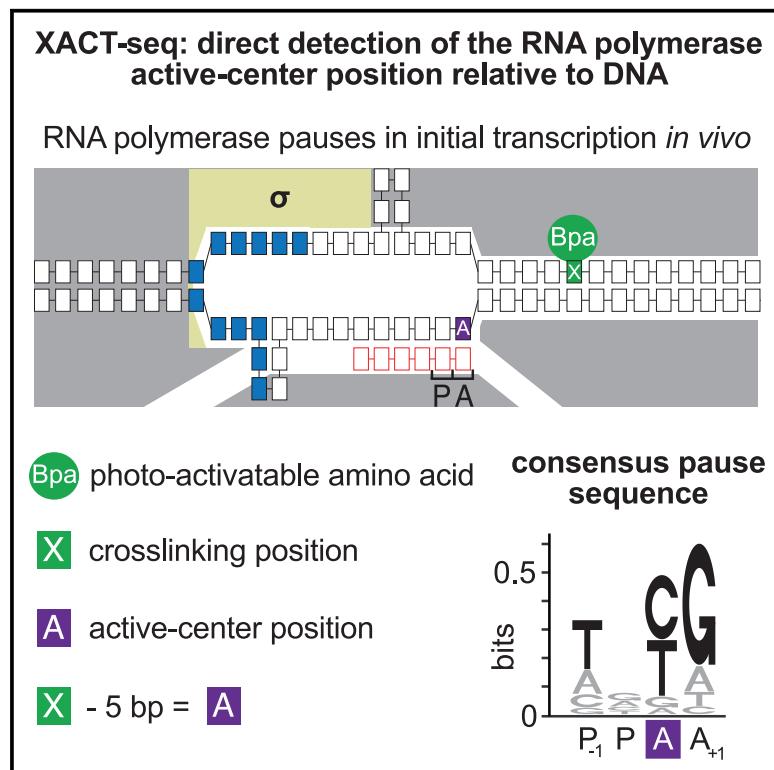


XACT-Seq Comprehensively Defines the Promoter-Position and Promoter-Sequence Determinants for Initial-Transcription Pausing

Graphical Abstract



Authors

Jared T. Winkelman,
Chirangini Pukhrambam,
Irina O. Vvedenskaya, ..., Premal Shah,
Richard H. Ebright, Bryce E. Nickels

Correspondence

ebright@waksman.rutgers.edu (R.H.E.),
bnickels@waksman.rutgers.edu (B.E.N.)

In Brief

Winkelman et al. report a protein-DNA photocrosslinking method that provides single-nucleotide-resolution readout of RNA polymerase active-center position relative to DNA and enables analysis of initial-transcription pausing. Analysis of 4^{11} ($\sim 4,000,000$) promoter sequences defines positional determinants and sequence determinants for initial-transcription pausing by bacterial RNA polymerase *in vitro* and *in vivo*.

Highlights

- XACT-seq detects RNA polymerase active-center position relative to DNA
- Initial-transcription pausing at 4^{11} ($\sim 4,000,000$) promoters was quantitated
- Consensus sequence element for initial-transcription pausing was identified
- Initial-transcription pausing and elongation pausing share mechanistic commonalities



Article

XACT-Seq Comprehensively Defines the Promoter-Position and Promoter-Sequence Determinants for Initial-Transcription Pausing

Jared T. Winkelman,^{1,2,3,6} Chirangini Pukhrambam,^{1,3,6} Irina O. Vvedenskaya,^{1,3} Yuanchao Zhang,^{1,4} Deanne M. Taylor,^{4,5} Premal Shah,¹ Richard H. Ebright,^{2,3,*} and Bryce E. Nickels^{1,3,7,*}

¹Department of Genetics, Rutgers University, Piscataway, NJ 08854, USA

²Department of Chemistry and Chemical Biology, Rutgers University, Piscataway, NJ 08854, USA

³Waksman Institute, Rutgers University, Piscataway, NJ 08854, USA

⁴Department of Biomedical and Health Informatics, The Children's Hospital of Philadelphia, Philadelphia, PA 19041, USA

⁵Department of Pediatrics, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA 19104, USA

⁶These authors contributed equally

⁷Lead Contact

*Correspondence: ebright@waksman.rutgers.edu (R.H.E.), bnickels@waksman.rutgers.edu (B.E.N.)

<https://doi.org/10.1016/j.molcel.2020.07.006>

SUMMARY

Pausing by RNA polymerase (RNAP) during transcription elongation, in which a translocating RNAP uses a “stepping” mechanism, has been studied extensively, but pausing by RNAP during initial transcription, in which a promoter-anchored RNAP uses a “scrunching” mechanism, has not. We report a method that directly defines the RNAP-active-center position relative to DNA with single-nucleotide resolution (XACT-seq; “cross-link-between-active-center-and-template sequencing”). We apply this method to detect and quantify pausing in initial transcription at 4¹¹ (~4,000,000) promoter sequences *in vivo* in *Escherichia coli*. The results show initial-transcription pausing can occur in each nucleotide addition during initial transcription, particularly the first 4 to 5 nucleotide additions. The results further show initial-transcription pausing occurs at sequences that resemble the consensus sequence element for transcription-elongation pausing. Our findings define the positional and sequence determinants for initial-transcription pausing and establish initial-transcription pausing is hard coded by sequence elements similar to those for transcription-elongation pausing.

INTRODUCTION

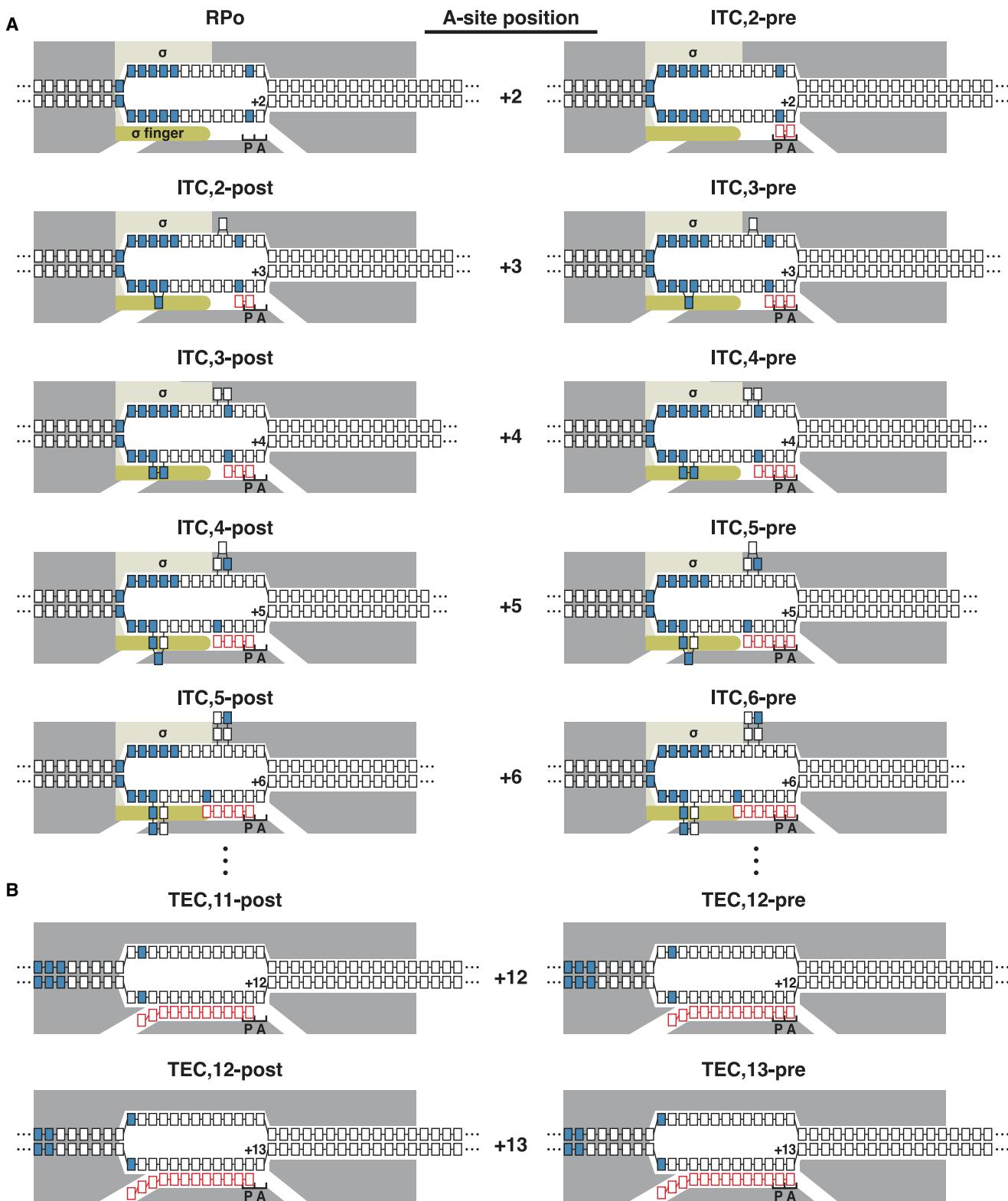
RNA polymerase (RNAP) initiates transcription by binding double-stranded promoter DNA, unwinding a turn of promoter DNA to yield an RNAP-promoter open complex (RPO) containing an ~13-bp single-stranded “transcription bubble” (Figure 1A), and selecting a transcription start site (TSS) (Ruff et al., 2015; Mazumder and Kapanidis, 2019; Winkelman et al., 2020). TSS selection entails placement of the start-site nucleotide (position +1) and the next nucleotide (position +2) of the template DNA strand into the RNAP-active-center product site (“P-site”) and addition site (“A-site”), respectively, and binding an initiating entity in the P-site and an extending NTP in the A-site.

The first ~10 nt of an RNA product are synthesized as an RNAP-promoter initial transcribing complex (ITC), in which RNAP remains anchored on promoter DNA through sequence-specific protein-DNA interactions (Figure 1A; Mazumder and Kapanidis, 2019; Winkelman et al., 2020). Initial transcription starts with phosphodiester bond formation between the initiating entity and the extending NTP to yield an initial RNA product (Figure 1A;

ITC,2). Each nucleotide-addition cycle after initial product formation requires translocation of the RNAP active center relative to DNA and RNA, starting from a “pre-translocated” state and yielding a “post-translocated” state (Figures 1A and 1B; Erie et al., 1992; Zhang and Landick, 2009; Larson et al., 2011; Belogurov and Artsimovitch, 2019). Translocation of the RNAP active center repositions the RNA 3' nucleotide from the A-site to the P-site, rendering the A-site available to bind the next extending NTP. Initial transcription proceeds until synthesis of an RNA product of a threshold length of ~10 nt (Mazumder and Kapanidis, 2019; Winkelman et al., 2020). Upon synthesis of a threshold-length RNA product, RNAP breaks the sequence-specific protein-DNA interactions that anchor it on promoter DNA, escapes the promoter, and synthesizes the rest of the RNA product as a transcription elongation complex (TEC) (Figure 1B).

There are two clear differences in the mechanism of initial transcription (performed by ITC) and transcription elongation (performed by TEC): (1) a different mechanism of RNAP active-center translocation and (2) a different RNAP subunit composition (Figure 1).





(legend on next page)

The first difference in the mechanisms of initial transcription and transcription elongation is a consequence of sequence-specific protein-DNA interactions that anchor RNAP on promoter DNA in initial transcription, but not in elongation (Larson et al., 2011; Belogurov and Artsimovitch, 2019; Mazumder and Kapanidis, 2019; Winkelman et al., 2020). These protein-DNA interactions prevent RNAP from moving relative to DNA in initial transcription, but not in elongation. Therefore, RNAP uses a different mechanism of RNAP active-center translocation in initial transcription versus elongation (Larson et al., 2011; Belogurov and Artsimovitch, 2019; Mazumder and Kapanidis, 2019; Winkelman et al., 2020). In initial transcription, RNAP uses a “scrunching” mechanism, in which, in each nucleotide-addition cycle, RNAP remains anchored to promoter DNA, unwinds one base pair of DNA downstream of the RNAP active center, pulls the unwound single-stranded DNA (ssDNA) into and past the RNAP active center, and accommodates the additional unwound ssDNA as bulges in the transcription bubble (Figure 1A; Kapanidis et al., 2006; Margeat et al., 2006; Revyakin et al., 2006). In contrast, in elongation, RNAP uses a “stepping” mechanism, in which, in each nucleotide-addition cycle, RNAP steps forward by 1 bp relative to the DNA (Figure 1B; Abbondanzieri et al., 2005).

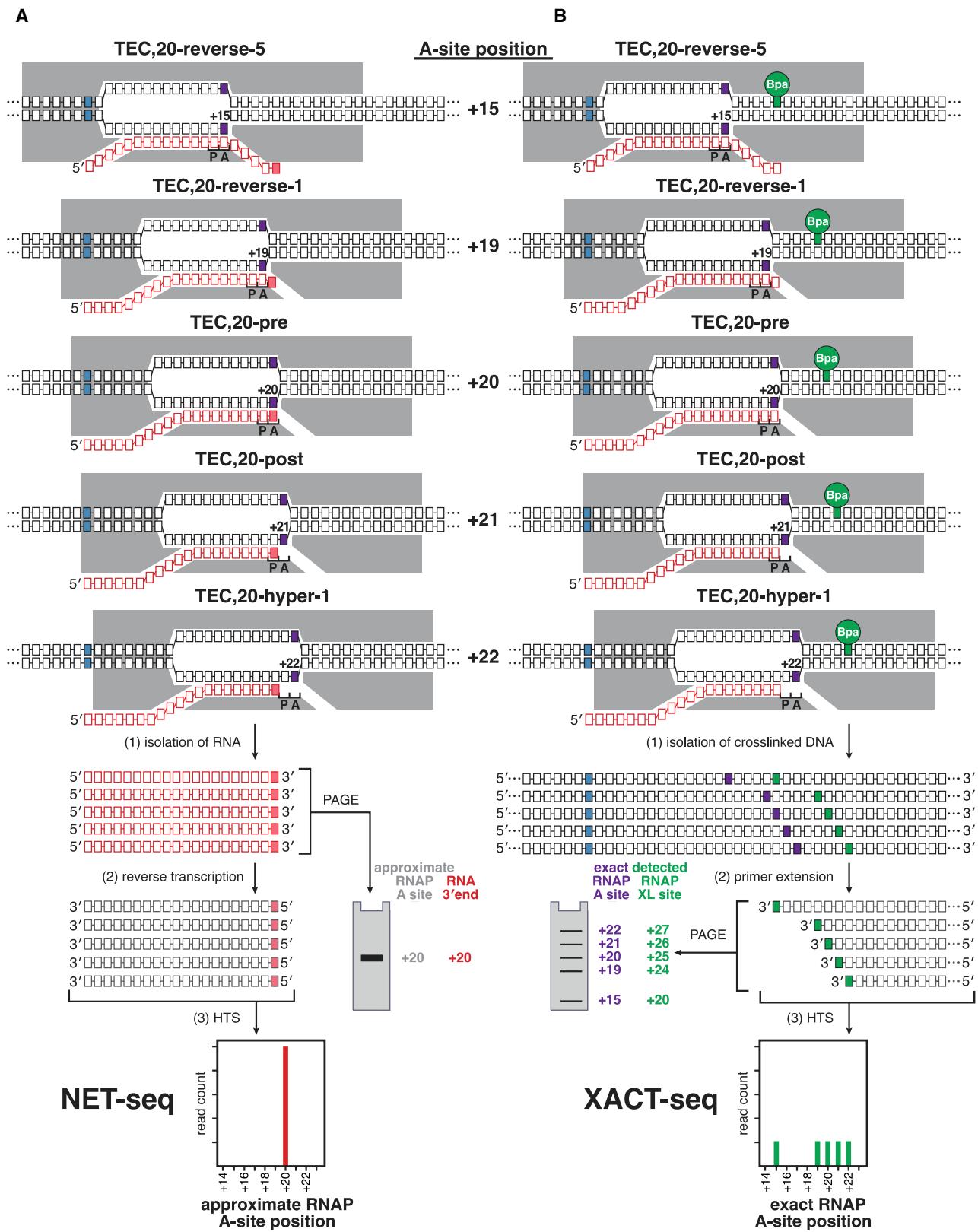
The second difference in the mechanisms of initial transcription and elongation is a consequence of the fact that initial transcription is carried out by a macromolecular assembly containing the initiation factor σ (Figure 1A), whereas transcription elongation is typically carried out by a macromolecular assembly lacking σ (Figure 1B; Mooney et al., 2005; Larson et al., 2011; Belogurov and Artsimovitch, 2019; Mazumder and Kapanidis, 2019; Winkelman et al., 2020). In the ITC, a module of σ referred to as the “ σ finger” reaches into the RNAP-active-center cleft and interacts with template-strand ssDNA in the transcription bubble close to the RNAP active center (Figure 1A; Severinov et al., 1994; Murakami et al., 2002; Kulbachinskiy and Mustaeve, 2006; Zhang et al., 2012; Basu et al., 2014). These interactions pre-organize template-strand ssDNA to engage the RNAP active center, thereby facilitating binding of initiating and extending NTPs (Murakami et al., 2002; Kulbachinskiy and Mustaeve, 2006; Zhang et al., 2012; Basu et al., 2014; Pupov et al., 2014). Interactions of the σ finger with template-strand ssDNA places the σ finger in the path that will be occupied by nascent RNA upon RNA extension (Murakami et al., 2002; Kulbachinskiy and Mustaeve, 2006; Zhang et al., 2012; Basu et al., 2014; Pupov et al., 2014; Zuo and Steitz, 2015). Thus, interactions of the σ finger with template-strand ssDNA presumably create an

obstacle that must be overcome during initial transcription. Specifically, when the RNA reaches a length of ~4 to ~5 nt (after ~2 to ~3 RNAP-active-center translocation steps), the RNA 5' end appears to contact, and make favorable interactions with, the σ finger, but when the RNA reaches a length of ~5 to ~7 nt (after ~3 to ~5 RNAP-active-center translocation steps), the RNA 5' end is expected to collide with, and clash with, the σ finger (Figure 1A; Murakami et al., 2002; Kulbachinskiy and Mustaeve, 2006; Zhang et al., 2012; Basu et al., 2014; Pupov et al., 2014; Zuo and Steitz, 2015). The occurrence at one point of a favorable interaction with the σ finger (after ~2 to ~3 translocation steps), and subsequently a clash with the σ finger (after ~3 to ~5 translocation steps), is expected to have position-specific effects on RNAP active-center translocation during initial transcription. In contrast, in elongation, where σ typically is absent (Mooney et al., 2005; Belogurov and Artsimovitch, 2019), no such position-specific effects on translocation are expected to occur.

