

Table S3. Comparing experimental mRNA expression distributions to simple models

	A	B	C	D	E	F
	tetO promoter without activator (basal)		tetO promoter with tTA activator		Constitutive DOA1 promoter	
	1xtetO**	7xtetO***	1xtetO	7xtetO	Higher	Lower
Ratio of mean mRNA at late G2/M to G1 as a measure of fold-change in transcription:						
\hat{R}_M (measured)	9.3	3.1	2.8	2.7	2.4	4.2
Theoretical corresponding f	Inf	4.3	3.6	3.3	2.7	8.9
Negative binomial fit to total distribution: The standard model equates a frequency and size of bursting to parameters of negative binomial fit to total population's stationary distribution.						
"Burst frequency"	0.4	0.5	2.2	1.2	4.1	1.1
"Burst size"	7.7	8.5	5.8	10.0	1.4	1.3
2-fold transcription increase: * Poisson transcription with S/G2/M transcription rate increased 2-fold over G1 transcription rate. The transcription rate is fit to the experimental total mean mRNA count.						
f	2	2	2	2	2	2
χ^2 fit p-value, Total	0	0	0	0	0.95	0.96
χ^2 fit p-value, G1	0	0	0	0	0.02	0.002
χ^2 fit p-value, G2	0	0	0	0.001	0.001	0.001

<i>f</i>-fold transcription increase: *						
Poisson transcription with S/G2/M transcription rate increased <i>f</i> -fold over G1 transcription rate. The transcription rate and <i>f</i> are fit to the experimental G1 and G2 mean mRNA count.						
<i>f</i>	Inf	100	4	9	4	12
χ^2 fit p-value, Total	0.06	0.002	0.14	0.07	0.004	0.12
χ^2 fit p-value, G1	0.69	0.17	0.46	0.84	0	0.002
χ^2 fit p-value, G2	0.004	0	0.18	0.007	0.78	0.69
<i>F</i>-fold transcription increase with variable timing of transition: *						
Poisson transcription with S/G2/M transcription rate increased <i>f</i> -fold over G1 transcription rate with a 40 minute uniformly distributed window of switching to S/G2/M transcription rates after the S/G1 transition. The transcription rate and <i>f</i> are fit to the experimental G1 and G2 mean mRNA count.						
<i>F</i>	Inf	100	6	13	7	18
χ^2 fit p-value, Total	0.85	0.003	0.13	0.15	0	0
χ^2 fit p-value, G1	0.35	0.06	0.30	0.73	0	0
χ^2 fit p-value, G2 *	0.01	0	0.84	0.76	0.06	0.27

* Result of a χ^2 goodness of fit test of the measured data against the model prediction. Cases that pass or fail are in black or gray text, respectively with $p = 0.05$ representing the cutoff.

** For basal expression from $P_{1_{\text{tetO}}}$, the G1 and S/G2/M expression differ more than expected for no transcription in G1. Thus the data is best fit where $f = \text{infinity}$, representing no G1 transcription.

*** For basal expression from $P_{7_{\text{tetO}}}$, because of high expression noise and the fact that 10% of cells have not turned on by late G2/M, specifying *f* by matching G1 and S/G2/M means gives a value of *f* (~7) that fits distributions poorly. The χ^2 goodness of fit was maximal and fairly constant over a range of approximately $50 < f < 100$. Thus, $f = 100$ was selected. For the model with variable timing of transitioning to G2 transcription rates, the estimated 40 minute window was extended to the full duration of S/G2/M.