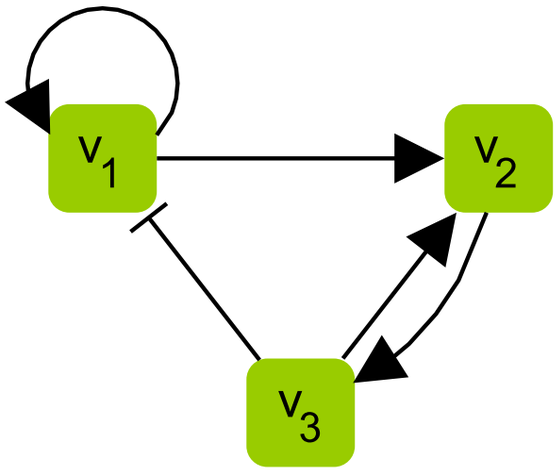
Boolean network modeling

(*a*) Network structure



(*b*) Boolean functions

$B_1(\sigma_1, \sigma_3) = \sigma_1$ OR NOT σ_3

$B_2(\sigma_1, \sigma_3) = \sigma_1$ AND σ_3

$B_3(\sigma_2) = \sigma_2$

(*c*) Truth tables

$B_1(\sigma_1, \sigma_3)$

σ_1	σ_3	σ_1
0	0	1
0	1	0
1	0	1
1	1	1

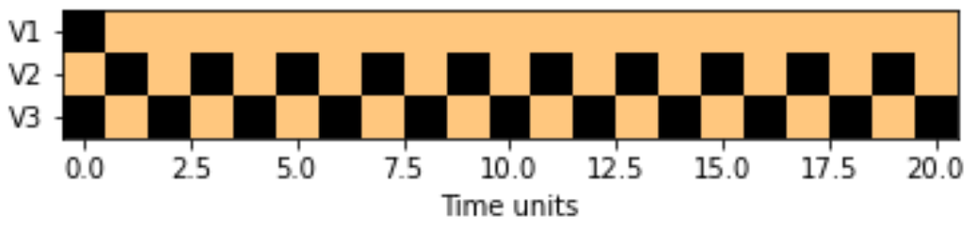
$B_2(\sigma_1, \sigma_3)$

σ_1	σ_3	σ_2
0	0	0
0	1	0
1	0	0
1	1	1

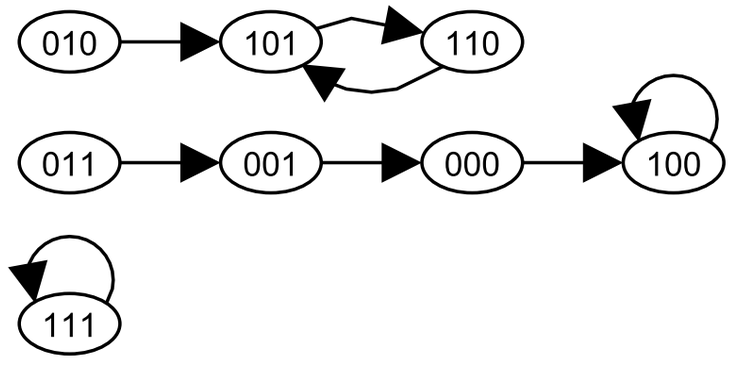
$B_3(\sigma_2)$

σ_2	σ_3
0	0
1	1

Dynamical behavior of the system



(*d*) State transition graph



Images from Wang et al. 2012, Phys Biol, doi:10.1088/1478-3975/9/5/055001

Global control of cell-cycle transcription by coupled CDK and network oscillators

David A. Orlando[1,2], Charles Y. Lin[1], Allister Bernard[3], Jean Y. Wang[1], Joshua E. S. Socolar[4], Edwin S. Iversen[5], Alexander J. Hartemink[3] & Steven B. Haase[1]

