Supplemental Data

Transcriptional Pulsing of a Developmental Gene

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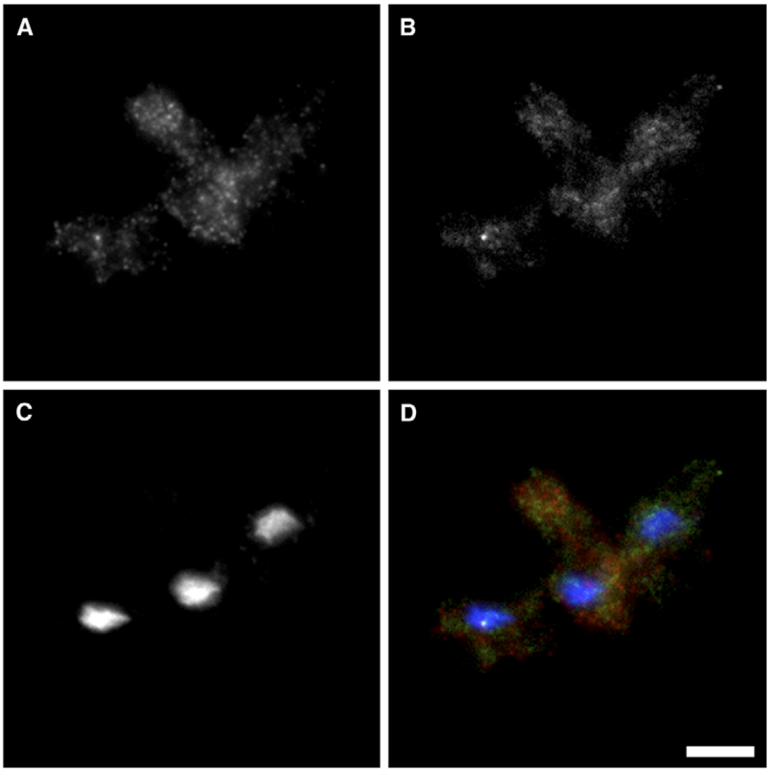

Figure S1. Nuclear Colocolization of RNA FISH of MS2 and dsc Probes

Nuclear colocalization of RNA FISH signals of MS2 (B) and dsc probes (A). (C) is the DAPI nuclear stain and (D) is the merge. RNA FISH protocol described in [S1]. Scale bar equals 5 μm.

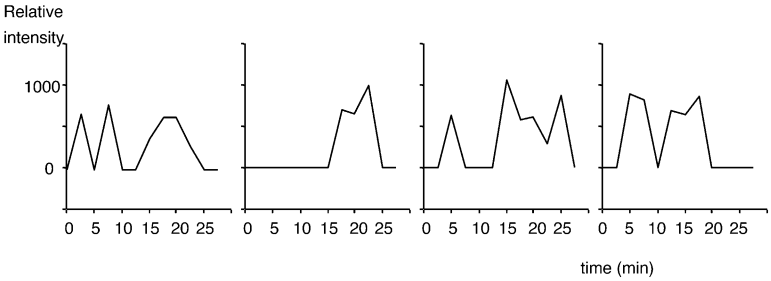

Figure S2. Intensity Time Series Data for the Transcriptional Pulsing of Four Typical Cells

Background subtracted pulse intensity at each time point was quantified by means of an automated script (described in text).

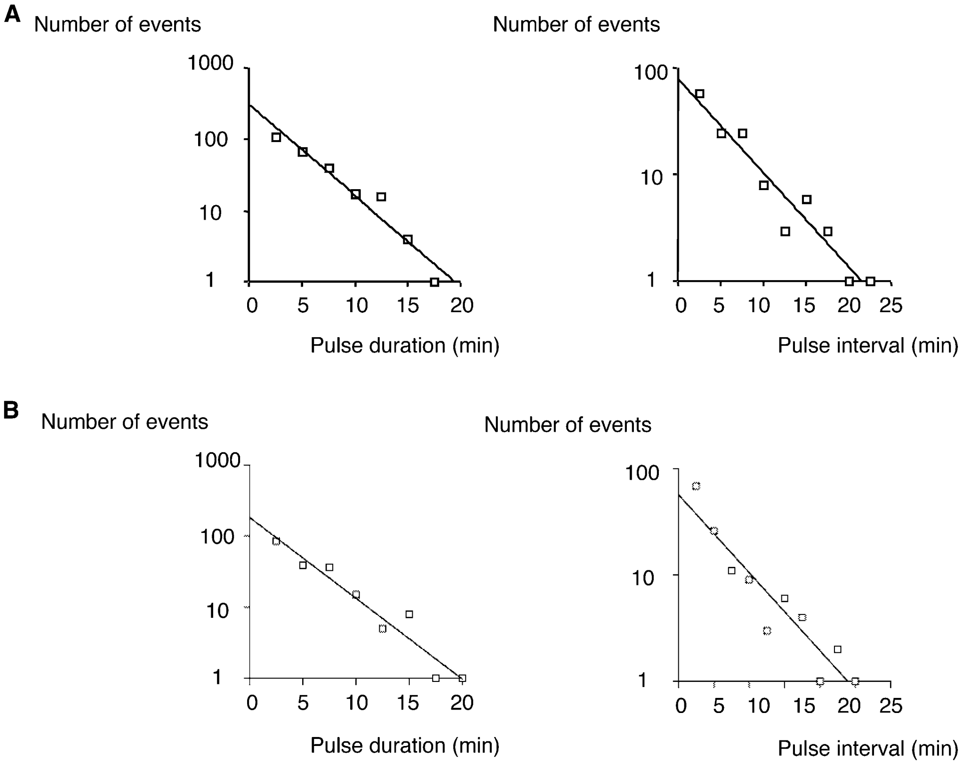

Figure S3. Frequency Distributions for Pulse Duration and Interval Fit Simple Exponential Functions

(A) Semilog plots of data from Figures 2B and 3B, showing the distribution of the lengths of pulses and intervals from the 0.5 hr time point.

(B) Semilog plots showing the distribution of the lengths of pulses and intervals from the 1.5 hr time point. All lines are fits to exponential functions ($r^2 > 0.99$).

Supplemental References

S1. Chubb, J.R., Bloomfield, G., Xu, Q., Kaller, M., Ivens, A., Skelton, J., Turner, B.M., Nellen, W., Shaulsky, G., Kay, R.R., et al. (2006). Developmental timing in *Dictyostelium* is regulated by the Set1 histone methyltransferase. Dev. Biol. *292*, 519–532.