In both initial transcription and elongation, in the presence of saturating NTPs, each nucleotide-addition cycle takes, on average, ~20 ms (Belogurov and Artsimovitch, 2019). In both initial transcription and elongation, pauses—nucleotide-addition cycles that occur on the second or longer timescales—are off-pathway states that potentially modulate gene-expression levels (Larson et al., 2011; Belogurov and Artsimovitch, 2019; Kang et al., 2019; Mazumder and Kapanidis, 2019). Transcription-elongation pausing has been the subject of extensive analysis, both *in vitro* and *in vivo* (Larson et al., 2011; Belogurov and Artsimovitch, 2019; Kang et al., 2019). The results establish that transcription-elongation pausing is determined by the sequence of the DNA template rather than TEC position relative to the TSS or the length of RNA in the TEC. For *Escherichia coli* RNAP, both *in vitro* and *in vivo*, transcription-elongation pausing occurs at DNA sequence elements that have the consensus sequence G₋₁₀N₋₉N₋₈N₋₇N₋₆N₋₅N₋₄N₋₃N₋₂Y₋₁G₊₁, where Y is a pyrimidine and Y₋₁ corresponds to the position of the RNA 3' end (Herbert et al., 2006; Larson et al., 2014; Vvedenskaya et al., 2014; Imashimizu et al., 2015; see also Kang et al., 2019 and Saba et al., 2019). In contrast, initial-transcription pausing has been subject to only limited studies *in vitro* (Duchi et al., 2016; Lerner et al., 2016; Dulin et al., 2018) and no studies *in vivo*. As a result, it is not known whether initial-transcription pausing occurs *in vivo*, it is not known what fraction of promoter sequences undergo initial-transcription pausing, the promoter-position dependence of initial-transcription pausing has not been defined, and the promoter-sequence determinants for initial-transcription pausing have not been defined.

Figure 1. Mechanisms of Initial Transcription and Transcription Elongation

(A) Initial transcription involves RNAP-active-center translocation through “DNA scrunching,” with RNAP in complex with initiation factor σ . Panel shows first six nucleotide-addition steps of initial transcription, starting from RNAP-promoter open complex (RPO) and yielding successive RNAP-promoter ITCs containing 2- to 6-nt RNA products (ITC,2–ITC,6). Following each nucleotide addition, the RNAP active center translocates forward through a DNA scrunching mechanism, from a pre-translocated state (pre; right column) to a post-translocated state (post; left column), and the RNAP-active-center A-site position advances by 1 bp. Gray, RNAP; yellow, σ ; dark yellow, σ finger; blue, -10 element and TSS; P and A, RNAP-active-center P-site and A-site, respectively; black boxes, DNA nucleotides (non-template-strand nucleotides above template-strand nucleotides); red boxes, RNA nucleotides; positions numbered relative to the TSS position, +1. (B) Transcription elongation involves RNAP-active-center translocation through “DNA stepping,” with RNAP not containing σ . Panel shows two nucleotide-addition steps of transcription elongation, from TEC containing 11 nt of RNA (TEC,11) to TEC containing 13 nt of RNA (TEC,13). Following each nucleotide addition, RNAP translocates forward through a DNA stepping mechanism, between a pre-translocated state (pre; right column) and a post-translocated state (post; left column), and the RNAP-active-center A-site position advances by 1 bp. Symbols and colors are as in (A).



(legend on next page)

RESULTS

Rationale

During RNA synthesis, the dwell time of the RNAP active center at each transcribed-region position, “RNAP occupancy,” is correlated with the tendency of RNAP to pause at that position. Accordingly, pause sites can be identified using methods that provide a measure of RNAP occupancy (Figure 2). Previously reported sequencing-based methods to monitor RNAP occupancies, such as native elongating transcript sequencing (NET-seq), rely on identifying and quantifying RNA 3' ends (Figure 2A; Churchman and Weissman, 2011, 2012; Larson et al., 2014; Vvedenskaya et al., 2014; Imashimizu et al., 2015). The identities of RNA 3' ends allow estimation of RNAP-active-center positions—subject to uncertainties, due to ability of RNAP to sample pre-translocated, post-translocated, reverse-translocated, and hyper-translocated states (Figures 2A and 2B; Larson et al., 2011; Belogurov and Artsimovitch, 2019)—and the quantities of RNA 3' ends allow estimation of RNAP-active-center dwell times. However, these methods provide only an indirect measure of RNAP-active-center positions relative to DNA (Figure 2A), and because these methods cannot be applied to RNAs less than ~15 nt in length (Figure S1), these methods are not suitable for analysis of initial transcription. Methods combining chromatin immunoprecipitation (ChIP) with sequencing, such as ChIP-seq and ChIP-exo, are alternative sequencing-based methods of mapping RNAP relative to DNA (Barski et al., 2007; Rhee and Pugh, 2012; Srivastava et al., 2013; Latif et al., 2018). However, these methods provide insufficient resolution for most purposes and define overall RNAP boundaries relative to DNA rather than RNAP-active-center positions.

Here, we describe a sequencing-based method to monitor RNAP occupancy that overcomes these limitations, providing a direct, single-nucleotide-resolution readout of RNAP-active-center position relative to DNA (Figure 2B), and that is suitable for analysis of initial transcription as well as elongation. The method entails formation of transcription complexes *in vitro* or *in vivo* using an RNAP derivative that has a photo-activatable crosslinking agent incorporated at a single, defined site in RNAP that, upon photo-activation *in vitro* or *in vivo*, forms covalent crosslinks with DNA at a defined position relative to the RNAP-active-center A-site; photo-activation to initiate covalent crosslinking of RNAP to DNA *in vitro* or *in vivo*; and high-throughput sequencing of primer extension products to define

crosslink positions and crosslink yields. We term this method “crosslink-between-active-center-and-template sequencing” (XACT-seq) (Figure 2B).

XACT-seq takes advantage of an RNAP derivative that has a photo-activatable crosslinking amino acid *p*-benzoyl-L-phenylalanine (Bpa) incorporated at RNAP- β' subunit residue R1148 (RNAP- β' ^{R1148Bpa}), which, upon photo-activation, forms covalent crosslinks with DNA at a position exactly 5 nt downstream of the RNAP-active-center A-site (Figure 2B; Yu et al., 2017). In previous work, we used this RNAP derivative for structural analysis of static, trapped transcription complexes (Winkelman et al., 2015, 2016a; Yu et al., 2017). In this work, we show this RNAP derivative exhibits transcription-elongation pausing and initial-transcription pausing properties indistinguishable from those of wild-type, unmodified RNAP (Figure 3), and we apply this RNAP derivative for analysis of actively transcribing complexes (Figures 4, 5, 6, S2–S4, S6, and S7).

RNAP-Active-Center A-Site Positions in Initial-Transcription Pausing at the lacCONS Promoter *In Vitro* and *In Vivo*

To demonstrate that the RNAP derivative that underpins XACT-seq, RNAP- β' ^{R1148Bpa}, enables detection of RNAP-active-center A-site positions in actively transcribing complexes and enables detection of initial-transcription pausing, we used RNAP- β' ^{R1148Bpa} to analyze actively transcribing complexes engaged in initial-transcription pausing (Figure 4). We analyzed initial-transcription pausing at the lacCONS promoter (*p*/*lacCONS*) (Figure 4A, top), the best-characterized example of initial-transcription pausing (Duchi et al., 2016; Lerner et al., 2016; Mazumder and Kapanidis, 2019). Lerner et al. (2016) and Duchi et al. (2016) showed *in vitro* that initial-transcription pausing occurs at *p*/*lacCONS* after ~4 to ~6 RNAP-active-center translocation steps. Duchi et al. (2016) and Dulin et al. (2018) further showed *in vitro* that this pause is reduced upon deletion of the σ finger (Duchi et al., 2016) and is increased upon substitution of the RNAP β -subunit residue 446 (β^{D446A}) (Dulin et al., 2018), a substitution that alters the sequence dependence of RNAP-active-center translocation behavior (Zhang et al., 2012; Vvedenskaya et al., 2014).

We first used RNAP- β' ^{R1148Bpa} to detect initial-transcription pausing at *p*/*lacCONS* *in vitro*. The results in Figure 4A, lanes 5,

Figure 2. Approaches to Map the RNAP-Active-Center A-Site Position: NET-Seq and XACT-Seq

(A) Approach to map the RNAP-active-center A-site position through analysis of RNA 3' ends. Procedure entails isolating nascent RNA and identifying and quantifying RNA 3' ends by polyacrylamide gel electrophoresis (PAGE) or high-throughput sequencing (HTS). The RNAP-active-center A-site position (purple box; numbered relative to TSS position, +1) is approximated based on the RNA 3' end (pink box); other symbols and colors are as in Figure 1. Different translocational states adopted by TEC containing single, defined 20-nt RNA product—e.g., reverse translocated by 5 bp (TEC,20-reverse-5), reverse translocated by 1 bp (TEC,20-reverse-1), pre-translocated (TEC, 20-pre), post-translocated (TEC,20-post), and hyper-translocated by 1 bp (TEC,20-hyper-1)—all yield the same RNA 3' end and therefore cannot be distinguished.

(B) Approach to map the RNAP-active-center A-site position through site-specific protein-DNA photocrosslinking, using RNAP derivative containing photo-activatable agent (green circle labeled Bpa) that crosslinks to DNA at defined distance from RNAP active center. Procedure entails UV-irradiating transcription complexes, isolating RNAP-crosslinked DNA, and identifying and quantifying crosslinking sites by analysis of primer extension products by PAGE or HTS. The RNAP-active-center A-site position (purple box; numbered relative to TSS position, +1) is defined based on identity of crosslinking site (green box). Symbols are as in (A). Different translocational states adopted by a TEC containing single, defined RNA product yield different crosslinking sites and therefore can be distinguished.

See also Figure S1.

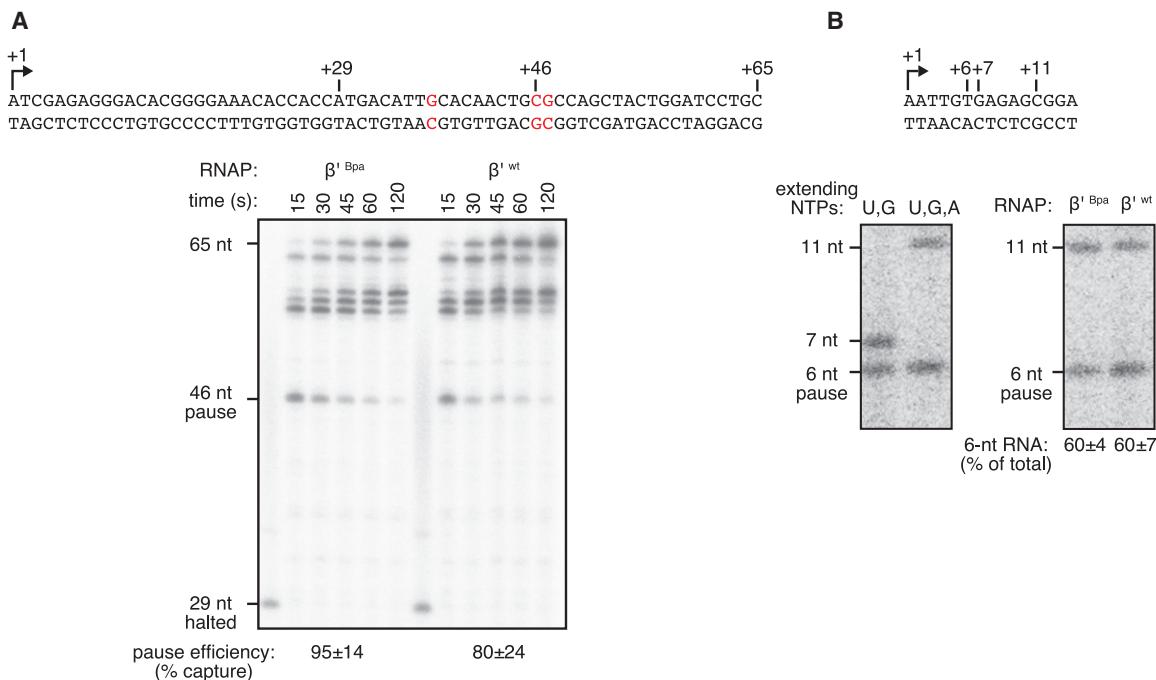


Figure 3. Incorporation of Bpa at RNAP- β' Subunit Residue R1148 Does Not Affect Pausing In Vitro

(A) Transcription-elongation pausing. Top: sequence of DNA template containing 65-bp transcribed region with consensus sequence element for transcription-elongation pausing (red) is shown. Bottom: PAGE analysis of products of transcription reactions performed with RNAP- β' R1148Bpa or RNAP- β' wt is shown. Gel shows RNA products at indicated times after addition of NTPs to complexes halted at position +29, +46, pause position. Pause-capture efficiencies (calculated as described in Landick et al., 1996) are means \pm SD ($n = 3$).

(B) Initial-transcription pausing. Top: sequence of placCONS initial-transcribed region is shown. Bottom left: products of reactions performed using ApA as initiating entity and NTP subsets that enable synthesis of RNA products of up to 7 nt (UTP/GTP) or up to 11 nt (UTP/GTP/ATP) are shown. Bottom right: products of reaction performed using ApA as initiating entity and NTP subset that enables synthesis of RNA products up to 11 nt, with RNAP- β' R1148Bpa (β' Bpa) or RNAP- β' wt (β' wt) are shown. Positions of 6-nt paused RNA product and 7- and 11-nt full-length RNA products are indicated. Percentages of 6-nt RNA products are means \pm SD ($n = 3$).

See also Figure S2.

8, and 11, confirm the previously reported ability of the RNAP- β' R1148Bpa to detect the A-site position with single-nucleotide resolution in static initial-transcribing complexes in the absence of NTP substrates *in vitro* (Winkelman et al., 2015, 2016a, 2016b; Yu et al., 2017). The results in Figure 4A, lanes 6, 9, and 12, demonstrate that the detected position of the A-site does not change upon addition of a 2-nt RNA (ApA), suggesting that the resulting ITC,2 is in a pre-translocated state (ITC,2-pre). The results in Figure 4A, lane 7, demonstrate the ability of RNAP- β' R1148Bpa to detect A-site positions—and to detect initial-transcription pausing—in active initial-transcribing complexes in the presence of all NTP substrates *in vitro*.

We observe strong pausing at a position corresponding to exactly 4 RNAP-active-center translocation steps relative to RPitc,2-pre (i.e., when the A-site is at promoter position +6; Figure 4A). We observe that RNAP occupancy at this position decreases upon deletion of the σ finger (Figure 4A, compare lanes 7 and 10) and increases upon substitution of RNAP β -subunit residue 446 (Figure 4A, compare lanes 7 and 13). The pause exhibits the previously reported hallmarks of initial-transcription pausing at placCONS: i.e., pausing after \sim 4 to \sim 6 active-center translocation steps (i.e., when the RNAP active-center A site is at promoter position +6 to +8;

Duchi et al., 2016; Lerner et al., 2016), a decrease in pausing upon deletion of the σ finger (Duchi et al., 2016; Figure S2), and an increase in pausing upon substitution of RNAP β -subunit residue 446 (Dulin et al., 2018; Figure S2). The pause is not reduced upon addition of transcript-cleavage factor GreB (Figures S2 and S3), indicating the pause does not involve a backtracked state (see Fish and Kane, 2002). We conclude that the pausing that occurs when the RNAP-active-center A-site is at promoter position +6 represents initial-transcription pausing.

