitsch L, Hughes J, McCarthy JEG (2004) Dynamics and processivity of 40S ribosome scanning on mRNA in yeast. *Mol. Microbiol.* **51**: 987–1001

Supplementary Figure 6. Comparison of Accurate Mass (AM) and Selected Reaction Monitoring (SRM) quantitation. Some proteins in the study were quantified by both AM and SRM approaches (see Materials and Methods section). For these proteins, the quantitation values were compared either for all peptides (top panel) or using the same peptide for each protein (lower panel).