

Table S4. Parameters increased *in silico* upper limit gene dosage search

Gene	gTOW	Max up	parameter category	Parameters changed			
	<i>in vivo</i> [#]	<i>in silico</i>		Parameter1	Parameter2	Parameter3	Parameter4
<i>BUB2</i>	118.5	32.0	constant	Bub2l	Bub2h		
<i>CDC6</i>	79.1	2.8	synthesis (constant, 2 regulated)	ksf6_r	ksf6_c	ksf6_r2	
<i>CDC14</i>	1.8	2.0	synthesis (constant)	ks14			
<i>CDC15</i>	157.7	256.0	constant	Cdc15T			
<i>CDC20</i>	70.6	16.0	synthesis (constant, regulated)	ks20_r	ks20_c		
<i>CDH1</i>	63.1	90.5	synthesis (constant)	kscdh			
<i>CLB1*</i>	72.1	8.0	synthesis (constant, regulted)	ksb2_r	ksb2_c		
<i>CLB2*</i>	31.3	8.0	synthesis (constant, regulted)	ksb2_r	ksb2_c		
<i>CLB5*</i>	8.8	32.0	synthesis (constant, regulated)	ksb5_c	ksb5_r		
<i>CLB6*</i>	142.2	32.0	synthesis (constant, regulated)	ksb5_c	ksb5_r		
<i>CLN1*</i>	56.7	5.7	synthesis (regulated)	ksn2_r			
<i>CLN2*</i>	116.9	5.7	synthesis (regulated)	ksn2_r			
<i>CLN3</i>	74.6	16.0	synthesis (assoc.MASS)	C0			
<i>ESP1</i>	164.7	1.4	constant	ESP1T			
<i>LTE1</i>	126.4	256.0	constant	lte1l	lte1h		
<i>MAD2</i>	95.7	128.0	constant	ki20_c	ki20_c		
<i>MBP1*</i>	95.6	4.0	GK function	ksn2_r	ksb5_r	ksf6_r2	ks1pds_r
<i>MCM1</i>	11.3	16.0	GK function	ks2pds_r	ksswi_r	ksb2_r	ks20_r
<i>NET1</i>	39.6	2.0	synthesis (constant)	ksnet			
<i>PDS1</i>	73.9	1.4	synthesis (2 regulated)	ks2pds_r	ks1pds_r		
<i>SIC1</i>	32.3	2.8	synthesis (constant, regulated)	ksc1_r	ksc1_c		
<i>SWI4*</i>	54.5	4.0	GK function	ksn2_r	ksb5_r	ksf6_r2	ks1pds_r
<i>SWI5</i>	62.5	2.0	synthesis (constant, regulated)	ksswi_r	ksswi_c		
<i>SWI6*</i>	155.3	4.0	GK function	ksn2_r	ksb5_r	ksf6_r2	ks1pds_r
<i>TEM1</i>	87.7	256.0	constant	TEM1T			

* *CLB1 /CLB2 , CLB5 /CLB6 , CLN1 /CLN2* and *MBP1 /SWI4 /SWI6* are implemented as single genes in the computational model. # The number is the copy number determined in the gTOW experiment (plasmid copy) + 1 (chromosomal copy).