We next used RNAP- β' R1148Bpa to detect initial-transcription pausing at placCONS *in vivo*. We produced, in *E. coli*, a Bpa-labeled, decahistidine-tagged RNAP- β' R1148Bpa in the presence of unlabeled, untagged, wild-type RNAP, using a three-plasmid system (Figure 4B, top) comprising (1) a plasmid carrying a gene for RNAP β' -subunit containing a nonsense codon (TAG) at position 1,148 and a decahistidine coding sequence; (2) a plasmid carrying genes for an engineered Bpa-specific UAG-suppressor tRNA and an engineered Bpa-specific aminoacyl-tRNA synthetase; and (3) a pSC101-derived plasmid containing placCONS (copy number \sim 5; Cohen and Chang, 1977). We then grew cells in medium containing Bpa, UV irradiated cells, lysed cells, purified

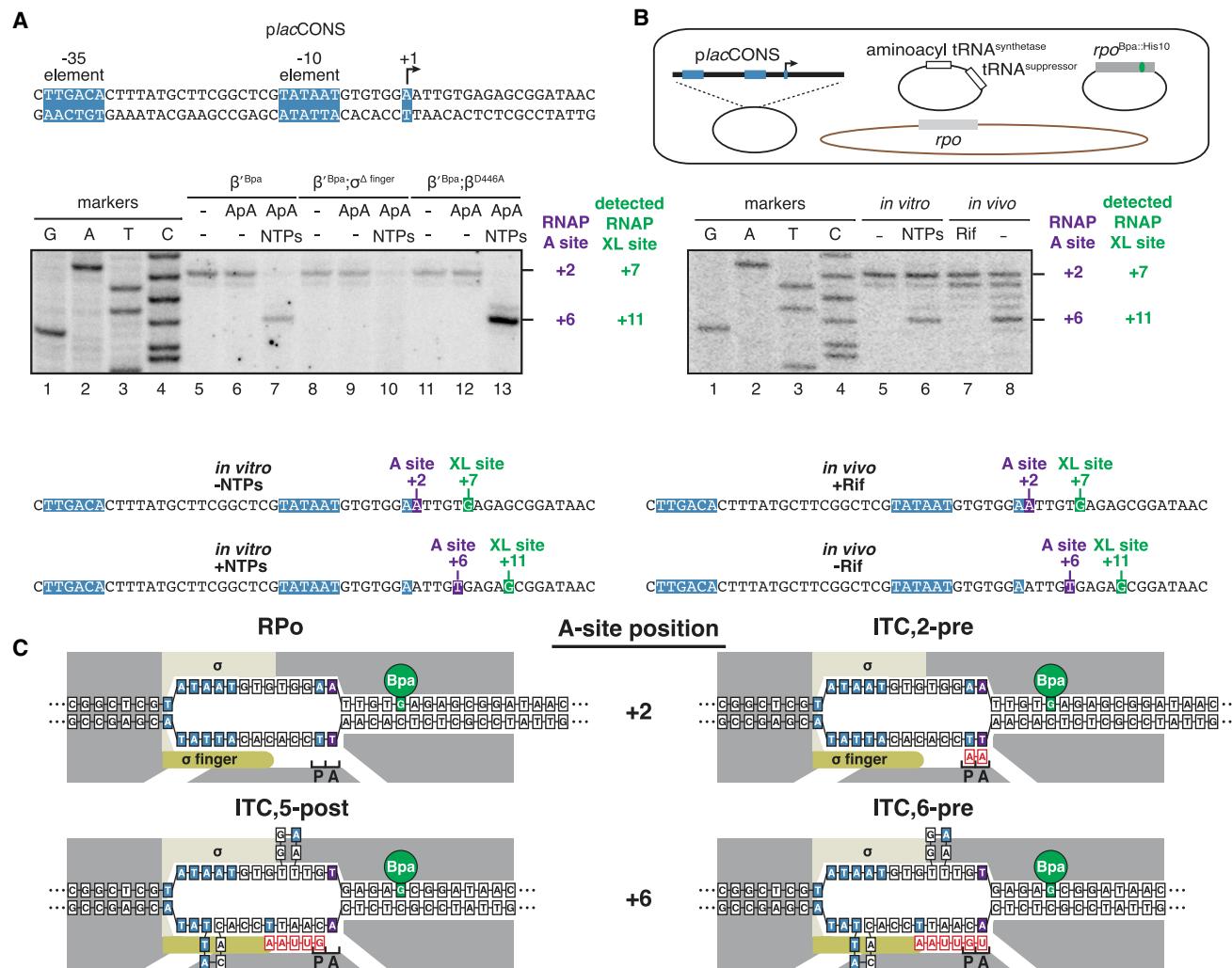


Figure 4. RNAP-Active-Center A-Site Positions in Initial-Transcription Pausing at the *lacCONS* Promoter In Vitro and In Vivo

(A) *In vitro*. Top: *lacCONS* is shown. Middle: primer extension mapping of crosslinking sites is shown. Bottom: position of RNAP-active-center A-site (purple) and nucleotide crosslinked to Bpa (green) defined relative to the TSS position is shown. Markers, sequence ladder generated using *lacCONS*. β' Bpa, RNAP- β' R1148Bpa, (β' Bpa, σ^Δ finger), RNAP- β' R1148Bpa containing σ finger deletion; (β' Bpa, β^{D446A}), RNAP- β' R1148Bpa containing β substitution D446A.

(B) *In vivo*. Top: three-plasmid merodiploid system for co-production, in *E. coli* cells, of decahistidine-tagged, RNAP- β' Bpa, in the presence of untagged wild-type RNAP is shown. First plasmid carries gene for RNAP- β' subunit (gray rectangle) with nonsense codon (green) at residue β' R1148; second plasmid carries genes for engineered Bpa-specific nonsense-suppressor tRNA and aminoacyl-tRNA synthetase (white rectangles); third plasmid carries *lacCONS*; and chromosome (brown oval) carries genes for wild-type RNAP subunits (light gray rectangle). Middle: primer-extension mapping of crosslinking sites is shown. Bottom: position of RNAP-active-center A-site (purple) and nucleotide crosslinked to Bpa (green) defined relative to the TSS position, +1, is shown. Rif, rifampin; markers, sequence ladder generated using *lacCONS*.

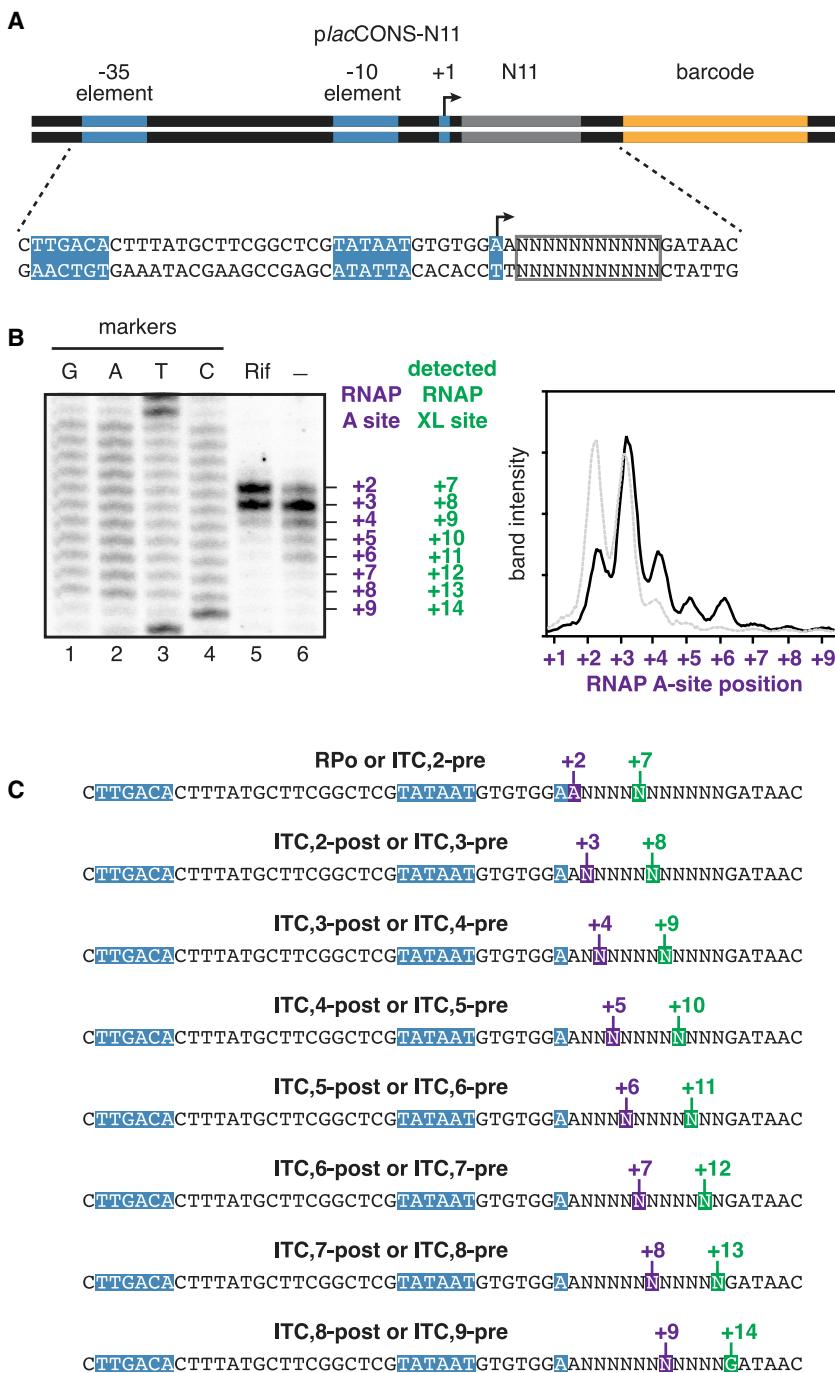
(C) Interpretation of results in (A) and (B). Symbols and colors are as in Figures 1 and 2.

See also Figure S3.

crosslinked material using immobilized metal-ion-affinity chromatography targeting the decahistidine tag on RNAP- β' R1148Bpa, and mapped crosslinks using primer extension (Figure 4B, middle). In order to trap static initial-transcribing complexes containing 2- to 3-nt RNA products *in vivo*, despite the presence of all NTP substrates *in vivo*, we used a chemical biology approach, exploiting the RNAP inhibitor rifampin (Rif), which blocks extension of RNA products beyond a

length of 2 to 3 nt (McClure and Cech, 1978). The results show matching crosslinking patterns *in vitro* and *in vivo* for the initial-transcription pause at promoter position +6 (Figure 4B).

The results in Figure 4 establish that RNAP- β' R1148Bpa enables detection of the RNAP-active-center A-site position in actively transcribing complexes. The results further establish that initial-transcription pausing at *lacCONS* occurs *in vivo*,



exhibits a similar promoter-position dependence *in vivo* as *in vitro*, and reveals the exact RNAP-active-center position in initial-transcription pausing at p/lacCONS. In particular, the results show that the RNAP-active-center A-site during initial-transcription pausing at p/lacCONS is located at promoter position +6 and thus, neglecting possible fractionally translocated states, show that pausing occurs in either RPitc,5-post (Figure 4C, bottom left) or RPitc,6-pre (Figure 4C, bottom right).

Figure 5. Promoter-Position Dependence of Initial-Transcription Pausing for a Library of 4¹¹ (~4,000,000) Promoters *In Vivo*

(A) p/lacCONS template library containing all possible sequences from promoter position +3 through +13 (p/lacCONS-N11). These promoter positions encompass expected positions of cross-linking of RNAP-β^{R1148Bpa} in initial transcription.

(B) Left: PAGE analysis of RNAP-active-center A-site positions *in vivo*. Right: histogram shows signals detected in absence (black line) or presence (gray line) of Rif. Markers, sequence ladder generated using p/lacCONS-N11.

(C) Position of RNAP-active-center A-site (purple) and nucleotide crosslinked to Bpa (green) defined relative to the TSS position, +1.

See also Figure S4.

The results in Figures 3 and S2 indicate that the paused complex contains a 6-nt RNA product. By combining results in Figure 4 defining the A-site position in the paused complex with results in Figures 3 and S2 defining the RNA-product length in the paused complex, we conclude that pausing occurs in RPitc,6 pre (Figure 4C, bottom right).

Promoter-Position Dependence of Initial-Transcription Pausing for a Library of 4¹¹ (~4,000,000) Promoters *In Vivo*

Having validated RNAP-β^{R1148Bpa} as a reagent for detection of the RNAP-active-center A-site position in actively transcribing complexes *in vitro* and *in vivo*, we next combined RNAP-β^{R1148Bpa} with a library of p/lacCONS derivatives (p/lacCONS-N11; Figure 5A) containing all possible sequences from promoter positions +3 to +13 (4¹¹; ~4,000,000 sequences), to enable multiplexed analysis of initial-transcription pausing on all possible initial-transcribed region sequences *in vivo*. We used a three-plasmid system analogous to that used in the previous section but having representatives of the p/lacCONS-N11 library of plasmids instead of the plasmid carrying p/lacCONS. We UV irradiated cells, lysed cells, isolated crosslinked material, and mapped crosslinks using primer extension as in the previous section. We used the same chemical-biology approach, exploiting the fact that the RNAP inhibitor Rif prevents extension of RNA products beyond the length of ~4 nt, to trap static initial-transcribing complexes corresponding to RPitc,2; RPitc,3; and RPitc,4 (Figure 5B).

To read out position-specific RNAP occupancies across the entire sampled initial-transcribed-region sequence space, we performed urea-PAGE of radiolabeled primer extension

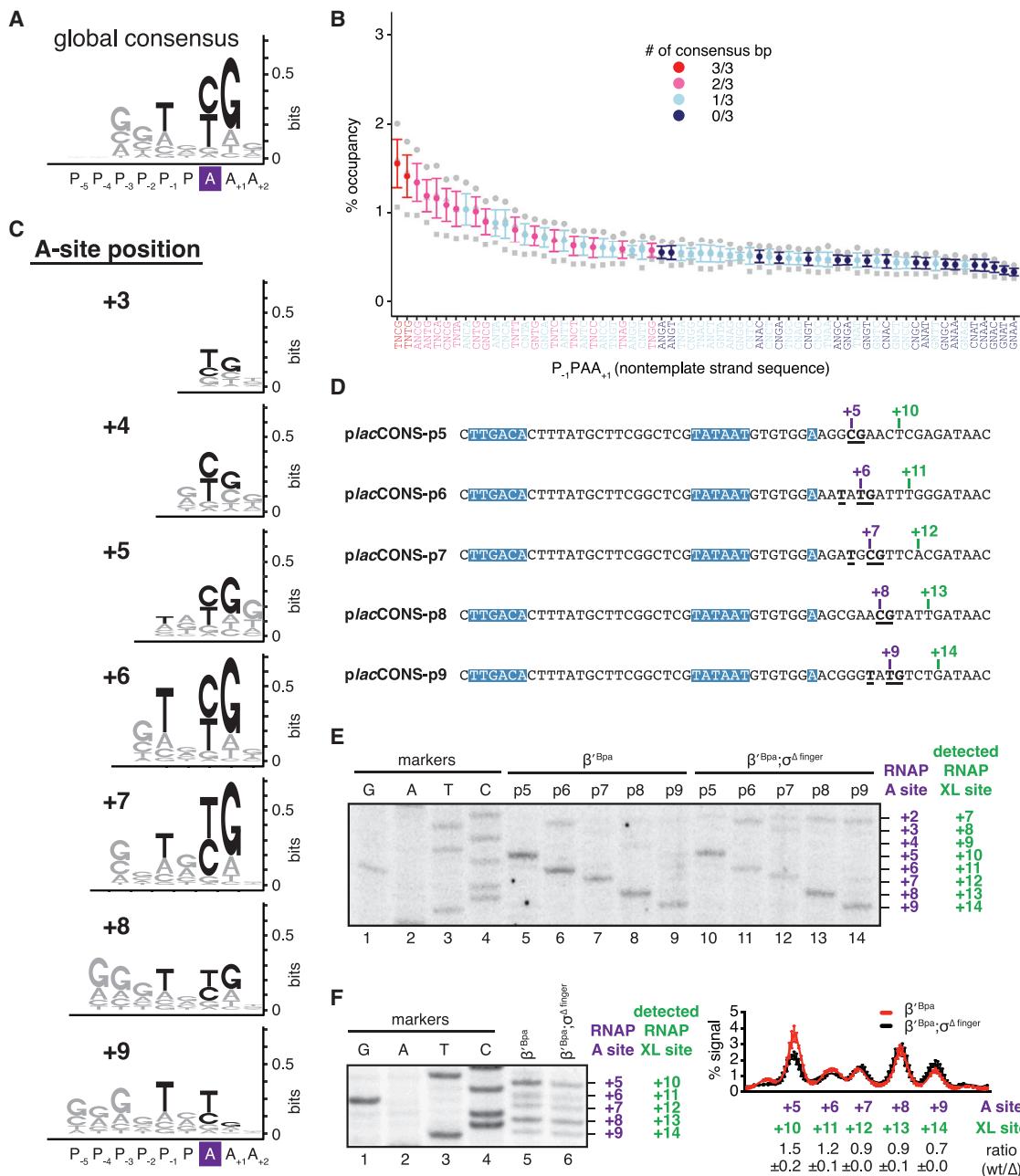


Figure 6. Promoter-Sequence Determinants for Initial-Transcription Pausing in a Library of 4¹¹ (~4,000,000) Promoters In Vivo

- (A) Position-independent, global, consensus sequence for initial-transcription pausing for RNAP-active-center A-site positions +5, +6, +7, +8, and +9. Consensus nucleotides are in black.
- (B) Percent occupancy at each initial-transcribed region tetranucleotide sequence for RNAP-active-center A-site positions +5, +6, +7, +8, and +9. Red, pink, cyan, and blue denote pause-site sequences with 3 of 3, 2 of 3, 1 of 3, and 0 of 3 matches to global consensus sequence, respectively. Mean \pm SEM ($n = 3$).
- (C) Position-specific consensus sequences for initial-transcription pausing for RNAP-active-center A-site positions +3, +4, +5, +6, +7, +8, and +9.
- (D) Representative sequences yielding high RNAP occupancy at positions +5, +6, +7, +8, and +9. Colors are as in Figure 5C.
- (E) RNAP-active-center A-site positions and crosslinking positions *in vitro* for sequences of (D). Lanes 1–4, sequence markers; lanes 5–9, data for RNAP- β' R1148Bpa, lanes 10–14, data for RNAP- β' R1148Bpa containing σ finger deletion.
- (F) RNAP-active-center A-site positions and crosslinking positions *in vitro* for sequences of (D) analyzed as pool. Histogram on right presents quantitation of RNAP occupancies at +5, +6, +7, +8, and +9, with data for RNAP- β' R1148Bpa in red and data for RNAP- β' R1148Bpa containing σ finger deletion in black. Ratios are means \pm SD ($n = 3$).
- See also Figures S5–S7.

products (Figure 5B). In the presence of Rif, we see two major bands and a minor band across the sampled initial-transcribed-region sequence space at positions corresponding to RPitc,2; RPitc,3; and RPitc,4—i.e., when the A-site is at promoter positions +2, +3, or +4 (see Figure 1A)—exactly as above for the *placCONS* initial-transcribed-region sequence (compare Figure 5B, lane 5, with Figure 4B, lane 7). In the absence of Rif, we observe a series of additional bands corresponding to positions of initial-transcription pausing (Figure 5B, lane 6). The prominence of the additional bands indicates that initial-transcription pausing is a prominent feature of transcription across the entire sampled initial-transcribed-region sequence space. As compared to the experiments in the presence of Rif, in the absence of Rif, we observe higher levels of RNAP occupancy at positions corresponding to exactly 1, 2, 3, 4, 5, 6, and 7 RNAP-active-center translocation steps relative to RPitc,2-pre (i.e., when the A-site is at promoter positions +3, +4, +5, +6, +7, +8, and +9; Figures 5B and 5C). RNAP occupancy levels are highest at positions corresponding to 1–4 RNAP-active-center translocation steps (i.e., when the A-site is at promoter positions +3, +4, +5, and +6; Figures 5B and 5C) and are lower for the positions corresponding to 5, 6, or 7 RNAP-active-center translocation steps (i.e., when the A-site is at promoter positions +7, +8, and +9; Figures 5B and 5C). Similar results are observed in parallel experiments using a promoter library that randomizes 20 bp of the initial-transcribed region, from position +2 through +21 (Figure S4). We conclude that, across the sampled initial-transcribed-region sequence space, initial-transcription pausing occurs at a large fraction of promoters and can occur at each position in the initial-transcribed region, with highest levels for promoter positions +3 through +6.

