Supplementary Table 1. Standard, minimum, and maximum values of parameters

Category	**Parameter**	**STD ($\min^{-1}$)**	**MIN ($\min^{-1}$)**	**MAX ($\min^{-1}$)**
binding constant of activator to DNA	h_t	0.002	9×10^{-4}	5×10^{-3}
dissociation constant of activator from DNA	f	0.08	0.05	0.16
transcription rate constant in the ON state	g_1	2	1.7	4
transcription rate constant in the OFF state	g_0	0.02	$< 1 \times 10^{-7}$	0.9
transcription rate constant in the constitutive expression **	g_2	0.2	0.1	0.6
degradation rate constant of mRNA **	k_2	ln2/5	ln2/9	ln2/4
translation rate constant	η	0.2	0.15	0.3
phosphorylation rate constant	h_p	1×10^{-2}	5×10^{-4}	0.2
dephosphorylation rate constant	h_p'	2×10^{-2}	2×10^{-3}	> 7
ubiquitination rate constant	h_u	5×10^{-3}	$< 1 \times 10^{-5}$	> 4
complex formation	h_b	0.1	$< 1 \times 10^{-6}$	> 10
degradation rate constant of unubiquitinated proteins *	k_1	ln2/120	$< \ln 2/10^4$	ln2/40
degradation rate constant of ubiquitinated proteins *	k_0	ln2/5	$< \ln 2/10^4$	$> \ln 2/10^{-3}$
exporting rate constant of Cdc14	h_r	ln2/160	$\ln 2/10^3$	$> \ln 2/10^{-2}$
importing rate constant of Cdc14	h_r'	ln2/10	$< \ln 2/10^5$	ln2/0.5

More than 300 reactions represented by the master equation are categorized into 15 types and a single parameter is assigned to each reaction type. Values in the third right column (STD) are used as the standard parameters. The standard limit cycle is robust when one of 15 parameters is varied in the range from the value of the second right column (MIN) to that of the first right column (MAX).

*Half-lives of ubiquitinated proteins are several minutes or less (see *Supporting Text*) and those of unubiquitinated proteins are >60 min (1-3).

**Transcription frequencies of *CLN1,2*, *CLN3*, *CLB1,2*, *CLB5,6*, *SIC1*, *CDC20*, *SWI5*, and *PDS1* are estimated to be ~10^{-2} mRNAs/min for asynchronous cells and half-lives of these mRNAs are estimated to be 9-17 min (4). These half-lives should include time needed for the export process of mRNA to cytoplasm. Because mRNA can be translated into proteins immediately after transcription in the present model, we set half-life of mRNA 5 min which is shorter than the experimental results.

References

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