

Table S2 Parameter Values and Ranges

Parameter	Description	Initial Value	Range and Unit	Average Value from parameter search	Average Value for min hes6 oscillations
δm	mRNA degradation	0.31	min ⁻¹		
$\delta m6$	<i>hes6</i> mRNA degradation	0.31	0-1 min ⁻¹	0.72	0.65
δP	protein degradation	0.15	min ⁻¹		
$\delta P6$	Hes6 protein degradation	0.15	0-1 min ⁻¹	0.12	0.061
δD	dimer degradation	0.15	min ⁻¹		
$\delta D6$	Hes6/Hes6 degradation	0.15	0-1 min ⁻¹	0.032	0.015
θm	maximum transcription	150	min ⁻¹		
$\theta m6$	maximum <i>hes6</i> transcription	150	0-10,000 min ⁻¹	1444	93
βP	translation	18.5	min ⁻¹		
$\beta P6$	Hes6 translation	18.5	0-100 min ⁻¹	18.3	62.8
r	critical concentration	13,900			
s	strength scaling factor	162.7	0-10,000	61.3	64.7
$k+$	dimer on rate	0.02	min ⁻¹		
$k-$	dimer off rate	1			
$k-_{Hes6/6}$	Hes6/Hes6 off rate	1	0-10	5.2	3.0
n	relative difference between weak and strong dimers	1.26	1-10	1.31	1.31
τm	transcriptional delay	5	min		
τ	translational delay	1.5	min		

Biochemical parameters used in computational model, their initial values and the average fitted values corresponding to Figure 5B. Transcription, translation and degradation rates are from (CINQUIN 2007) along with r and s values, which were scaled to account for the different number of repressive dimers in our simulation and the assumption of independent, rather than competitive, repressors.