Promoter-Sequence Determinants for Initial-Transcription Pausing in a Library of 4^{11} ($\sim 4,000,000$) Promoters *In Vivo*

To quantify the promoter-position dependence and define the promoter-sequence determinants for initial-transcription pausing, for the library of 4^{11} ($\sim 4,000,000$) initial-transcribed-region sequences, we performed the full XACT-seq protocol (Figure S5). We used the same three-plasmid system and the same procedure of UV irradiation, cell lysis, purification of crosslinked material, and primer extension as in the previous sections. We then used high-throughput sequencing of primer extension products to determine yields of crosslinks at positions +2 to +25, thus providing a measure of the total RNAP A-site occupancy at positions –3 to +20. We assigned sites of initial-transcription pausing as sites having >50% of the total RNAP A-site occupancy at a single position from +3 to +9. The results confirm and quantify the finding in the preceding section that a substantial fraction of promoter initial-transcribed-region sequences ($\sim 15\%$) show initial-transcription pausing (Table S1) and that pausing can occur when the A-site is at each promoter position from +3 through +9, with highest levels occurring when the A-site is at positions +3 through +7 and lower levels when the A-site is at positions +8 and +9 (Table S1).

To confirm that the pause sites detected by XACT-seq represent above-background transcription-dependent phenomena, we performed a parallel XACT-seq analysis in the presence of

Rif, which blocks synthesis of RNA products greater than ~ 3 to 4 nt. This allows us, for pausing at positions +5, +6, +7, +8, and +9, to define, definitively, the number of sequences that are above-background, transcription-dependent pausing (Table S1). Observed pauses detected for A-site positions +8 and +9 are low, but these numbers are bona fide, above-background, transcription-dependent pausing (Table S1, column 3).

A global alignment of sequences showing the highest RNAP occupancies at positions +5, +6, +7, +8, and +9—aligning by the A-site position—yields a clear consensus sequence: $T_{P-1}N_pY_A G_{A+1}$, where Y is pyrimidine and Y_A is the position of the A-site (Figure 6A). A plot of RNAP occupancy as a function of initial-transcribed-region tetranucleotide sequence shows RNAP occupancy is strongly correlated with match to the consensus sequence (Figure 6B). Separate alignments of sequences showing the highest RNAP occupancy for each promoter position from +3 through +9 yield, in all cases, a consensus sequence resembling the global alignment (Figure 6C). At positions +6 and +7, the consensus sequence is especially strong (≥ 0.3 bits). At other positions, the match to consensus is evident, but the strength of the consensus is lower (≤ 0.3 bits). Plots of RNAP occupancy as a function of initial-transcribed-region sequence show that RNAP occupancy strongly correlates with match to the consensus sequence for each position (Figure S6). We note that *placCONS*, the promoter previously shown to exhibit initial-transcription pausing at a position in the range +5 to +7 *in vitro* (Duchi et al., 2016; Lerner et al., 2016; Dulin et al., 2018), and shown here to exhibit initial transcription pausing when the RNAP-active center A-site is at position +6 *in vitro* and *in vivo* (Figure 4), contains a 3-of-3 match to the consensus sequence in the register that would yield initial transcription pausing at position +6 (compare Figure 4A and Figure 6A).

Representative individual initial-transcribed-region sequences showing initial-transcription pausing were analyzed individually, both *in vitro* and *in vivo*, and showed clear pausing at the expected positions *in vitro* and *in vivo* (Figures 6D–6F and S7). The staircase pattern in Figures 6E (*in vitro*) and S7C (*in vivo*) shows graphically that initial-transcription pausing can occur when the A-site is at each promoter position in the tested range.

We performed analogous experiments with individual initial-transcribed-region sequences using an RNAP holoenzyme derivative containing a deletion of the σ finger (Figures 6E and 6F). Qualitatively, the results for wild-type RNAP holoenzyme and the derivative containing the σ finger deletion were identical (Figures 6E and 6F), indicating that sequence, rather than position-dependent collision with the σ finger, is the crucial determinant for initial-transcription pausing. Quantitatively, however, we observe reductions in RNAP occupancies for the RNAP holoenzyme containing a deletion of the σ finger, relative to wild-type RNAP holoenzyme, for promoter positions +5 and +6, but not for promoter positions +7, +8, and +9 (Figures 6E and 6F). We infer that the σ finger contributes quantitatively to pausing when the A-site is at promoter positions +5 and +6, which are positions where collision of the RNA 5' end and the σ finger potentially may occur (Murakami et al., 2002; Kulbachinskii and Mustaev, 2006; Zhang et al., 2012; Basu et al., 2014; Pupov et al.,

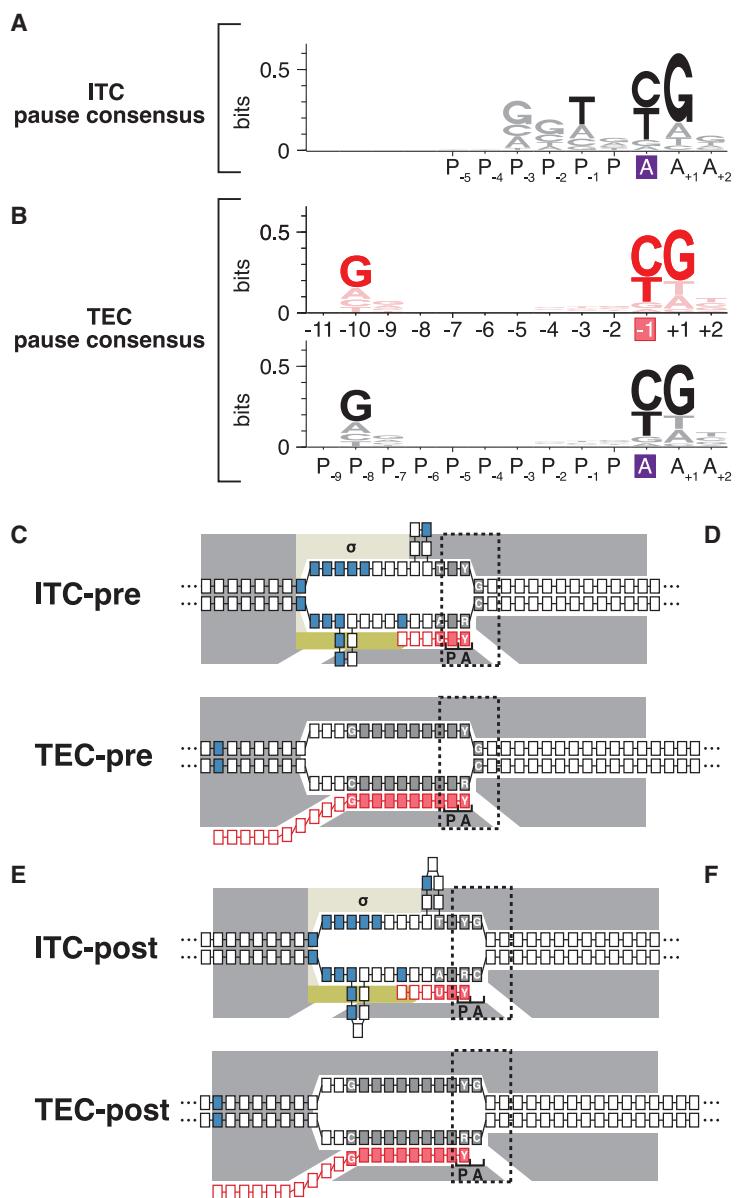


Figure 7. Relationship between Sequence Determinants for Initial-Transcription Pausing and Transcription-Elongation Pausing

(A) Consensus sequence for initial-transcription pausing. Positions are labeled relative to the RNAP-active-center A-site (purple box) and P-site.

(B) Consensus sequence for transcription-elongation pausing (Vvedenskaya et al., 2014). Top: positions numbered relative to RNA 3' end (pink box) are shown. Bottom: positions numbered relative to RNAP-active-center A-site (purple box) and P-site are shown.

(C) Positions of consensus-sequence nucleotides in pre-translocated-state complexes in initial-transcription pausing (ITC-pre) and transcription-elongation pausing (TEC-pre). Gray boxes with white lettering, high-information-content DNA nucleotides of consensus sequence; gray boxes without white lettering, low-information-content nucleotides of consensus sequence; pink boxes with white lettering, high-information-content RNA nucleotides of consensus sequence. Dotted rectangle, region enlarged in (D). Other symbols and colors are as in Figure 1.

(D) Enlarged view, showing unfavorable interaction of RNAP β residue D446 with nontemplate-strand pyrimidine (Y) at A-site (crossed-out bracket labeled β D446).

(E) Positions of consensus-sequence nucleotides in post-translocated-state complexes in initial transcription pausing (ITC-post) and transcription-elongation pausing (TEC-post). Dotted rectangle, region enlarged in (F).

(F) Enlarged view showing favorable interaction of RNAP β residue D446 with nontemplate-strand purine (R) at A-site (bracket labeled β D446).

2014; Zuo and Steitz, 2015). Considering the results in Figure 6 as a whole, we conclude that sequence is the crucial determinant of initial-transcription pausing. We further conclude that sequence is the crucial determinant of initial-transcription pausing at each promoter position from position +3 to position +9 and that the consensus sequences for initial-transcription pausing are similar or identical at each position.

Relationship between Sequence Determinants for Initial-Transcription Pausing and Transcription-Elongation Pausing

Our results define the consensus sequence for initial-transcription pausing as $T_{P-1}N_PYAG_{A+1}$ (Figure 7A). This is both the global consensus sequence for initial-transcription

pausing irrespective of position and, in most and possibly all cases, the position-specific sequence for initial-transcription pausing at each initial-transcribed region position (Figures 6A–6C).

Three groups previously have used NET-seq to define the consensus sequence for transcription-elongation

pausing as $G_{-10}N_{-9}N_{-8}N_{-7}N_{-6}N_{-5}N_{-4}N_{-3}N_{-2}Y_{-1}G_{+1}$, where Y_{-1} is the position of the RNA 3' end (Figure 7B, top; Larson et al., 2014; Vvedenskaya et al., 2014; Imashimizu et al., 2015). Mapping of TEC translocational state by analysis of pyrophosphorylation kinetics (Vvedenskaya et al., 2014) and by cryoelectron microscopy (cryo-EM) structure determination (Guo et al., 2018; Kang et al., 2018; Vos et al., 2018) indicates that TECs paused at the consensus sequence element assume a pre-translocated or fractionally translocated state. Accordingly, the consensus sequence for transcription-elongation pausing can be expressed as $G_{P-8}N_{P-7}N_{P-6}N_{P-5}N_{P-4}N_{P-3}N_{P-2}N_{P-1}N_PY_A G_{A+1}$, where Y_A is the position of the A-site (Figure 7B, bottom). The consensus sequence for transcription-elongation pausing, $G_{P-8}N_{P-7}N_{P-6}N_{P-5}N_{P-4}N_{P-3}N_{P-2}N_{P-1}N_PY_A G_{A+1}$, comprises a

highly conserved downstream segment, $\underline{Y_A}G_{A+1}$ (Larson et al., 2014; Vvedenskaya et al., 2014; Imashimizu et al., 2015). In the paused TEC, the $G_{A+1}:C_{A+1}$ nucleotide pair is located at the downstream end of the transcription bubble and must be broken for RNAP forward translocation, and the DNA-template-strand P_A interacts with the RNAP active center (Figures 7C and 7E; Vvedenskaya et al., 2014; see also Saba et al., 2019); the identities of nucleotides at these positions affect RNAP-translocation behavior through sequence-dependent effects on DNA duplex thermal stability and sequence-dependent effects on interactions of the DNA template strand with the RNAP active center (Vvedenskaya et al., 2014). The consensus sequence element for transcription-elongation pausing also comprises a less highly conserved upstream segment, G_{P-8} (Larson et al., 2014; Vvedenskaya et al., 2014; Imashimizu et al., 2015). In the paused TEC, the $G_{P-8}:C_{P-8}$ RNA:DNA base pair is located at the upstream end of the RNA-DNA hybrid and must be broken for RNAP translocation (Figures 7C and 7E; Vvedenskaya et al., 2014); sequence at these positions affects RNAP-translocation behavior through effects on RNA-DNA duplex thermal stability (Vvedenskaya et al., 2014).

The consensus sequence for initial-transcription pausing defined in this work, $T_{P-1}N_P\underline{Y_A}G_{A+1}$ (Figure 7A), exhibits a striking resemblance to the downstream, most highly conserved portion of the consensus sequence for transcription-elongation pausing: $\underline{Y_A}G_{A+1}$ (Figure 7B, bottom). This resemblance extends both to the sequence and the position of the A-site relative to sequence. Consistent with the conclusion that the consensus sequence for initial-transcription pausing, $T_{P-1}N_P\underline{Y_A}G_{A+1}$, may be functionally related to the downstream, most highly conserved portion of the consensus sequence for transcription-elongation pausing, $\underline{Y_A}G_{A+1}$, the consensus sequence for initial-transcription pausing contains T at position P_{-1} (Figure 7A), and two groups defining the consensus sequence for transcription-elongation pausing identified T as the optimal nucleotide at the corresponding position (Larson et al., 2014; Imashimizu et al., 2015). The observation that the consensus sequence for initial-transcription pausing does not contain a sequence corresponding to the upstream, less highly conserved portion of the consensus sequence for elongation pausing, G_{P-8} , is explained by the fact that ITCs contain short RNA products and short RNA:DNA hybrids that do not extend to this upstream position.

We suggest that the resemblance of the consensus sequence for initial-transcription pausing and the downstream portion of the consensus sequence for transcription-elongation pausing reflects a functional relationship. We infer that initial-transcription pausing and transcription-elongation pausing share mechanistic commonalities. Consistent with this proposal, substitution of the RNAP β -subunit residue 446 (β^{D446A}) increases sequence-dependent pausing in both initial transcription (Figures 4A, S2, S7D, and S7F; Dulin et al., 2018) and transcription elongation (Vvedenskaya et al., 2014).

DISCUSSION

XACT-seq provides a high-throughput, direct, single-nucleotide-resolution readout of the RNAP-active-center A-site position relative to DNA during transcription in living cells. Here, using

the reagent that underpins XACT-seq, we (1) defined the RNAP-active-center A-site position at placCONS (Figure 4), (2) demonstrated initial-transcription pausing occurs at a substantial fraction of promoter initial-transcribed-region sequences *in vivo* (Figures 5 and S4), (3) showed that initial-transcription pausing can occur at each promoter position from +3 to +9 (Figures 5 and S4), and (4) showed that the σ finger contributes quantitatively to pausing at promoter positions +5 and +6, presumably through collision with the RNA 5' end (Figures 4, 6E, and 6F). Next, using XACT-seq and sampling a library of 4^{11} ($\sim 4,000,000$) promoter initial-transcribed-region sequences, we (1) confirmed that initial-transcription pausing occurs *in vivo* (Figures 6 and S6; Table S1), (2) confirmed and quantified that initial-transcription pausing occurs at a substantial fraction ($\sim 15\%$) of initial-transcribed-region sequences (Figure 6C; Table S1), (3) confirmed and quantified that initial-transcription pausing can occur at each position in the initial-transcribed region (high prevalence for positions +3 to +7; lower prevalence for positions +8 and +9; Figure 6C; Table S1), (4) showed that initial-transcription pausing is determined primarily by promoter sequence (Figures 6 and S6), (5) defined the consensus sequence for initial-transcription pausing as $T_{P-1}N_P\underline{Y_A}G_{A+1}$ (Figure 6A), and (6) showed that the consensus sequence for initial-transcription pausing resembles the consensus sequence for transcription-elongation pausing, suggesting that initial-transcription pausing and transcription-elongation pausing share mechanistic commonalities (Figure 7). A major finding is that initial-transcription pausing and transcription-elongation pausing appear to be fundamentally similar, with the key mechanistic difference, a “scrunching” mechanism of RNAP-active-center translocation in the former versus a “stepping” mechanism of RNAP-active-center translocation in the latter, having no detectable effect and the key structural difference, the presence of the initiation factor σ in the former, but not the latter, having only a quantitative, modulatory effect on initial-transcription pausing.

