Table S4. Transcription related parameters for $\mathbf{2}$ doub/h, $37^{\circ} \mathbf{C}$. Transcription related parameters as defined in [28], obtained here for 2 doub/h. Values in bold were estimated. See S1.2 in Text S1 for further explanations.

| Genetic parameter | Units | P1 $^{\mathrm{a}}$ | $\mathbf{P 2}^{\mathrm{a}}$ | constitutive $^{\mathrm{a}}$ | repressable $^{\text {a }}$ | pause $^{\mathrm{a}}$ |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| $D_{i}=V_{\text {cell }}(2$ doub/h $) \cdot d_{i}$ | average copies per cell | $27^{\mathrm{b}}$ | $27^{\mathrm{b}}$ | $40.4^{\mathrm{c}}$ | $\mathbf{4 0 8 . 4}^{\mathrm{d}}$ | $161.8^{\mathrm{e}}$ |
| $V_{i}^{\max }$ | min/min | $110^{\mathrm{f}}$ | $110^{\mathrm{f}}$ | $33^{\mathrm{g}}$ | $1.5^{\mathrm{h}}$ | $3.3^{\mathrm{i}}$ |
| $c_{i}$ | nuc/sec | $85^{\mathrm{j}}$ | $85^{\mathrm{j}}$ | $52^{\mathrm{j}}$ | $52^{\mathrm{j}}$ | $\mathbf{0 . 8 9}^{\mathrm{d}}$ |
| $K_{m, i}$ | molec/cell | $1240^{\mathrm{l}}$ | $2531^{\mathrm{k}}$ | $405^{\mathrm{k}}$ | $405^{\mathrm{k}}$ | $405^{\mathrm{k}}$ |
| $L_{i}$ | base pairs | $6000^{\mathrm{m}}$ | $6000^{\mathrm{m}}$ | $2000^{\mathrm{m}}$ | $1000^{\mathrm{m}}$ | $1000^{\mathrm{m}}$ |

${ }^{a}$ Promoter classes as defined by [28].
${ }^{\mathrm{b}}$ The average number of copies of the $r r n$ operon per cell, $D_{r r n}(\mu)$, is given by Eq. S7: $D_{r n}(\mu)=\sum_{j=1}^{7} 2^{\mu\left(C\left(1-m j_{j}^{(m)}\right)+D\right)}$, where $m_{j}^{(r r n)}$ are the rrn operon map locations given in Table S1.
${ }^{c}$ According to [28], $\left[\mathrm{P}_{\text {constitutive }}\right]=1.5\left[\mathrm{P}_{\text {rrn }}\right]$, in order to fit to (1) transcription of all r-proteins and (2) mRNA synthesis rate. This is consistent with the length of the r-protein gene class given in Table S 1 : the total DNA per chromosome associated with this gene class is roughly $40.4 /(27 / 7=\text { gene dosage per gene })^{*}(2000 \mathrm{bp})=20,948=$ total length of constitutive class coding genes, compared with $L_{r \text {-protein }}=21252$ (Table S1).
${ }^{\mathrm{d}}$ Estimated value - see S1.2.
${ }^{\mathrm{e}}$ According to [28], based on known fractions of intermittently inactive RNAp in the cell $\left[\mathrm{P}_{\text {pause }}\right]=6\left[\mathrm{P}_{\mathrm{rm}}\right]$.
${ }^{\mathrm{f}}$ Estimated in [3]. Assumed to be growth rate independent [28].
${ }^{\mathrm{g}}$ As measured for the spc ribosomal promoter, which is a representative promoter for this class (see [28]).
${ }^{\text {h }}$ As measured for $\beta$-lactamase promoter, which is taken to be a representative promoter for this class (see [28]).
${ }^{i}$ Maximum initiation rate was set to be ten fold lower than the $\mathrm{V}^{\max }$ for the constitutive gene class, assuming pause genes are blocked $90 \%$ of the time [28].
${ }^{j}$ See table 3 in [17].
${ }^{\mathrm{k}}$ Constitutive promoter binding affinities scale according to cell volume with respect to their values at 2.5 doub $/ \mathrm{h}$ and are taken from [28]. Volumes are given in Table S2.
${ }^{1}$ Taken from table 5 of [105]: $\mathrm{K}_{\mathrm{P} 1}: \mathrm{K}_{\mathrm{P} 2}$ at $(2.14$ doub $/ \mathrm{h})=0.49: 1$, i.e. $1240=0.49 * 2531$.
${ }^{\mathrm{m}}$ See tables 1 and 2 in [28].

