Electronic Supplementary Material (ESI) for Molecular BioSystems.

ESI Table 1. The initial reactant concentrations and source references.

Reactant	Initial concentration	Unit	Source references
SCFAcoeff	(1.00 → 3.60)	µM	*N/A*
TR	0.05	µM	[1,2]
TRac	0	µM	
HST	0.3	µM	[1,2]
HSTac	0	µM	
βeta	1.1	µM	[3]
MT	5.5	µM	[4-7]
tuGDP	3	µM	
tuGTP	1.5	µM	

ESI Table 2. The kinetic reactions, rate constants, rate laws and ODEs used in the modeled system.

Equation; activator	Rate constant	Rate law	ODE
TR → *TRac; SCFAcoeff*	k1f	irr. mass action, activated	d[*TRac*]/dt = - (k1b[*TRac*]) + (k1f [*TR*] [*SCFAcoeff*])
TRac → *TR*	k1b	irr. mass action	
HST → *HSTac; TRac*	k2f	irr. mass action, activated	d[*HSTac*]/dt = - (k2b[*HSTac*]) + (k2f [*HST*] [*TRac*])
HSTac → *HST*	k2b	irr. mass action	
→ *βeta; HSTac*	k3f	zero order, activated	d[*βeta*]/dt = - (k3b[*βeta*]) + (k3f [*HSTac*])
βeta →	k3b	irr. mass action	
tuGTP → *MT*	k4; k4x	non-linear second order	d[*MT*]/dt = - (k5[*MT*][*βeta*]) + ([*tuGTP*] (k4x + k4 [*MT*]^2))
MT → *tuGDP; βeta*	k5	irr. mass action, activated	d[*tuGDP*]/dt = - (k6 [*tuGDP*]) + (k5[*MT*][*βeta*])
tuGDP → *tuGTP*	k6	irr. mass action	d[*tuGTP*]/dt = - ([*tuGTP*] (k4x + k4 [*MT*]^2)) + (k6 [*tuGTP*])

irr: irreversible; f: denotes a forward reaction; b: denotes a backward reaction

ESI Table 3. The forward and reverse kinetic rate constants in the modelled pathway.

Reaction	Rate constant	Value	Units	Range	Source references
TR acetylation	k1f	0.30	$\mu M^{-1}s^{-1}$	0.2 to 5 s^{-1}	[1,8]
TR deacetylation	k1b	0.25	s^{-1}		
Histone acetylation	k2f	0.275	$\mu M^{-1}s^{-1}$	0.35 s^{-1} ; 0.3 s^{-1}	[9]
Histone deacetylation	k2b	0.05	s^{-1}		
βeta synthesis	k3f	0.23	s^{-1}	0.01–0.6 s^{-1}	[10,11]
βeta degradation	k3b	0.30	s^{-1}	0.06–2 s^{-1}	
MT rescue	k4	50			
	k4x	0.081	s^{-1}	upper & lower	[12]
MT catastrophe	k5	1	$\mu M^{-1}s^{-1}$	constraints	
tuGDP phosphorylation	k6	0.0065	s^{-1}		

f: denotes a forward reaction; b: denotes a backward reaction

ESI Table 4. Published experimental data for MT dynamicity parameters in **(A)** interphase cells and control cells for MT destabilising and stabilising treatments; **(B)** mitotic cells and cells undergoing MT-destabilising and MT-stabilising treatments.

(A)

MT dynamicity parameter	**Interphase cells[a]**	**control cells (destabilising)[b]**	**control cells (stabilising)[b]**
catastrophe frequency [s^{-1}]	0.023	0.004	0.012
rescue frequency [s^{-1}]	0.108	0.036	0.020
% time elongating	15.9	66.2	38.7
% time shortening	12.2	7.2	19.9
% time pausing	*72.0*	*28.9*	*39.4*
growth rate [µm. min^{-1}]	9.875	3.6	4.8
shrinkage rate [µm. min^{-1}]	14.50	9.5	6.4

(B)

MT dynamicity parameter	**Mitotic cells[a]**	**MT-destabilised cells[b]**	**MT-stabilised cells[b]**
catastrophe frequency [s^{-1}]	0.089	0.018	0.006
rescue frequency [s^{-1}]	0.033	0.021	0.038
% time elongating	50.5	34.1	63.8
% time shortening	38.1	29.0	7.6
% time pausing	11.4	38.7	29.0
growth rate [µm. min^{-1}]	13.12	6.0	4.0
shrinkage rate [µm. min^{-1}]	15.15	6.9	10.0

Mean values: [a] Rusan *et al*. (2001); [b] Kline-Smith & Walczak (2002) [6,13]

ESI Table 5. The sensitivities of the model outcomes to the initial parameters. The results show the summarised, scaled sensitivities: **(A)** the influences of the initial concentrations of the reactants on the reaction fluxes; **(B)** the influences of the kinetic rate constants on the temporal concentrations of the reactants.

A

Variable: initial concentration	**Target function: fluxes of reactions**
TR	46.73
HST	54.14
βeta	10.87
MT	75.86
tuGDP	41.43
tuGTP	21.03

B

Variable: kinetic rate constant	**Target function: temporal concentrations**
k1f (*TR*-acetylation)	20.40
k1b (*TR*-deacetylation)	19.13
k2f (*HST*-acetylation)	46.70
k2b (*HST*-deacetylation)	39.78
k3f (*βeta*-synthesis)	54.09
k3b (*β*eta-degradation)	48.44
k4 (rescue)	68.51
k4x (rescue-x)	30.62
k5 (catastrophe)	67.14
k6 (phosphorylation)	144.71

f: denotes a forward reaction; b: denotes a backward reaction

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