Supplemental Material to Yao et al., submitted to *J. Bacteriol.* 8/3/2011

Fig. S1. Relationship of PABLO ligation yield to rate constants for mRNA degradation. The top line is a schematic of full-length, 5'-triphosphorylated Δ*ermC* mRNA or Δ*ermC*-del mRNA (deletion endpoints shown by square brackets). The 5'-monophosphorylated version of these mRNAs is shown on the line below. Rate constants for various processes that contribute to the cellular amounts of Δ*ermC* and Δ*ermC*-del mRNAs are indicated.

Fig. S1
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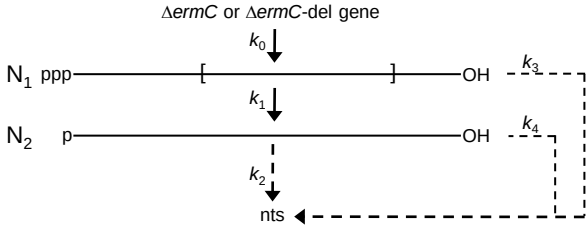

G = concentration of the gene
N_1 = concentration of tri-P RNA
N_2 = concentration of mono-P RNA
k_0 = rate constant for transcription
k_1 = rate constant for conversion of N_1 to N_2 by a pyrophosphohydrolase
k_2 = rate constant for RNA degradation by the 5' exonuclease activity of RNase J1
k_3 = rate constant for tri-P RNA degradation by RNase Y
k_4 = rate constant for mono-P RNA degradation by RNase Y

The system is described by two differential equations:

$$\frac{dN_1}{dt} = k_0 G - (k_1 + k_3)N_1$$

$$\frac{dN_2}{dt} = k_1 N_1 - (k_2 + k_4)N_2$$

At steady state: $\frac{dN_1}{dt} = 0$, $\frac{dN_2}{dt} = 0$

and $$\frac{N_2}{N_1} = \frac{k_1}{k_2 + k_4}$$

Ligation yield: $$\frac{N_2}{N_2 + N_1} = \frac{k_1}{k_1 + k_2 + k_4}$$

Thus, the ligation yield is inversely related to the rate constant k_4. Because k_4 is smaller for Δ*ermC*-del mRNA than for Δ*ermC* mRNA, the ligation yield will be higher for Δ*ermC*-del than for Δ*ermC*.