We applied XACT-seq to analysis of a library of 4^{11} ($\sim 4,000,000$) initial-transcribed region sequences. However, in principle, the sequence of other promoter regions also may impact pausing. Therefore, repeating XACT-seq with libraries containing randomized segments within other promoter regions potentially could reveal additional determinants of initial-transcription pausing. In addition, the *in vivo* experiments reported in this work were performed in the context of a plasmid-borne promoter. A priority for future work will be to use XACT-seq to analyze pausing in the context of the bacterial chromosome.

In this report, we focused on results for initial-transcription pausing. However, the same experiments also provide information for pausing in subsequent stages of transcription, including pausing at the moment of promoter escape and formation of a TEC, promoter-proximal σ -dependent pausing by TECs, and sequence-dependent elongation pausing by TECs. The findings for these stages of transcription will be reported elsewhere.

We used the model bacterium *E. coli* to develop and first apply XACT-seq, but XACT-seq could be applied to organisms with more complex genomes. Bpa has previously been incorporated into RNAP subunits in yeast (Chen et al., 2007) and can be incorporated into proteins in mammalian cells (Hino et al., 2005).

Methods for UV irradiation, DNA fragmentation, RNAP purification, and sequencing library preparation would be similar for each organism. A priority for future work will be to apply XACT-seq for analysis of RNAP-active-center A-site positions *ex vivo* on isolated DNA or chromatin or *in vivo* in living cells, providing a basis for “RNAP profiling” analogous to existing methods for ribosome profiling (Ingolia et al., 2009). Combining XACT-seq and NET-seq for genome-wide analysis of RNAP-active-center A-site positions and RNA 3'-end positions, respectively, each with single-nucleotide resolution, should provide an unprecedentedly rich description of the sequence-dependent, factor-dependent transcriptional landscape.

STAR★METHODS

Detailed methods are provided in the online version of this paper and include the following:

- KEY RESOURCES TABLE

- RESOURCE AVAILABILITY

- Lead Contact
 - Materials Availability
 - Data and Code Availability

- EXPERIMENTAL MODEL AND SUBJECT DETAILS

- METHOD DETAILS

- Plasmids
 - Proteins
 - Oligonucleotides
 - Templates for *in vitro* assays
 - *In vitro* transcription assays: transcription-elongation pausing
 - *In vitro* transcription assays: initial-transcription pausing
 - Determination of RNAP-active-center A-site positions by protein-DNA photo-crosslinking *in vitro*
 - Determination of RNAP-active-center A-site positions by protein-DNA photo-crosslinking *in vivo*
 - XACT-seq: primer extension
 - XACT-seq: 3'-adaptor ligation and library amplification
 - XACT-seq: analysis of template sequences in the plac-CONS-N11 library
 - XACT-seq: data analysis

- QUANTIFICATION AND STATISTICAL ANALYSIS

SUPPLEMENTAL INFORMATION

Supplemental Information can be found online at <https://doi.org/10.1016/j.molcel.2020.07.006>.

ACKNOWLEDGMENTS

Work was supported by NIH grants GM124976 (P.S.), GM041376 (R.H.E.), and GM118059 (B.E.N.). J.T.W. was supported by a fellowship from the Helen Hay Whitney Foundation.

AUTHOR CONTRIBUTIONS

Conceptualization, J.T.W., R.H.E., and B.E.N.; Methodology, J.T.W., C.P., Y.Z., I.O.V., and P.S.; Formal Analysis, J.T.W., C.P., P.S., Y.Z., and D.M.T.; Investigation, J.T.W., C.P., and I.O.V.; Writing, J.T.W., R.H.E., and B.E.N.;

Visualization, J.T.W., R.H.E., and B.E.N.; Supervision, D.M.T., R.H.E., and B.E.N.; Project Administration, R.H.E. and B.E.N.; Funding Acquisition, P.S., R.H.E., and B.E.N.

DECLARATION OF INTERESTS

The authors declare no competing interests.

Received: December 21, 2019

Revised: July 7, 2020

Accepted: July 7, 2020

Published: August 3, 2020

REFERENCES

- Abbondanzieri, E.A., Greenleaf, W.J., Shaevitz, J.W., Landick, R., and Block, S.M. (2005). Direct observation of base-pair stepping by RNA polymerase. *Nature* 438, 460–465.
- Artsimovitch, I., and Landick, R. (2000). Pausing by bacterial RNA polymerase is mediated by mechanistically distinct classes of signals. *Proc. Natl. Acad. Sci. USA* 97, 7090–7095.
- Artsimovitch, I., Svetlov, V., Murakami, K.S., and Landick, R. (2003). Co-over-expression of *Escherichia coli* RNA polymerase subunits allows isolation and analysis of mutant enzymes lacking lineage-specific sequence insertions. *J. Biol. Chem.* 278, 12344–12355.
- Barski, A., Cuddapah, S., Cui, K., Roh, T.Y., Schones, D.E., Wang, Z., Wei, G., Chepelev, I., and Zhao, K. (2007). High-resolution profiling of histone methylations in the human genome. *Cell* 129, 823–837.
- Basu, R.S., Warner, B.A., Molodtsov, V., Pupov, D., Esyunina, D., Fernández-Tornero, C., Kulbachinskiy, A., and Murakami, K.S. (2014). Structural basis of transcription initiation by bacterial RNA polymerase holoenzyme. *J. Biol. Chem.* 289, 24549–24559.
- Belogurov, G.A., and Artsimovitch, I. (2019). The mechanisms of substrate selection, catalysis, and translocation by the elongating RNA polymerase. *J. Mol. Biol.* 431, 3975–4006.
- Borukhov, S., Sagitov, V., and Goldfarb, A. (1993). Transcript cleavage factors from *E. coli*. *Cell* 72, 459–466.
- Chen, H.T., Warfield, L., and Hahn, S. (2007). The positions of TFIIF and TFIIE in the RNA polymerase II transcription preinitiation complex. *Nat. Struct. Mol. Biol.* 14, 696–703.
- Chin, J.W., Martin, A.B., King, D.S., Wang, L., and Schultz, P.G. (2002). Addition of a photocrosslinking amino acid to the genetic code of *Escherichia coli*. *Proc. Natl. Acad. Sci. USA* 99, 11020–11024.
- Churchman, L.S., and Weissman, J.S. (2011). Nascent transcript sequencing visualizes transcription at nucleotide resolution. *Nature* 469, 368–373.
- Churchman, L.S., and Weissman, J.S. (2012). Native elongating transcript sequencing (NET-seq). *Curr. Protoc. Mol. Biol. Chapter 4. Unit 4.14.1–4.14.17.*
- Cohen, S.N., and Chang, A.C. (1977). Revised interpretation of the origin of the pSC101 plasmid. *J. Bacteriol.* 132, 734–737.
- Duchi, D., Bauer, D.L., Fernandez, L., Evans, G., Robb, N., Hwang, L.C., Gryte, K., Tomescu, A., Zawadzki, P., Morichaud, Z., et al. (2016). RNA polymerase pausing during initial transcription. *Mol. Cell* 63, 939–950.
- Dulin, D., Bauer, D.L.V., Malinen, A.M., Bakermans, J.J.W., Kaller, M., Morichaud, Z., Petushkov, I., Depken, M., Brodolin, K., Kulbachinskiy, A., and Kapanidis, A.N. (2018). Pausing controls branching between productive and non-productive pathways during initial transcription in bacteria. *Nat. Commun.* 9, 1478.
- Erie, D.A., Yager, T.D., and von Hippel, P.H. (1992). The single-nucleotide addition cycle in transcription: a biophysical and biochemical perspective. *Annu. Rev. Biophys. Biomol. Struct.* 21, 379–415.
- Fish, R.N., and Kane, C.M. (2002). Promoting elongation with transcript cleavage stimulatory factors. *Biochim. Biophys. Acta* 1577, 287–307.

- Guo, X., Myasnikov, A.G., Chen, J., Crucifix, C., Papai, G., Takacs, M., Schultz, P., and Weixlbaumer, A. (2018). Structural basis for NusA stabilized transcriptional pausing. *Mol. Cell* 69, 816–827.e4.
- Herbert, K.M., La Porta, A., Wong, B.J., Mooney, R.A., Neuman, K.C., Landick, R., and Block, S.M. (2006). Sequence-resolved detection of pausing by single RNA polymerase molecules. *Cell* 125, 1083–1094.
- Hino, N., Okazaki, Y., Kobayashi, T., Hayashi, A., Sakamoto, K., and Yokoyama, S. (2005). Protein photo-cross-linking in mammalian cells by site-specific incorporation of a photoreactive amino acid. *Nat. Methods* 2, 201–206.
- Imashimizu, M., Takahashi, H., Oshima, T., McIntosh, C., Bubunenko, M., Court, D.L., and Kashlev, M. (2015). Visualizing translocation dynamics and nascent transcript errors in paused RNA polymerases *in vivo*. *Genome Biol.* 16, 98.
- Ingolia, N.T., Ghaemmaghami, S., Newman, J.R., and Weissman, J.S. (2009). Genome-wide analysis *in vivo* of translation with nucleotide resolution using ribosome profiling. *Science* 324, 218–223.
- Kang, J.Y., Mishanina, T.V., Bellecourt, M.J., Mooney, R.A., Darst, S.A., and Landick, R. (2018). RNA polymerase accommodates a pause RNA hairpin by global conformational rearrangements that prolong pausing. *Mol. Cell* 69, 802–815.e1.
- Kang, J.Y., Mishanina, T.V., Landick, R., and Darst, S.A. (2019). Mechanisms of transcriptional pausing in bacteria. *J. Mol. Biol.* 431, 4007–4029.
- Kapanidis, A.N., Margeat, E., Ho, S.O., Kortkhonjia, E., Weiss, S., and Ebright, R.H. (2006). Initial transcription by RNA polymerase proceeds through a DNA-scrunching mechanism. *Science* 314, 1144–1147.
- Kulbachinskiy, A., and Mustaev, A. (2006). Region 3.2 of the σ subunit contributes to the binding of the 3'-initiating nucleotide in the RNA polymerase active center and facilitates promoter clearance during initiation. *J. Biol. Chem.* 281, 18273–18276.
- Landick, R., Wang, D., and Chan, C.L. (1996). Quantitative analysis of transcriptional pausing by *Escherichia coli* RNA polymerase: his leader pause site as paradigm. *Methods Enzymol.* 274, 334–353.
- Larson, M.H., Landick, R., and Block, S.M. (2011). Single-molecule studies of RNA polymerase: one singular sensation, every little step it takes. *Mol. Cell* 41, 249–262.
- Larson, M.H., Mooney, R.A., Peters, J.M., Windgassen, T., Nayak, D., Gross, C.A., Block, S.M., Greenleaf, W.J., Landick, R., and Weissman, J.S. (2014). A pause sequence enriched at translation start sites drives transcription dynamics *in vivo*. *Science* 344, 1042–1047.
- Latif, H., Federowicz, S., Ebrahim, A., Tarasova, J., Szubin, R., Utrilla, J., Zengler, K., and Palsson, B.O. (2018). ChIP-exo interrogation of Crp, DNA, and RNAP holoenzyme interactions. *PLoS ONE* 13, e0197272.
- Lerner, E., Chung, S., Allen, B.L., Wang, S., Lee, J., Lu, S.W., Grimaud, L.W., Ingariola, A., Michalet, X., Alhadid, Y., et al. (2016). Backtracked and paused transcription initiation intermediate of *Escherichia coli* RNA polymerase. *Proc. Natl. Acad. Sci. USA* 113, E6562–E6571.
- Margeat, E., Kapanidis, A.N., Tinnefeld, P., Wang, Y., Mukhopadhyay, J., Ebright, R.H., and Weiss, S. (2006). Direct observation of abortive initiation and promoter escape within single immobilized transcription complexes. *Biophys. J.* 90, 1419–1431.
- Marr, M.T., and Roberts, J.W. (1997). Promoter recognition as measured by binding of polymerase to nontemplate strand oligonucleotide. *Science* 276, 1258–1260.
- Mazumder, A., and Kapanidis, A.N. (2019). Recent advances in understanding σ⁷⁰-dependent transcription initiation mechanisms. *J. Mol. Biol.* 431, 3947–3959.
- McClure, W.R., and Cech, C.L. (1978). On the mechanism of rifampicin inhibition of RNA synthesis. *J. Biol. Chem.* 253, 8949–8956.
- Mooney, R.A., Darst, S.A., and Landick, R. (2005). Sigma and RNA polymerase: an on-again, off-again relationship? *Mol. Cell* 20, 335–345.
- Murakami, K.S., Masuda, S., and Darst, S.A. (2002). Structural basis of transcription initiation: RNA polymerase holoenzyme at 4 Å resolution. *Science* 296, 1280–1284.
- Pupov, D., Kuzin, I., Bass, I., and Kulbachinskiy, A. (2014). Distinct functions of the RNA polymerase σ subunit region 3.2 in RNA priming and promoter escape. *Nucleic Acids Res.* 42, 4494–4504.
- Revyakin, A., Liu, C., Ebright, R.H., and Strick, T.R. (2006). Abortive initiation and productive initiation by RNA polymerase involve DNA scrunching. *Science* 314, 1139–1143.
- Rhee, H.S., and Pugh, B.F. (2012). Genome-wide structure and organization of eukaryotic pre-initiation complexes. *Nature* 483, 295–301.
- Ruff, E.F., Record, M.T., Jr., and Artsimovitch, I. (2015). Initial events in bacterial transcription initiation. *Biomolecules* 5, 1035–1062.
- Saba, J., Chua, X.Y., Mishanina, T.V., Nayak, D., Windgassen, T.A., Mooney, R.A., and Landick, R. (2019). The elemental mechanism of transcriptional pausing. *eLife* 8, e40981.
- Sambrook, J., Russell, D., and Sambrook, J. (2006). The Condensed Protocols from Molecular Cloning: A Laboratory Manual (Cold Spring Harbor Laboratory).
- Severinov, K., Fenyö, D., Severinova, E., Mustaev, A., Chait, B.T., Goldfarb, A., and Darst, S.A. (1994). The sigma subunit conserved region 3 is part of "5'-face" of active center of *Escherichia coli* RNA polymerase. *J. Biol. Chem.* 269, 20826–20828.
- Srivastava, D.B., Leon, K., Osmundson, J., Garner, A.L., Weiss, L.A., Westblade, L.F., Glickman, M.S., Landick, R., Darst, S.A., Stallings, C.L., and Campbell, E.A. (2013). Structure and function of CarD, an essential mycobacterial transcription factor. *Proc. Natl. Acad. Sci. USA* 110, 12619–12624.
- Vos, S.M., Farnung, L., Urlaub, H., and Cramer, P. (2018). Structure of paused transcription complex Pol II-DSIF-NELF. *Nature* 560, 601–606.
- Vvedenskaya, I.O., Vahedian-Movahed, H., Bird, J.G., Knoblauch, J.G., Goldman, S.R., Zhang, Y., Ebright, R.H., and Nickels, B.E. (2014). Interactions between RNA polymerase and the "core recognition element" counteract pausing. *Science* 344, 1285–1289.
- Vvedenskaya, I.O., Zhang, Y., Goldman, S.R., Valenti, A., Visone, V., Taylor, D.M., Ebright, R.H., and Nickels, B.E. (2015). Massively systematic transcript end readout, "MASTER": transcription start site selection, transcriptional slippage, and transcript yields. *Mol. Cell* 60, 953–965.
- Vvedenskaya, I.O., Bird, J.G., Zhang, Y., Zhang, Y., Jiao, X., Barvik, I., Krásný, L., Kledjian, M., Taylor, D.M., Ebright, R.H., et al. (2018a). "CapZyme-seq" comprehensively defines promoter-sequence determinants for RNA 5' capping with NAD⁺. *Mol. Cell* 70, 553–564.e9.
- Vvedenskaya, I.O., Goldman, S.R., and Nickels, B.E. (2018b). Analysis of bacterial transcription by "massively systematic transcript end readout," MASTER. *Methods Enzymol.* 612, 269–302.
- Winkelman, J.T., Winkelman, B.T., Boyce, J., Maloney, M.F., Chen, A.Y., Ross, W., and Gourse, R.L. (2015). Crosslink mapping at amino acid-base resolution reveals the path of scrunched DNA in initial transcribing complexes. *Mol. Cell* 59, 768–780.
- Wagih, O. (2017). ggseqlogo: a versatile R package for drawing sequence logos. *Bioinformatics*.
- Wickham, H. (2016). *ggplot2: Elegant Graphics for Data Analysis* (New York: Springer-Verlag).
- Wickham, H., François, R., Henry, L., and Müller, K. (2020). *dplyr: A Grammar of Data Manipulation*. R package version 0.8.4.
- Winkelman, J.T., Chandrangsu, P., Ross, W., and Gourse, R.L. (2016a). Open complex scrunching before nucleotide addition accounts for the unusual transcription start site of *E. coli* ribosomal RNA promoters. *Proc. Natl. Acad. Sci. USA* 113, E1787–E1795.
- Winkelman, J.T., Nickels, B.E., and Ebright, R.H. (2020). The transition from transcription initiation to transcription elongation: start-site selection, initial transcription, and promoter escape. In *RNA Polymerase as a Molecular*

- Motor, Second Edition, R. Landick, J. Wang, and T. Strick, eds. (RSC Publishing).
- Winkelman, J.T., Vvedenskaya, I.O., Zhang, Y., Zhang, Y., Bird, J.G., Taylor, D.M., Gourse, R.L., Ebright, R.H., and Nickels, B.E. (2016b). Multiplexed protein-DNA cross-linking: scrunching in transcription start site selection. *Science* 351, 1090–1093.
- Yu, L., Winkelman, J.T., Pukhrambam, C., Strick, T.R., Nickels, B.E., and Ebright, R.H. (2017). The mechanism of variability in transcription start site selection. *eLife* 6, e32038.
- Zhang, L.R., and Landick, R. (2009). Substrate loading, nucleotide addition, and translocation by RNA polymerase. In *RNA Polymerases as Molecular Motors*, H. Buc and S. Strick, eds. (Royal Society of Chemistry).
- Zhang, Y., Feng, Y., Chatterjee, S., Tuske, S., Ho, M.X., Arnold, E., and Ebright, R.H. (2012). Structural basis of transcription initiation. *Science* 338, 1076–1080.
- Zuo, Y., and Steitz, T.A. (2015). Crystal structures of the *E. coli* transcription initiation complexes with a complete bubble. *Mol. Cell* 58, 534–540.

