

## Supplemental Data

### Retention of Transcription Initiation

#### Factor $\sigma^{70}$ in Transcription Elongation:

#### Single-Molecule Analysis

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##### A *lacUV5-11(Cy5,+25)*

```
AGGC TTTACA CTTTATGCTTCCGGCTCG TATAAT GTGTGGA AATTGTGAGAG GGATAACAATTC  
TCCG AATGT GAAATACGAAGGCCGAGC ATATTA CACACCT TAACACTCT CCTATTGTTAAAG - Cy5
```

##### *lacUV5-14(Cy5,+28)*

```
AGGC TTTACA CTTTATGCTTCCGGCTCG TATAAT GTGTGGA AATTGTGAGGAGGAC GGATAACAATTC  
TCCG AATGT GAAATACGAAGGCCGAGC ATATTA CACACCT TAACACTCT CCTATTGTTAAAG - Cy5
```

##### *lacUV5-50(Cy5,+64)*

```
AGGC TTTACA CTTTATGCTTCCGGCTCG TATAAT GTGTGGA AATTGTGAGAGGTTAGTTGATTGTATTGA . . .  
TCCG AATGT GAAATACGAAGGCCGAGC ATATTA CACACCT TAACACTCTCCAATCAACTAACATAACT . . .  
. . . GTTGATTGGATTGAGTGAGAG GGATAACAATTC  
. . . CAACTAACCTAACTCACTCT CCTATTGTTAAAG - Cy5
```

##### *lacUV5-11(Cy5,-40)*

```
Cy5-AGGC TTTACA CTTTATGCTTCCGGCTCG TATAAT GTGTGGA AATTGTGAGAG GGATAACAATTC  
TCCG AATGT GAAATACGAAGGCCGAGC ATATTA CACACCT TAACACTCT CCTATTGTTAAAG
```

##### B *lacUV5(A+2G)-11(Cy5,+25)*

```
AGGC TTTACA CTTTATGCTTCCGGCTCG TATAAT GTGTGGA AATTGTGAGAG GGATAACAATTC  
TCCG AATGT GAAATACGAAGGCCGAGC ATATTA CACACCT TAACACTCT CCTATTGTTAAAG - Cy5
```

##### *lacUV5(A+2G)-14(Cy5,+28)*

```
AGGC TTTACA CTTTATGCTTCCGGCTCG TATAAT GTGTGGA AATTGTGAGGAGGAC GGATAACAATTC  
TCCG AATGT GAAATACGAAGGCCGAGC ATATTA CACACCT TAACACTCT CCTATTGTTAAAG - Cy5
```

##### *lacUV5(A+2G)-50(Cy5,+64)*

```
AGGC TTTACA CTTTATGCTTCCGGCTCG TATAAT GTGTGGA AATTGTGAGAGGTTAGTTGATTGTATTGA . . .  
TCCG AATGT GAAATACGAAGGCCGAGC ATATTA CACACCT TAACACTCTCCAATCAACTAACATAACT . . .  
. . . GTTGATTGGATTGAGTGAGAG GGATAACAATTC  
. . . CAACTAACCTAACTCACTCT CCTATTGTTAAAG - Cy5
```

##### *lacUV5(A+2G)-11(Cy5,-40)*

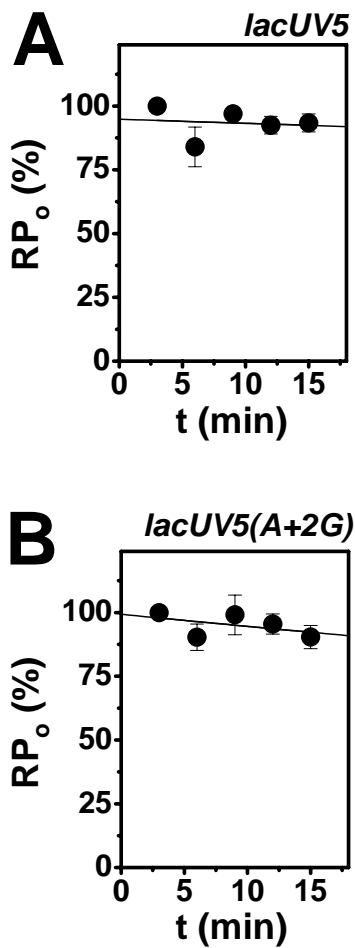
```
Cy5-AGGC TTTACA CTTTATGCTTCCGGCTCG TATAAT GTGTGGA AATTGTGAGAG GGATAACAATTC  
TCCG AATGT GAAATACGAAGGCCGAGC ATATTA CACACCT TAACACTCT CCTATTGTTAAAG
```

**Figure S1.** DNA fragments.

(A) DNA fragments used in the analysis of RD<sub>e</sub> initiated on *lacUV5* and halted after synthesis of 11, 14, or 50 nt of RNA (*lacUV5* derivatives having no guanine residues on the template strand from positions +1 to +11, +1 to +14, or +11 to +50)(Mukhopadhyay et al., 2001; Mukhopadhyay et al., 2003; Nickels et al., 2004). The first 3 DNA fragments are used for leading-edge FRET analysis and thus have fluorophore Cy5 at position +25, +28, and +64. The 4<sup>th</sup> DNA fragment is used for trailing-edge FRET analysis and thus has fluorophore Cy5 at position -40. Black boxes, transcription start site (with arrow), promoter -10 element and promoter -35 element; red boxes, halt site.

(B) DNA fragments used in the analysis of RD<sub>e</sub> initiated on *lacUV5(A+2G)* (Nickels et al., 2004) and halted after synthesis of 11, 14, or 50 nt of RNA (Mukhopadhyay et al., 2001; Mukhopadhyay et al., 2003; Nickels et al., 2004). The first 3 DNA fragments are used for leading-edge FRET analysis and thus have FRET acceptor Cy5 at position +25, +28, and +64. The 4<sup>th</sup> DNA fragment is used for trailing-edge FRET analysis and thus has FRET acceptor Cy5 at position -40.

## Leading-edge FRET: $RP_o$



**Figure S2.**  $\sigma^{70}$  retention in  $RP_o$ .

(A) Extent of  $\sigma^{70}$  retention in  $RP_o$  at *lacUV5*. The y-intercept ( $t = 0$  min) corresponds to the beginning of data acquisition; the data are normalized to the 3-min data point. Error bars, standard error of mean (SEM) for 4 independent measurements. Solid lines, single-exponential fits. The half-life of  $\sigma^{70}$  retention is  $>2$  h.

(B) As panel (A), but for  $RP_o$  at *lacUV5(A+2G)* (substituted *lacUV5* derivative lacking determinant for sequence-specific  $\sigma^{70}$ -DNA interaction in initial transcribed region). The half-life of  $\sigma^{70}$  retention is  $>2$  h.

**Table S1.** Relative equilibrium binding constants ( $K_{b,x}/K_{b,wild-type}$ ) for RNAP core binding of  $\sigma^{70}$  derivatives used in this work (data from fluorescence-detected electrophoretic mobility shift experiments).

<b>Sigma derivative</b>	<b><math>K_{b,x}/K_{b,wild-type}</math></b>
<b>unlabelled wild-type sigma</b>	[1.0]
<b>TMR366-sigma</b>	0.5±0.1
<b>TMR596-sigma</b>	1.1±0.1