**Supplementary File 2**

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| **Para-meter** | **Biological meaning** | **Unit** | **Description** |
| $$r\_{1}$$ | $$\frac{bulk transcription rate}{total protein number}$$ | $10^{-3}$/min | This parameter was estimated as $r\_{1}=θ\_{RNAP}β\_{mRNA} /T\_{RNAP}$, where $θ\_{RNAP}$ is the number of RNAPs normalized by the number of proteins; $β\_{mRNA}$ is the fraction of RNAPs engaged in transcription, and $T\_{RNAP}$ is the mean mRNA synthesis time. |
| $$r\_{2}$$ | $$\frac{bulk translation rate}{total protein number}$$ | $10^{-3}$/min | This parameter was estimated by $r\_{2}=θ\_{ribo} /T\_{ribo}$, where $θ\_{ribo}$ is the number of ribosomes normalized by the number of proteins, and $ T\_{ribo}$ is the mean protein synthesis time. |
| $$K\_{1}$$ | Saturation level of DNA with respect to RNAP binding | 1/$μm^{3}$ | This parameter was estimates from $α\_{RNAP}=\frac{[Z]}{K\_{1}+[Z]}$ , where $α\_{RNAP}$ is measured in this work and $\left[Z\right]\_{avg}$, the mean genome copy.  |
| $$K\_{2}$$ | Saturation level of mRNA with respect to ribosome binding | 1/$μm^{3}$ | This parameter was estimated as $α\_{ribo}=\frac{[X]}{K\_{2}+[X]}$ , where $α\_{ribo}$ is measured in this work and $[X]$, the mRNA concentration.  |
| $$δ$$ | mRNA degradation rate | 1/min | $δ=1/τ\_{L}$, where $τ\_{L}$ is the mRNA lifetime  |
| $$c$$ | $$\frac{cell volume}{protein number}$$ | $$10^{-6}μm^{3}$$ | Cell volumes of different culture conditions were measured in this work.  |
| $$c'$$ | $$\frac{cell area}{protein number}$$ | $$10^{-6}μm^{2}$$ | Cell area of different culture conditions was measured in this work.  |
| $$[Z]\_{avg}$$ | Average genome concentrationof normal-growing cells | genome/$μm^{3}$ | Estimated by averaging the genome concentration over the cell cycle, see Appendix 1 for details.  |