STAR★METHODS

KEY RESOURCES TABLE

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Bacterial and Virus Strains		
NiCo21(DE3)	NEB	C2529H
ElectroMax DH10B-T1 ^R electrocompetent cells	Thermo Fisher	1521050
Chemicals, Peptides, and Recombinant Proteins		
Nuclease-free water (not DEPC-treated)	Thermo Fisher	AM9932
H-Bpa-OH	Bachem	F-2800
Bacto agar	VWR	90000-760
Bacto tryptone	VWR	90000-286
Bacto yeast extract	VWR	90000-726
L-Arabinose	Calbiochem	178680
IPTG	Gold Biotech	I2481C50
Chloramphenicol	Gold Biotech	C-105-25
Spectinomycin	Gold Biotech	S0188-25
Streptomycin	Fisher Scientific	15140122
Carbenicillin	Gold Biotech	C-103-25
Rifampicin	Gold Biotech	R-120-25
SOC Outgrowth Medium	NEB	B9020S
dNTP solution mix, 10 mM of each NTP	NEB	N0447S
NTP set (ultra-pure), 100 mM solutions	GE Healthcare	27-2025-01
Tris base (Amresco)	VWR	97061-800
Boric Acid (ACS grade)	VWR	97061-980
EDTA disodium salt dyhydrate	VWR	97061-018
0.5 M EDTA pH 8	Thermo Fisher	AM9260G
Sodium Chloride	EMD Millipore	SX0420-3
Sodium hydroxide	VWR	BDH0292-500G
Potassium Chloride	EMD Millipore	7300-500GM
Sodium Acetate, trihydrate	VWR	MK736406
β-mercaptoethanol	Omnipur	60-24-2
Lysozyme	VWR	EM-5980
Formamide, deionized	VWR	EM-4610
Sodium dodecylsulfate (SDS)	VWR	97064-470
Magnesium chloride hexahydrate	VWR	EM-5980
Glycerol (ACS grade)	VWR	EMGX0185-5
Bovine Serum Albumin (BSA) fraction V	VWR	101174-932
Betaine Solution	VWR	101375-612
Bromophenol Blue	VWR	EM-BX1410-7
Xylene Cyanol	Sigma-Aldrich	X4126-10G
Amaranth Dye	VWR	200030-400
Temed (JT Baker)	VWR	JT4098-1
Ammonium Persulfate	VWR	97064-594
Dithiothreitol (DTT)	Gold Bio	DTT50
Glycogen from Oyster (type II)	Sigma-Aldrich	G8751
Hydrochloric Acid (ACS plus)	Fisher Scientific	A144-212

(Continued on next page)

Continued

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Ethyl Alcohol	Pharmco-AAPER	111000200
Isopropyl Alcohol	BDH	BDH1133-1LP
DMSO	VWR	EM-2951
Heparin sulfate	Sigma-Aldrich	H-3393
GeneMate LE Quick Dissolve agarose	BioExpress	E-3119-500
SequaGel sequencing system	National Diagnostics	EC833
10% TBE-Urea gels, 1mm x 10 wells	Thermo Fisher	EC6875Box
10% TBE gels, 1mm x 10 wells	Thermo Fisher	EC6275Box
alpha-32P CTP EasyTide 250 uCi	Perkin Elmer	BLU508H250UC
alpha-32P GTP EasyTide 250 uCi	Perkin Elmer	BLU506H250UC
alpha-32P UTP EasyTide 250 uCi	Perkin Elmer	BLU507H250UC
Gamma-32P ATP EasyTide 250 uCi	Perkin Elmer	BLU502Z001MC
Low Range ssRNA Ladder	NEB	N0364S
O'Gene Ruler Ultra Low Range DNA Ladder	Thermo Fisher	SM1223
6X Orange DNA Loading Dye	Thermo Fisher	R0631
SYBR Gold nucleic acid gel stain	Thermo Fisher	S11494
B-Per Bacterial Extraction Reagent	Thermo Fisher	78248
Amicon Ultra-4 100K MWCO	Fisher Scientific	UFC810024
Acid phenol:chloroform (CHCl_3) pH 4.5	Thermo Fisher	AM9720
Ni-NTA agarose	QIAGEN	30230
MagneHis Ni-Particles	Promega	V8560
DNase I	Zymo Research	E1009A
T4 RNA Ligase 1 (ssRNA Ligase)	NEB	M0204L
5' App DNA/RNA ligase	NEB	M0319S
T4 Polynucleotide Kinase (PNK)	NEB	M0201S
Superscript III Reverse Transcriptase	Thermo Fisher	18080-044
RNase H	Thermo Fisher	AM2293
Phusion HF Master Mix	Thermo Fisher	F-548L
Taq DNA polymerase	NEB	M0273
5X Detergent-free Phusion HF Buffer Pack	NEB	B0520S
Phusion Flash HF master mix	Thermo Fisher	F-548L
<i>E. coli</i> RNA polymerase core (β' -10xHis)	Artsimovitch et al., 2003	N/A
<i>E. coli</i> σ^{70} -6xHis	Marr and Roberts, 1997	N/A
Critical Commercial Assays		
Sequenase Cycle Sequencing Kit	Thermo Fisher	785001KT
QIAprep Spin Miniprep Kit	QIAGEN	27106
Qubit dsDNA HS assay kit	Thermo Fisher	Q32851
Qubit ssDNA Assay kit	Thermo Fisher	Q10212
Micellula DNA Emulsion PCR Kit	Chimerix	3600-02
QIAquick PCR purification kit	QIAGEN	28104
Deposited Data		
High throughput sequencing data	NIH Sequence Read Archive	study accession number: PRJNA615362
Experimental Models: Organisms/Strains		
NiCo21(DE3)	NEB	C2529H
Oligonucleotides		
DNA/RNA Oligos listed in Oligonucleotides table	Integrated DNA Technologies (IDT)	N/A
ApA	Trilink	N/A

(Continued on next page)

Continued

REAGENT or RESOURCE	SOURCE	IDENTIFIER
ApU	Trilink	N/A
Recombinant DNA		
pIA900	Gift of I. Artsimovitch	N/A
pIA900-RNAP- β' R1148Bpa	Winkelman et al., 2015	N/A
pIA900- β D446A RNAP- β' R1148Bpa	This work	N/A
p σ ⁷⁰ -His	Gift of J. Roberts	N/A
p σ ⁷⁰ Δ finger-His	This work	N/A
pMASTER-lacCONS-N11	This work	N/A
pMASTER-lacCONS-N20	This work	N/A
pCDF-CP	Yu et al., 2017	N/A
pEVOL-pBpF	Chin et al., 2002	N/A
pCDF-lacCONS	Yu et al., 2017	N/A
pCDF-lacCONS-p5	This work	N/A
pCDF-lacCONS-p6	This work	N/A
pCDF-lacCONS-p7	This work	N/A
pCDF-lacCONS-p8	This work	N/A
pCDF-lacCONS-p9	This work	N/A
pIA171	Artsimovitch and Landick, 2000	N/A
Software and Algorithms		
Excel	Microsoft	2011
ImageQuant	GE Healthcare	TL 5.1
SigmaPlot	Systat Software Inc.	Ver. 10
XACT-seq	This work	https://github.com/NickelsLabRutgers/XACT-seq
R programming language	R Core Team	http://www.R-project.org/
ggplot2	Wickham, 2016	https://www.springer.com/us/book/9780387981413
dplyr	Wickham et al., 2020	https://cran.r-project.org/web/packages/dplyr/index.html
Pymol	Schrodinger, LLC	https://pymol.org/2/
Illustrator	Adobe	Ver. CS6
Other		
Molecular Dynamics PhosphorImager	GE Healthcare	Typhoon 9400
Illumina high-throughput sequencing (NextSeq)	Waksman Genomics Core Facility, Rutgers University	N/A

RESOURCE AVAILABILITY**Lead Contact**

Further information and requests for resources and reagents should be directed to and will be fulfilled by the Lead Contact, Bryce Nickels (bnickels@waksman.rutgers.edu).

Materials Availability

This study did not generate new unique reagents.

Data and Code Availability

Original data for all replicates are available at <http://data.mendeley.com/datasets/p5cscgdd5x/1>.

Unprocessed sequencing reads have been deposited in the NIH/NCBI Sequence Read Archive under the study accession number PRJNA615362. Source code and documentation for analysis of sequencing data are provided at <https://github.com/NickelsLabRutgers/XACT-seq>.

EXPERIMENTAL MODEL AND SUBJECT DETAILS

For all *in vivo* crosslinking assays, *Escherichia coli* was grown at 37°C in LB broth containing 1 mM Bpa, 100 µg/ml carbenicillin, 50 µg/ml spectinomycin, 50 µg/ml streptomycin, and 25 µg/ml chloramphenicol. For plasmid maintenance and protein expression, *Escherichia coli* was grown at 37°C in LB broth supplemented with the appropriate antibiotic.

METHOD DETAILS

Plasmids

To generate plasmid pIA900-βD446A RNAP- β' ^{R1148Bpa}, we performed PCR using ~20 ng of pIA900-RNAP- β' ^{R1148Bpa} ([Winkelmann et al., 2015](#)) in 12.5 µl reactions containing 0.8 µM oligo JW44 and 1 X Phusion HF Master Mix (Thermo Fischer Scientific) (95°C for 2 min; 95°C for 15 s, 55°C for 15 s, 72°C for 5 min; 30 cycles; 72°C for 6 min). Next, to remove the wild-type plasmid template, 20 units of DpnI (New England Biolabs) was added, the reaction was incubated at 37°C for 16 h, 1 µl of the reaction was introduced into electrocompetent DH10B cells (Thermo Fischer Scientific), and cells were plated on LB agar plates containing 100 µg/ml carbenicillin to select for transformants.

To generate plasmid $\rho\sigma^{70}\Delta$ finger-His, we performed PCR using 4 ng of plasmid $\rho\sigma^{70}$ -His ([Marr and Roberts, 1997](#)) in 50 µl reactions containing 0.8 µM oligo JW268, 0.8 µM oligo JW269, and 1 X Phusion HF Master Mix (2 min at 95°C; 95°C for 15 s, 55°C for 15 s, 72°C for 4 min (30 x); 2 min at 72°C). 30 units of DpnI was added, the reaction was incubated at 37°C for 16 h, and DNA was recovered using a PCR purification kit (QIAGEN). The recovered DNA was treated with 10 units of T4 polynucleotide kinase (PNK) (New England Biolabs) in 1 X T4 PNK buffer containing 20 µM ATP for 30 min at 37°C, 400 units of T4 DNA ligase (New England Biolabs) was added, reactions were incubated at 16°C for 16 h, 1 µl of the reaction was introduced into electrocompetent DH10B cells, and cells were plated on LB agar plates containing 50 µg/ml kanamycin, and recombinant plasmid DNA was isolated from individual transformants.

Plasmid pCDF-CP ([Yu et al., 2017](#)) contains a CloDF13 replication origin, a selectable marker conferring resistance to spectinomycin, and two BglII recognition sites that are used to introduce DNA fragments upstream of transcription terminator tR2. Plasmid pCDF-lacCONS ([Yu et al., 2017](#)) is a derivative of pCDF-CP containing sequences from positions -88 to +70 of *placCONS* inserted into BglII-digested pCDF-CP.

To generate plasmids pCDF-lacCONS-p5, -p6, -p7, -p8, and -p9, which contain the sequences between positions +3 and +13 shown in [Figure 6D](#), we performed PCR using 1 ng of pCDF-lacCONS in 25 µl reactions containing 1 X Phusion HF Master Mix, 0.8 µM oligo JW80 and 0.8 µM oligo JW433, JW408, JW409, JW580, or JW575, respectively. 1 µl of this reaction was used as a template in PCR reactions (50 µl) containing 1 X Phusion HF Master Mix, 0.8 µM JW79, and 0.8 µM JW80. Amplicons were treated with BglII and BglII-digested fragments were ligated into BglII-digested pCDF-CP. The ligation mixture was transformed into NEB 5-alpha competent cells (New England Biolabs), cells plated on LB agar plates containing 50 µg/ml spectinomycin, and recombinant plasmid DNA was isolated from individual transformants.

Plasmid-borne promoter libraries *placCONS-N11* and *placCONS-N20* were generated using a procedure described in ([Vvedenskaya et al. 2015, 2018b](#)) that provides a “self-assembling barcode,” in which for each DNA molecule in the library a first randomized sequence in a region of interest is associated with a known corresponding second randomized sequence that serves as a barcode. The procedure involves synthesis of three oligos for use in PCR. One oligo, which serves as the template for PCR amplification, contains a first randomized sequence spanning the region of interest and a second randomized sequence that serves as a barcode. The other oligos, which serve as amplification primers, contain 5' end sequences that introduce BglII recognition sequences and 3' end sequences complementary to the template oligo. Libraries *placCONS-N11*, containing up to 4¹¹ initial-transcribed region sequences from position +3 to position +13, was constructed using oligo JW153 as the template and oligos s1219 and s1220 as amplification primers. Library *placCONS-N20*, containing up to 4²⁰ initial-transcribed region sequences from position +2 to position +21, was constructed using oligo JW203 as the template and oligos s1219 and s1220 as amplification primers. Amplicons were treated with BglII and BglII-digested fragments were ligated into BglII-digested pCDF-CP. The ligation mixture was transformed into NEB 5-alpha competent cells, cells plated on LB agar plates containing 50 µg/ml spectinomycin, and recombinant plasmid DNA was isolated from ~10⁷ transformants.

Plasmid pEVOL-pBpF contains genes directing the synthesis of an engineered Bpa-specific UAG-suppressor tRNA and an engineered Bpa-specific aminoacyl-tRNA synthetase that charges the amber suppressor tRNA with Bpa (Addgene; [Chin et al., 2002](#)).

Proteins

Wild-type RNAP core enzyme was prepared from *E. coli* strain NiCo21(DE3) (New England Biolabs) containing plasmid pIA900 ([Art-simovitch et al., 2003](#)) using procedures described in [Winkelmann et al. \(2015\)](#).

Bpa-containing RNAP core enzyme derivatives RNAP- β' ^{R1148Bpa} and βD446A RNAP- β' ^{R1148Bpa} were prepared from *E. coli* strain NiCo21(DE3) (New England Biolabs) containing plasmid pEVOL-pBpF and plasmid pIA900-RNAP- β' ^{R1148Bpa} ([Winkelmann et al., 2015](#)) or plasmid pIA900-βD446A RNAP- β' ^{R1148Bpa}, using procedures described in [Winkelmann et al. \(2015\)](#).

Wild-type σ^{70} or a σ^{70} derivative containing a deletion of the σ finger (residues 513–519), were prepared from *E. coli* strain NiCo21(DE3) containing plasmid $\rho\sigma^{70}$ -His (gift of J. Roberts; [Marr and Roberts, 1997](#)) or plasmid $\rho\sigma^{70}$ -His Δ finger using procedures described in [Marr and Roberts \(1997\)](#). To form RNAP holoenzyme, 1 µM RNAP core enzyme and 5 µM wild-type σ^{70} or Δ finger

σ^{70} in 10 mM Tris-Cl (pH 8.0), 100 mM KCl, 10 mM MgCl₂, 0.1 mM EDTA, 1 mM DTT, and 50% glycerol were incubated for 30 min at 25°C. GreB was purified using procedures described in [Borukhov et al. \(1993\)](#).

Oligonucleotides

Oligodeoxyribonucleotides ([Table S2](#)) were purchased from IDT. Diribonucleotides ApA and ApU (HPLC-purified) were purchased from TriLink Biotechnologies.

Templates for *in vitro* assays

Linear DNA templates used for *in vitro* assays in [Figures 3B, 4, S2](#), and [S3A](#) contain sequences from positions -88 to +70 of *plac*-CONS. Templates used for *in vitro* assays in [Figures 6E, 6F](#), and [S7](#) contain sequences from positions -88 to +70 of *plac*CONS-p5, *plac*CONS-p6, *plac*CONS-p7, *plac*CONS-p8, or *plac*CONS-p9. Templates were generated by PCR in reactions containing 1 X Phusion HF Master Mix, 0.8 μ M primer JW61, 0.8 μ M primer JW62, and ~1 pg of plasmids *plac*CONS-p5, -p6, -p7, -p8, or -p9. Reaction products were purified using a PCR purification kit. The linear DNA template used for *in vitro* transcription assays in [Figure 3A](#) contained sequences from positions -93 to +9 of the T7A1 promoter, a T-less tract from +10 to +29, a T at +30, followed by a 35-bp sequence containing the *yrbL* consensus pause sequence ([Vvedenskaya et al., 2014](#)). This template was generated by PCR in reactions containing 1 X Phusion HF Master Mix, 0.8 μ M primer JB49, 0.8 μ M primer JB105, and ~1 pg of plasmid pIA171 ([Artsimovitch and Landick, 2000](#)).

