Table S1: Description of model input and outputs.

	Input	Description	Value
1	*M*	Mitogen level	1.8 (normal simulations). 2.3 (cyclin E$^{-/-}$, final model). 11 (cyclin D$^{-/-}$ final model).
2	*p53_damage*	Level of p53	Value of *p53*(*t*) from upstream network (initial model). 1 during arrest, 0 during free cycling (fitting and final model).
3	*Chk2_damage*	Level of Chk2	Value of *Chk2*(*t*) from upstream network (initial model). 1 during arrest, 0 during free cycling (fitting and final model).
4	*CycD_ko*	Cyclin D knockout	1 (cyclin D$^{-/-}$ simulations) 0 (all other simulations)
5	*CycE_ko*	Cyclin E knockout	1 (cyclin E$^{-/-}$ simulations) 0 (all other simulations)
6	*CHX*	Cycloheximide level	0.25 (cycloheximide-induced arrest simulations) 0 (all other simulations)
7	*p53_basal*	Basal p53 level	0.75 (p53$^{+/+}$ simulations) 0 (all other simulations)
8	*Arrest_I*	p53-dependent p21 activation	0 or 1, depending on whether this arrest mechanism is active
9	*Arrest_II*	Chk2-dependent Cdc25 phosphorylation	0 or 1
10	*Arrest_III*	p53-dependent Cyclin A and Cyclin B repression	0 or 1

	Output	Description	Species contained	Quantities Influenced

1	*CycET*	Total cyclin E	`CycE+TriE+ TriE21`	Steady-state level reached during arrest
2	*CycBT*	Total cyclin B	`CycB+pB+BCKI +pBCKI`	Steady-state level reached during arrest
3	*CycE*	Active cyclin E	`CycE`	Time of the G1/S transition
4	*pB*	Phosphorylated cyclin B	`pB`	Time of the S/G2 transition
5	*Cdc20A*	APC/C$^{\text{Cdc20A}}$	`Cdc20A`	Time of mitosis