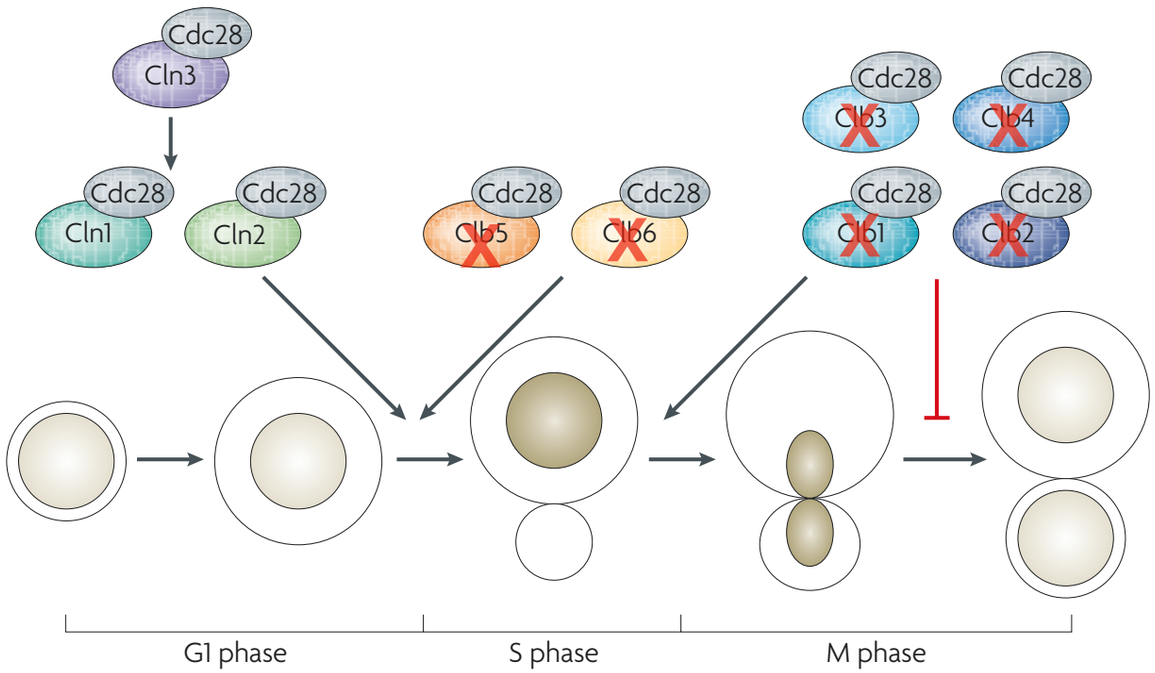


Image from Bloom and Cross, doi:10.1038/nrm2105

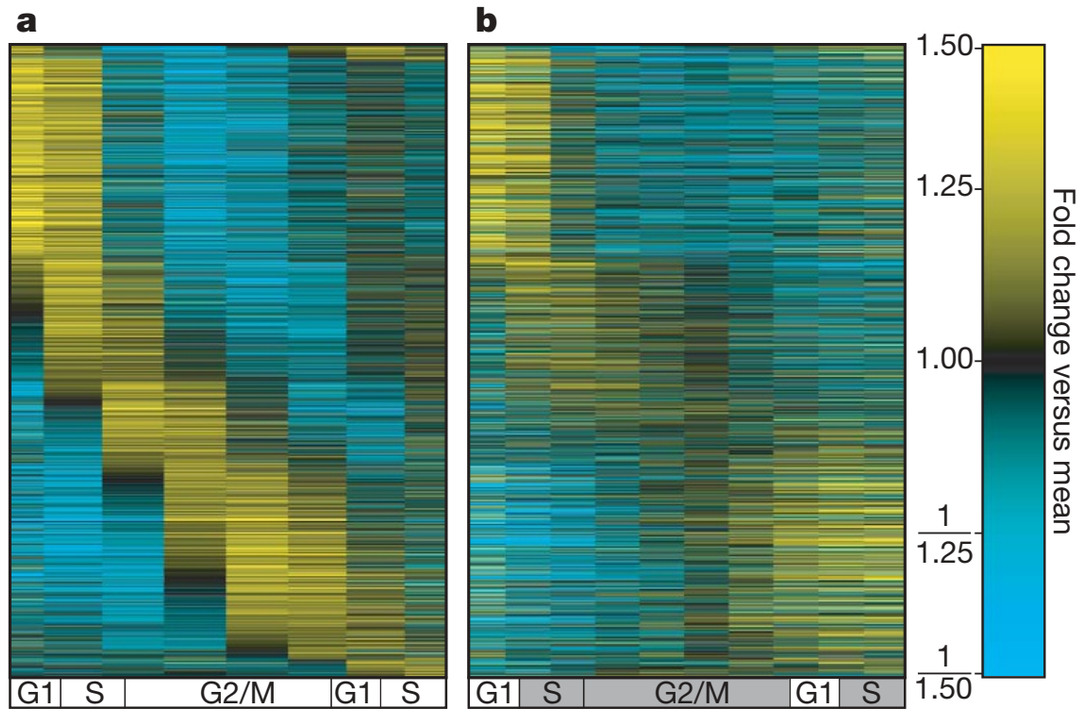
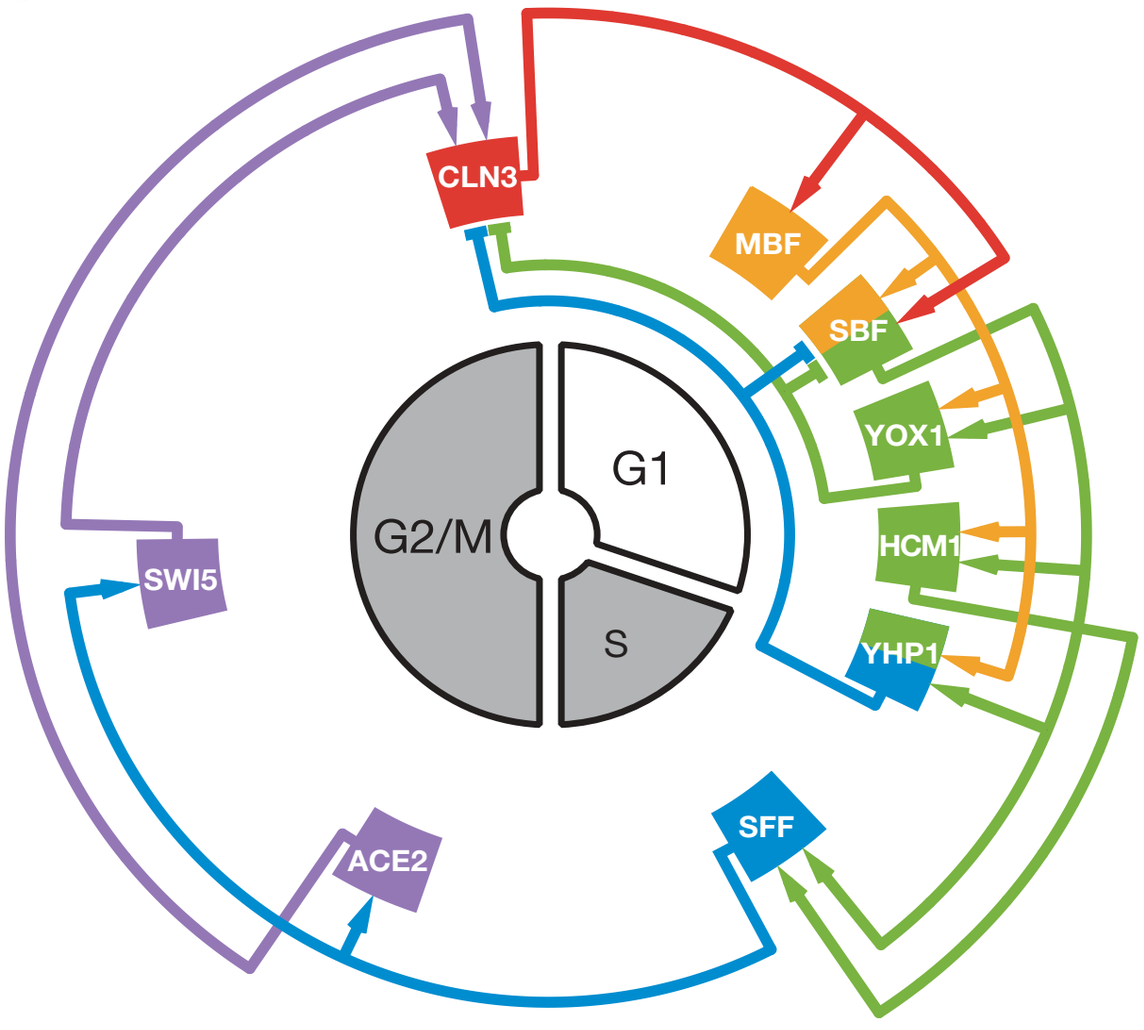


Figure 1 | Dynamics of periodic transcripts in wild-type and cyclin-mutant cells. Heat maps depicting mRNA levels of periodic genes for wild-type (**a**) and cyclin-mutant (**b**) cells. Each row in **a** and **b** represents data for the same gene (Supplementary Table 1). Transcript levels are expressed as a $\log_2$-fold change relative to mean expression. Transcript levels at each point in the time series were mapped onto a cell-cycle timeline (see Methods). The S and G2/M phases of the cyclin-mutant timeline are shaded, indicating that, by conventional definitions, cyclin-mutant cells arrest at the G1/S-phase border.

c



a Initial Regulatory Logic Choice

TF	Activation Rule
MBF	CLN3
SBF	(CLN3 $\vee$ MBF) $\wedge$ $\neg$(YOX1 $\wedge$ YHP1)
YOX1	MBF $\wedge$ SBF
HCM1	MBF $\wedge$ SBF
YHP1	MBF $\vee$ SBF
SFF	SBF $\wedge$ HCM1
ACE2	SFF
SWI5	SFF
CLN3	(SWI5 $\wedge$ ACE2) $\wedge$ $\neg$(YOX1 $\wedge$ YHP1)