In vitro transcription assays: transcription-elongation pausing

40 nM of the T7A1-*yrbL* DNA template was mixed with 150 nM RNAP holoenzyme in 1X RB and incubated at 37°C for 5 minutes to form open complexes. Complexes were stalled at position +29 by addition of 100 μ M ApU, 2.5 μ M ATP, 2.5 μ M CTP [cold CTP + 5 μ Ci 32P- α -CTP (Perkin Elmer; 3000 Ci/mmol)], 1 μ M GTP and incubation at 37°C for 15 minutes. NTPs and heparin were then added to final concentrations of: 200 μ M ATP, 200 μ M UTP, 200 μ M CTP, 10 μ M GTP and 40 μ g/ml heparin. Aliquots were taken before addition of UTP, and 15, 30, 45, 60, and 120 s after addition of UTP and mixed with an equal volume of 2 X RNA loading dye. Samples were heated at 95°C for 1 min, cooled to room temperature, and run on 12% TBE-Urea polyacrylamide gels (UreaGel system, National Diagnostics). Autoradiography of gels was performed as above. Pause-capture efficiency was calculated as described in [Landick et al. \(1996\)](#). Values of pause-capture efficiency reported in [Figure 3A](#) are means \pm SD of three independent experiments.

In vitro transcription assays: initial-transcription pausing

For reactions in [Figures 3B](#) and [S2A](#), 8 μ L reactions containing 4 nM of the *lac*CONS DNA template, 20 nM RNAP holoenzyme, 100 μ M ApA, 1X RB, and 100 nM GreB (where indicated) were incubated for 2 min at 25°C. For reactions halted at position +7 ([Figure 3B, left](#)), 2 μ L of 50 μ M UTP and 50 μ M GTP (final concentration of 10 μ M UTP, and 10 μ M GTP [cold GTP + 5 μ Ci 32P- α -GTP (Perkin Elmer; 3000 Ci/mmol)]) were added. For reactions halted at position +11, 2 μ L of 50 μ M ATP, 50 μ M UTP and 50 μ M GTP (final concentration of 10 μ M ATP, 10 μ M UTP, and 10 μ M GTP [cold GTP + 5 μ Ci 32P- α -GTP (Perkin Elmer; 3000 Ci/mmol)]) were added. After addition of NTPs, reactions were incubated for 5 min at 25°C, and 10 μ L of 2 X RNA loading dye was added. Samples were heated at 95°C for 1 min, cooled to room temperature, and run on 20% TBE-Urea polyacrylamide gels (UreaGel system, National Diagnostics). Autoradiography of gels was performed as above. The intensity of the 6- and 11-nt RNA products were used to calculate the percentage of the total RNA products that were 6 nt using the formula: % 6-nt RNA = 100 x ((6-nt RNA / (6-nt RNA + 11-nt RNA))). Values reported in [Figures 3B, right](#) and [S2B](#) are means \pm SD of three independent experiments.

Determination of RNAP-active-center A-site positions by protein-DNA photo-crosslinking *in vitro*

In vitro photo-crosslinking and crosslink mapping experiments were done using procedures described in [Yu et al. \(2017\)](#). For the experiments in [Figures 4A](#) and [4B](#), 50 μ L reactions containing 20 nM RNAP holoenzyme, 4 nM template, 100 μ M ApA dinucleotide (where indicated), and 1 X RB [10 mM Tris-Cl, pH 8.0, 70 mM NaCl, 10 mM MgCl₂, and 0.1 mg/ml bovine serum albumin (BSA)] were incubated for 5 min at 25°C, 5 μ L of 100 μ M ATP, 100 μ M CTP, 100 μ M GTP, and 100 μ M UTP (final concentration of 10 μ M ATP, 10 μ M CTP, 10 μ M GTP, and 10 μ M UTP) were added (where indicated), reactions were incubated 2 min at 25°C, and subjected to UV irradiation for 2 min at 25°C in a Rayonet RPR-100 photochemical reactor equipped with 16 \times 350 nm tubes (Southern New England Ultraviolet). For the experiments in [Figure 6E](#), 50 μ L reactions containing 20 nM RNAP holoenzyme, 4 nM template, and 1 X RB were incubated for 5 min at 25°C, 5 μ L of 1 mM ATP, 1 mM CTP, 1 mM GTP, and 1 mM UTP were added, reactions were incubated 2 min at 25°C, and subjected to UV irradiation for 2 min at 25°C. For the experiments in [Figure 6F](#), 50 μ L reactions containing 50 nM RNAP holoenzyme, 20 nM template (4 nM of *plac*CONS-p5, -p6, -p7, -p8, and -p9), and 1 X RB were incubated for 5 min at 25°C, 5 μ L of 1 mM ATP, 1 mM CTP, 1 mM GTP, and 1 mM UTP was added, reactions were incubated 2 min at 25°C, and subjected to UV irradiation for 2 min at 25°C.

To denature RNAP-DNA complexes, reactions were mixed with 15 μ L 5 M NaCl and 6 μ L 100 μ g/ml heparin, incubated for 5 min at 95°C and then cooled to 4°C. Crosslinked RNAP-DNA complexes were isolated by adding 20 μ L MagneHis Ni-particles (Promega) equilibrated and suspended in 1 X *Taq* DNA polymerase buffer, 10 μ g/ml heparin, and 0.1 mg/ml BSA; MagneHis Ni-particles were collected using a magnetic microfuge tube rack; particles were washed with 1 X *Taq* DNA polymerase buffer, 10 μ g/ml heparin, and 0.1 mg/ml BSA, washed twice with 50 μ L 1 X *Taq* DNA polymerase buffer (New England Biolabs), and particles (which contained

bound RNAP-DNA complexes) were resuspended in 10 μl 1 X *Taq* DNA polymerase buffer. Primer extension reactions (12.5 μl) were performed by combining 2 μl of the recovered RNAP-DNA complexes, 1 μl of 1 μM ^{32}P -5' end-labeled primer JW61 [200 Bq/fmol; prepared using [γ ^{32}P]-ATP (PerkinElmer) and T4 polynucleotide kinase (New England Biolabs) as described in (Sambrook et al., 2006)], 1 μl 10 X dNTPs (2.5 mM dATP, 2.5 mM dCTP, 2.5 mM dGTP, 2.5 mM dTTP, 0.25 μl 5 U/ μl *Taq* DNA polymerase (New England Biolabs), 5 μl 5 M betaine, 0.625 μl 100% dimethyl sulfoxide, and 1.25 μl 10 X *Taq* DNA polymerase buffer; 40 cycles of 30 s at 95°C, 30 s at 55°C, and 30 s at 72°C. Reactions were stopped by addition of 12.5 μl 1 X TBE, 8 M urea, 0.025% xylene cyanol, and 0.025% bromophenol blue; radiolabeled products were separated by electrophoresis on 10% 8M urea slab gels (equilibrated and run in 1 X TBE) and visualized by storage-phosphor imaging (Typhoon 9400 variable-mode imager; GE Life Science). Positions of RNAP-DNA crosslinking were determined by comparison to products of a DNA-nucleotide sequencing reaction generated using oligo JW61 and a linear DNA template containing sequences from positions –88 to +70 of *placCONS* (Thermo Sequenase Cycle Sequencing Kit; Affymetrix).

For the experiment in Figure 4, values of %XL₊₁₁ were calculated using the formula:

%XL₊₁₁ = ((XL₊₁₁ / (XL₊₇ + XL₊₁₁)), where XL₊₇ and XL₊₁₁ correspond to the intensity of the bands at positions +7 and +11, respectively. The values of %XL₊₁₁, which are reported in Figure S2B, are means \pm SD of three independent experiments.

Histogram of band intensities shown in Figures 5B, 6F, and S4B represent the means \pm SD of three independent experiments.

Determination of RNAP-active-center A-site positions by protein-DNA photo-crosslinking *in vivo*

In vivo photo-crosslinking and crosslink mapping experiments of Figures 4B, 5B, and S7 were done essentially as described in Yu et al. (2017) except the RNAP active site was not mutationally inactivated. Analysis of RNAP-active-center A-site positions *in vivo* for *placCONS* transcription complexes was performed by sequential introduction of plasmid pCDF-*lacCONS*, plasmid pIA900-RNAP- β' ^{R1148Bpa}, and plasmid pEVOL-pBpF into *E. coli* strain NiCo21(DE3) by transformation. After the final transformation step, cells were plated on LB agar containing 100 $\mu\text{g}/\text{ml}$ carbenicillin, 50 $\mu\text{g}/\text{ml}$ spectinomycin, 50 $\mu\text{g}/\text{ml}$ streptomycin, and 25 $\mu\text{g}/\text{ml}$ chloramphenicol; at least 1,000 individual colonies were scraped from the plate, combined, and used to inoculate 250 mL LB broth containing 1 mM Bpa (Bachem), 100 $\mu\text{g}/\text{ml}$ carbenicillin, 50 $\mu\text{g}/\text{ml}$ spectinomycin, 50 $\mu\text{g}/\text{ml}$ streptomycin, and 25 $\mu\text{g}/\text{ml}$ chloramphenicol in a 1000 mL flask (Bellco) to yield OD₆₀₀ = 0.3; the culture was placed in the dark and shaken (220 rpm) for 1 h at 37°C; isopropyl- β -D-thiogalactoside (IPTG) was added to 1 mM; and the culture was placed in the dark and shaken (220 rpm) for 3 h at 37°C.

Analysis of RNAP-active-center A-site positions *in vivo* for *placCONS*-N11 and *placCONS*-N20 transcription complexes was performed by sequential introduction into *E. coli* strain NiCo21(DE3) of the pCDF-*lacCONS*-N11 library (yielding ~2 million transformants) or the *placCONS*-N20 library (yielding ~2 million transformants), plasmid pIA900-RNAP- β' ^{R1148Bpa} (yielding ~15 million transformants), and plasmid pEVOL-pBpF (yielding ~4 million transformants). After the final transformation step, cells were plated on ~10–15 LB agar plates containing 100 $\mu\text{g}/\text{ml}$ carbenicillin, 50 $\mu\text{g}/\text{ml}$ spectinomycin, 50 $\mu\text{g}/\text{ml}$ streptomycin, and 25 $\mu\text{g}/\text{ml}$ chloramphenicol to yield a lawn. Colonies were scraped from the surface of the plates, combined, and used to inoculate 250 mL LB broth containing 1 mM Bpa, 100 $\mu\text{g}/\text{ml}$ carbenicillin, 50 $\mu\text{g}/\text{ml}$ spectinomycin, 50 $\mu\text{g}/\text{ml}$ streptomycin, and 25 $\mu\text{g}/\text{ml}$ chloramphenicol in a 1000 mL flask to yield OD₆₀₀ = 0.3; the culture was placed in the dark and shaken (220 rpm) for 1 h at 37°C; IPTG was added to 1 mM; and the culture was placed in the dark and shaken (220 rpm) for 3 h at 37°C. To measure background signal, a portion of the cell cultures containing pCDF-*lacCONS*, pCDF-*lacCONS*-N11, or pCDF-*lacCONS*-N20 were removed, rifampin was added to a final concentration of 200 $\mu\text{g}/\text{ml}$, and the culture was shaken for 10 min prior to UV irradiation.

Cell suspensions (9 ml) were removed from each culture to a 13 mm x 100 mm borosilicate glass test tube (VWR) and subjected to UV irradiation for 20 min at 25°C. Cells were collected by centrifugation (3000 x g; 15 min at 4°C) and cell pellets were stored at –20°C. To lyse cells, the frozen cell pellets were incubated at 4°C for 30 min, re-suspended in 40 mL of 50 mM Na₂HPO₄ (pH 8.0), 1.4 M NaCl, 20 mM imidazole, 14 mM β -mercaptoethanol, 0.1% Tween 20, and 5% ethanol containing 2 mg egg white lysozyme, and sonicated for 5 min at 4°C. Lysates were centrifuged (23,000 x g; 30 min at 4°C), supernatants were added to 1 mL Ni-NTA-agarose (QIAGEN) in 50 mM Na₂HPO₄ (pH 8.0), 1.4 M NaCl, 20 mM imidazole, 0.1% Tween 20, 5 mM β -mercaptoethanol, and 5% ethanol, and the mixture was incubated 30 min at 4°C with gentle rocking. The slurry was loaded into a 15 mL polyprop column (BioRad) to collect the Ni-NTA-agarose resin. The resin was washed with 10 mL of 1 X WB (50 mM Na₂HPO₄, pH 8.0, 300 mM NaCl, 30 mM imidazole, 0.1% Tween 20, 5 mM β -mercaptoethanol, and 5% ethanol) and His-tagged RNAP was eluted from the resin with 3 mL of 1 X WB containing 300 mM imidazole. The eluate was concentrated to 0.2 mL in 20 mM Tris-Cl (pH 8.0), 200 mM KCl, 20 mM MgCl₂, 0.2 mM EDTA, and 1 mM DTT using a 100K MWCO Amicon Ultra-4 centrifugal filter (EMD Millipore), 0.2 mL glycerol was added, and the sample was stored at –20°C.

To denature RNAP-DNA complexes, 25 μL of the concentrated eluate was mixed with 25 μL water, 15 μL 5 M NaCl, and 6 μL 100 $\mu\text{g}/\text{ml}$ heparin, incubated at 95°C for 5 min, then incubated at 4°C for 5 min. Crosslinked RNAP-DNA complexes were isolated by adding 20 μl MagneHis Ni-particles equilibrated and suspended in 1 X *Taq* DNA polymerase buffer, 10 $\mu\text{g}/\text{ml}$ heparin, and 0.1 mg/ml BSA; MagneHis Ni-particles were collected using a magnetic microfuge tube rack; particles were washed with 50 μl 10 mM Tris-Cl, pH 8.0, 1.2 M NaCl, 10 mM MgCl₂, 10 $\mu\text{g}/\text{ml}$ heparin, and 0.1 mg/ml BSA, washed twice with 50 μl 1 X *Taq* DNA polymerase buffer (New England Biolabs), and the particles (which contained bound RNAP-DNA complexes) were resuspended in 10 μl 1 X *Taq* DNA polymerase buffer. Primer extension reactions and analysis of radiolabeled products generated in these reactions were performed

using procedures identical to those used in the analysis of p_ElacCONS *in vitro* (see above) using material isolated from cells containing pCDF-lacCONS (Figure 4B), cells containing the pCDF-lacCONS-N11 library (Figure 5B), or cells containing the pCDF-lacCONS-N20 library (Figure S4). XACT-seq experiments (see below) were performed using denatured RNAP-DNA complexes isolated from cells containing the pCDF-lacCONS-N11 library.

XACT-seq: primer extension

Primer extension reactions (50 µl) were performed by combining 8 µl of recovered RNAP-DNA complexes, 1 µl of 1 µM primer s128a, 5 µL 10 X dNTPs (2.5 mM dATP, 2.5 mM dCTP, 2.5 mM dGTP, 2.5 mM dTTP), 1 µL 5 U/µl Taq DNA polymerase, 20 µL 5 M betaine, 2.5 µL 100% dimethyl sulfoxide, and 5 µl 10 X Taq DNA polymerase buffer, and cycling 40 times through 30 s at 95°C, 30 s at 55°C, and 30 s at 72°C. Primer extension products were isolated by ethanol precipitation, washed twice with 80% cold ethanol, resuspended in 20 µl water, and mixed with 20 µl of 2 X RNA loading dye (95% deionized formamide, 18 mM EDTA, 0.25% SDS, xylene cyanol, bromophenol blue, amaranth).

Primer extension products were separated by electrophoresis on 10% 7M urea slab gels (equilibrated and run in 1 X TBE). The gel was stained with SYBR Gold nucleic acid gel stain (Life Technologies) and ssDNA products ~35- to ~75-nt in size were excised from the gel. To elute nucleic acids from the gel, the gel fragment was crushed as described in Vvedenskaya et al. (2018a), 350 µL of 0.3 M NaCl in 1 X TE buffer was added, the mixture was incubated for 10 min at 70°C, and the supernatant was collected using a Spin-X column (Corning). The elution procedure was repeated, supernatants were combined, and nucleic acids were recovered by ethanol precipitation, washed twice with 80% cold ethanol, and resuspended in 5 µL of nuclease-free water.

XACT-seq: 3'-adaptor ligation and library amplification

The recovered primer extension products (5 µl) were combined with 1 µL 10 X NEB buffer 1, ~0.8 µM 3'-adaptor oligo s1248 [5' adenylated and 3' end blocked oligo containing ten randomized nucleotides (10N) at the 5' end], 5 mM MnCl₂ and 1 µM of 5'-AppDNA/RNA ligase (New England Biolabs) in a final volume of 10 µl. The mixture was incubated for 1 h at 65°C followed by 3 min at 90°C, and cooled to 4°C for 5 min. The reaction was combined with 15 µL of mixture containing 10 U of T4 RNA ligase 1 (New England Biolabs), 1 X T4 RNA ligase 1 reaction buffer, 12% PEG 8000, 10 mM DTT, 60 µg/mL BSA. Reactions were incubated at 16°C for 16 h.

Adaptor-ligated products were separated by electrophoresis on 10% 7M urea slab gels (equilibrated and run in 1 X TBE). The gel was stained with SYBR Gold nucleic acid gel stain and species ranging from ~60 to ~100-nt (for reactions containing oligo s1248 and primer extension products) or ~50 and 90 nt (for reactions containing oligo s1248 and oligo JW402) were isolated by gel excision. The gel fragment was crushed, 700 µL of 0.3M NaCl in 1 X TE buffer was added, the mixture was incubated for 2 h at 37°C, the supernatant was collected using a Spin-X column (Corning). The elution procedure was repeated, supernatants were combined, and nucleic acids were recovered by ethanol precipitation, washed twice with 80% cold ethanol, and resuspended in 13 µL of nuclease-free water.

Adaptor-ligated DNA (5 µl) were used as template in emulsion PCR (ePCR). Reactions contained 1 X Detergent-free Phusion HF reaction buffer containing 5 µg/ml BSA, 0.4 mM dNTPs, 0.5 µM Illumina RP1 primer, 0.5 µM Illumina index primer and 0.04 U/µl Phusion HF polymerase [95°C for 10 s, 95°C for 5 s, 60°C for 5 s, 72°C for 15 s (20 cycles), 72°C for 5 min]. Amplicons were recovered using a Micellula DNA Emulsion and Purification Kit. The emulsion was broken, DNA was purified according to the manufacturer's recommendations, recovered by ethanol precipitation, and resuspended in 20 µL of nuclease-free water. Reaction products were separated by electrophoresis on a non-denaturing 10% slab gel (equilibrated and run in 1 X TBE), and amplicons between ~160 bp and ~170 bp were isolated by gel excision. The gel fragment was crushed, 600 µL of 0.3M NaCl in 1 X TE buffer was added, the mixture was incubated for 2 h at 37°C, the supernatant was collected using a Spin-X column. The elution procedure was repeated, supernatants were combined, and nucleic acids were recovered by ethanol precipitation, washed twice with 80% cold ethanol, and resuspended in 20 µL of nuclease-free water.

Libraries generated by this procedure are: CP21/CP21D, CP23/CP23D, CP27/CP27C, CP22/CP22D, CP24/CP24D, and CP28/CP28C (where “/” indicates libraries that are technical replicates). Libraries CP21/CP21D, CP23/CP23D, and CP27/CP27C are generated from material isolated from cells not treated with rifampin. Libraries CP22/CP22D, CP24/CP24D, and CP28/CP28C are generated from material isolated from cells treated with rifampin. Each library was analyzed by HTS using an Illumina NextSeq with custom sequencing primer s1115. Results were used to define the RNAP occupancy at each position from -3 to +20 on each promoter sequence as described below.

XACT-seq: analysis of template sequences in the placCONS-N11 library

We performed ePCR reactions with ~10⁹ molecules of the p_ElacCONS-N11 plasmid library, 1 X Detergent-free Phusion HF reaction buffer, 5 µg/ml BSA, 0.4 mM dNTPs, 0.5 µM Illumina RP1 primer, 0.5 µM Illumina index primer and 0.04 U/µl Phusion HF polymerase [95°C for 10 s, 95°C for 5 s, 60°C for 5 s, 72°C for 15 s (20 cycles), 72°C for 5 min]. Amplicons were recovered using a Micellula DNA Emulsion and Purification Kit. The emulsion was broken, DNA was purified according to the manufacturer's recommendations, recovered by ethanol precipitation, and resuspended in 20 µL of nuclease-free water. Products were subjected to electrophoresis on a non-denaturing 10% slab gel (equilibrated and run in 1 X TBE), the 204 bp fragment was excised from the gel. The gel fragment was crushed, 600 µL of 0.3M NaCl in 1 X TE buffer was added, the mixture was incubated for 2 h at 37°C, the supernatant was collected using a Spin-X column. The elution procedure was repeated, supernatants were combined, and nucleic acids were

recovered by ethanol precipitation, washed twice with 80% cold ethanol, and resuspended in 20 μ L of nuclease-free water. The library generated by this procedure, CP26T, was analyzed by HTS using an Illumina NextSeq with custom sequencing primer s1115. Results were used to identify barcodes associated with each initial-transcribed region sequences in the placCONS-N11 library (see below).

XACT-seq: data analysis

We selected sequencing reads in sample CP26T that matched sequences from positions -39 to +2 and from positions +14 to +31 of placCONS-N11 (aggct**ttgacactt**tatgc~~tcgg~~tcg**tataat**tg~~tg~~gaannnnnnnnnngataacaattcaacaatnnnnnnnnnnnt~~gg~~attctcg~~gg~~tgccagg; -35 element and -10 element are in bold; randomized sequences in the initial-transcribed region, +3 to +13, and in the barcode region, +32 to +48, are underlined). From this subset of reads, we identified barcodes associated with each initial-transcribed region sequence. Barcode sequences were used to identify initial-transcribed region sequences associated with primer extension products in libraries CP21/CP21D, CP23/CP23D, CP27/CP27C, CP22/CP22D, CP24/CP24D, and CP28/CP28C. The 3' end sequence of each primer extension product was used to identify positions of RNAP-DNA crosslinking and corresponding RNAP active-center A-site positions located 5 nt upstream. Next, we calculated the read count corresponding to crosslinks at each position (X) from +2 to +25 (RC_X) and the total number of reads derived from crosslinks at all positions from +2 to +25 (RC_{total}). The percent occupancy for each RNAP active-center A-site position from -3 to +20 was calculated using the formula: $100 \times (RC_X / RC_{total})$, where X is the position 5 nt downstream of the A site.

Table S1, column 1 shows the total number of template sequences where % occupancy at positions +3, +4, +5, +6, +7, +8, or +9 is $\geq 50\%$ in at least 2 of 3 replicates. Values of above-background pausing in Table S1, column 3 were calculated by eliminating pause sites where % occupancy at positions +5, +6, +7, +8, or +9 is $\geq 10\%$. The sequence logo shown in Figure 6A was generated using nontemplate-strand sequences for templates with $RC_{total} \geq 10$ having % occupancy values in the top 0.1% for promoter positions +5, +6, +7, +8, and +9. The sequence logos shown in Figure 6C were generated using templates with $RC_{total} \geq 10$ having % occupancy values in the top 0.1% for promoter positions +3, +4, +5, +6, +7, +8, or +9. Each sequence logo was generated from 480 out of 480,000 sequences for which $RC_{total} \geq 10$ (Wagh, 2017).

The plot shown in Figure 6B depicts mean % occupancy for nontemplate-strand tetranucleotide sequences at RNAP active-center positions P₋₁, P, A, and A₊₁ for promoter position +5, +6, +7, +8, and +9. Plots shows the mean and SEM calculated from three biological replicates. The plots shown in Figure S6 depict mean % occupancy for nontemplate-strand dinucleotide sequences at RNAP active-center positions A and A₊₁ for promoter positions +3 or +4 or for nontemplate-strand tetranucleotide sequences at RNAP active-center positions P₋₁, P, A, and A₊₁ for promoter positions +5, +6, +7, +8, or +9.

QUANTIFICATION AND STATISTICAL ANALYSIS

Statistical details of experiments including the number of replicates (n) and dispersion and precision measures can be found in the figure legends and [Method Details](#).

Supplemental Information

XACT-Seq Comprehensively Defines the Promoter-Position and Promoter-Sequence Determinants for Initial-Transcription Pausing

Jared T. Winkelman, Chirangini Pukhrambam, Irina O. Vvedenskaya, Yuanchao Zhang, Deanne M. Taylor, Premal Shah, Richard H. Ebright, and Bryce E. Nickels

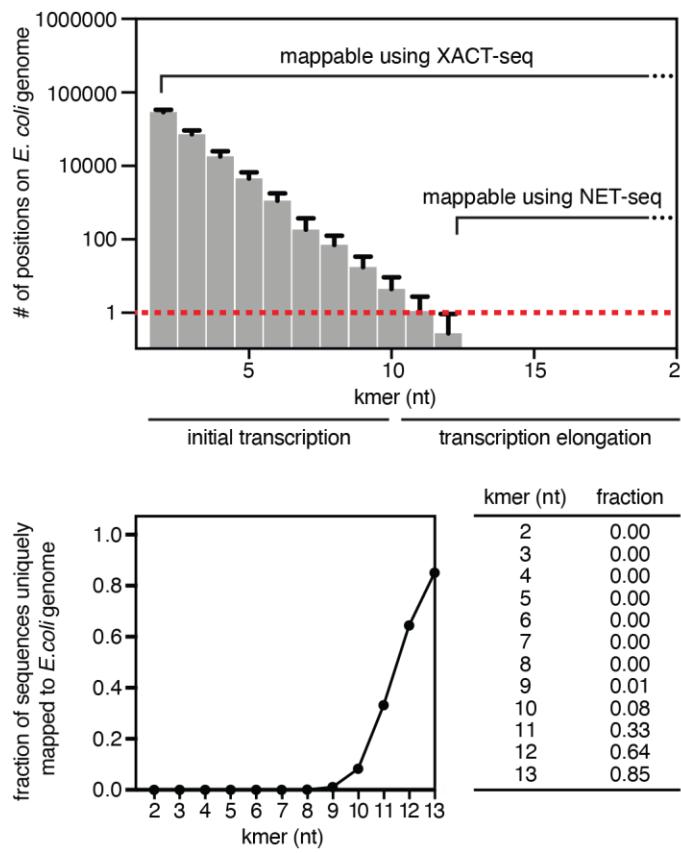
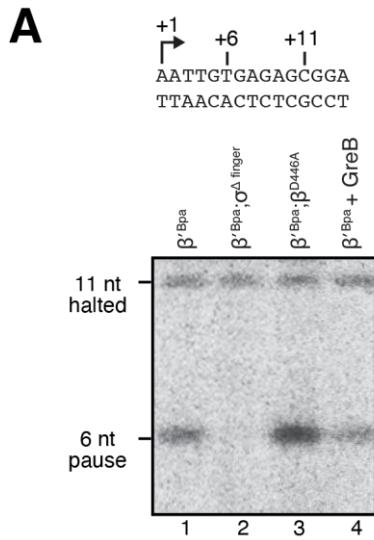


Figure S1. Inapplicability of RNA-based sequencing methods, such as NET-seq, for analysis of initial transcription, related to Figure 2.

Relationship between RNA product length and number of occurrences of sequence on the *E. coli* genome. Top, plot of mean \pm SD of the number of occurrences of sequences on the *E. coli* genome as a function of RNA length. Bottom, fraction of sequences uniquely mappable to the *E. coli* genome as a function of RNA length. Because essentially all RNA products ≤ 10 nt, and a substantial number of RNA products ≤ 13 nt, have more than one occurrence on the *E. coli* genome, and because many RNA product sequences ≤ 13 nt are not uniquely mappable to the *E. coli* genome, RNA-based sequencing methods cannot be used to study initial transcription. In contrast, because RNAP-active-center A-site positions for RNA products of any length are mappable to the *E. coli* genome using XACT-seq, this method can be used for analysis of initial transcription.



B

RNAP	6-nt RNA (% of total)	%XL ₊₁₁
β' Bpa	60 ± 4	68 ± 9
β' Bpa; σ^Δ finger	7 ± 4	19 ± 11
β' Bpa; β D446A	75 ± 2	95 ± 4
β' Bpa + GreB	48 ± 2	79 ± 6

Figure S2. Initial-transcription pausing at placCONS *in vitro*: quantitation of RNA 3' ends, related to Figure 3.

(A) Top, sequence of placCONS initial-transcribed region. Bottom, PAGE analysis of products of transcription reactions. Reactions performed using ApA as the initiating entity and using [α^{32} P]-GTP, ATP, and UTP as extending nucleotides, yields halted TECs containing +11 nt RNA products. Positions of the 11-nt RNA product associated with halted complexes and the 6-nt RNA product associated with paused complexes are indicated. +6, position of pausing; +11, position of halting; β' Bpa, RNAP- β' R1148Bpa; β' Bpa; σ^Δ finger, RNAP- β' R1148Bpa containing the σ finger deletion; β' Bpa; β D446A, RNAP- β' R1148Bpa containing β substitution D446A.

(B) Pause efficiencies calculated by quantification of yields of 6-nt RNA products or yields of crosslinks at position +11 (%XL₊₁₁; see Figure 4A). Percentage of 6-nt RNA products or +11 crosslinks are means ± SD from three independent experiments.

placCONS
 -35 element -10 element +1
 CTTGACA CTTTATGCTTCGGCTCG TATAAT GTGTGG AATTGTGAGAGCGGATAAC
 GAACTGT GAAATACGAAGCCGAGC ATATTACACACC TAAACACTCTCGCTATTG

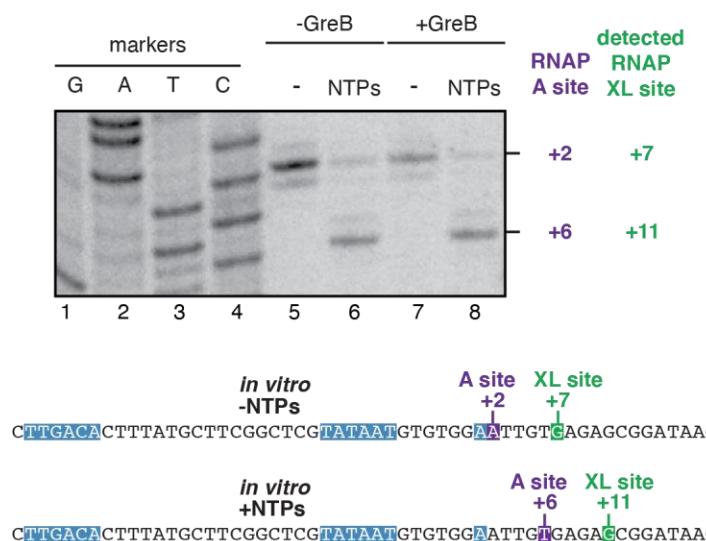


Figure S3. RNAP-active-center A-site positions in initial-transcription pausing at placCONS *in vitro*: effect of GreB, related to Figure 4.

Top, *lacCONS* promoter (placCONS). Middle, results of protein-DNA photocrosslinking assays. PAGE analysis of primer-extension products identifies positions of nucleotides crosslinked to Bpa. Bottom, position of RNAP-active-center A-site (purple) and nucleotide crosslinked to Bpa (green) defined relative to the TSS position. Markers, DNA sequence ladder generated using the placCONS template. Symbols and colors as in Figures 1 and 2.

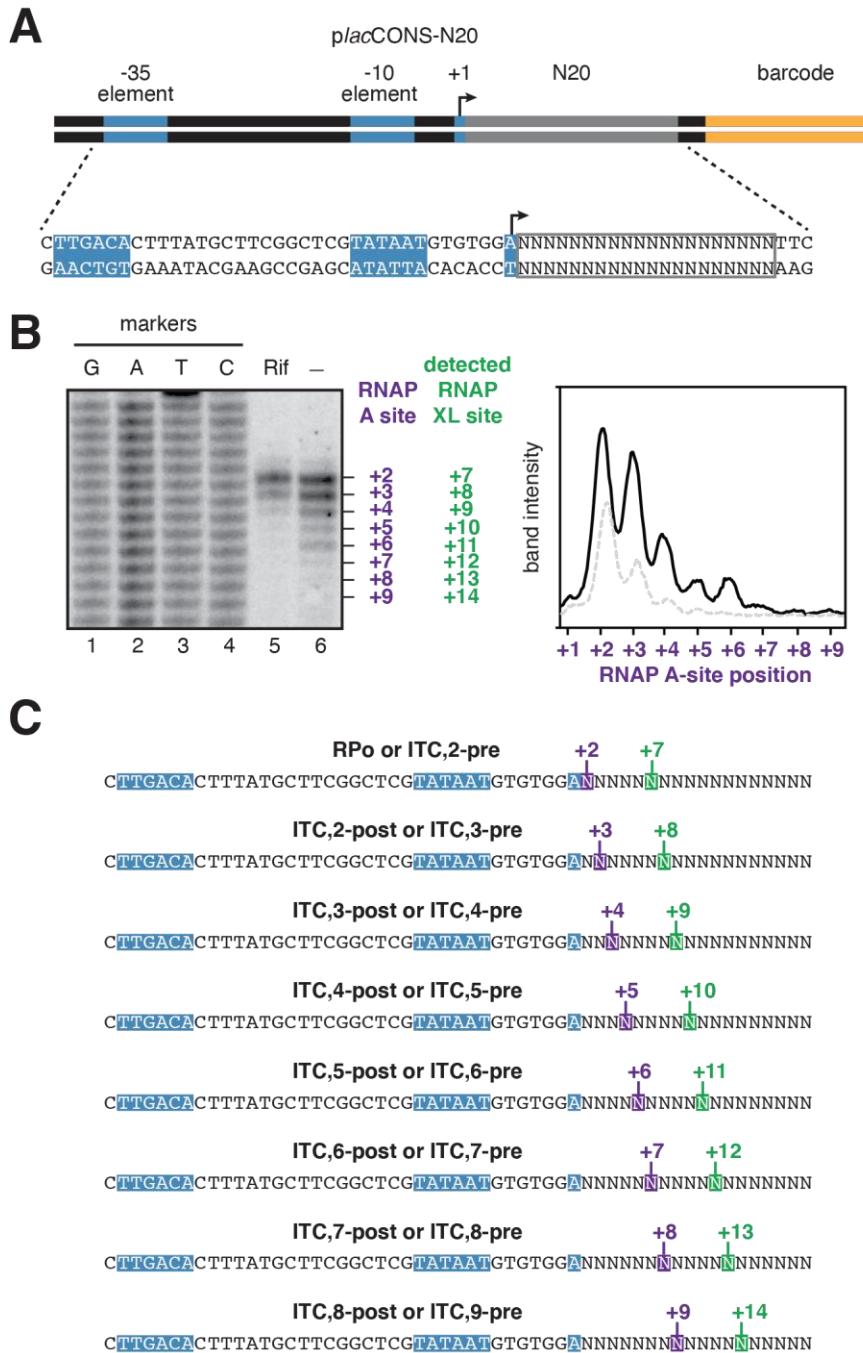


Figure S4. Promoter-position dependence of initial-transcription pausing for a library of up to 4^{20} promoter sequences *in vivo*, related to Figure 5.

(A) placCONS template library containing randomized sequences from promoter position +2 to promoter position +21 (placCONS-N20).

(B) Left, PAGE analysis of RNAP-active-center A-site positions *in vivo*. Markers, DNA sequence ladder generated using placCONS-N20. Right, histogram showing signals detected in absence (black line) or presence (grey line) of Rif.

(C) Position of RNAP-active-center A-site (purple) and nucleotide crosslinked to Bpa (green) defined relative to the TSS position, +1.

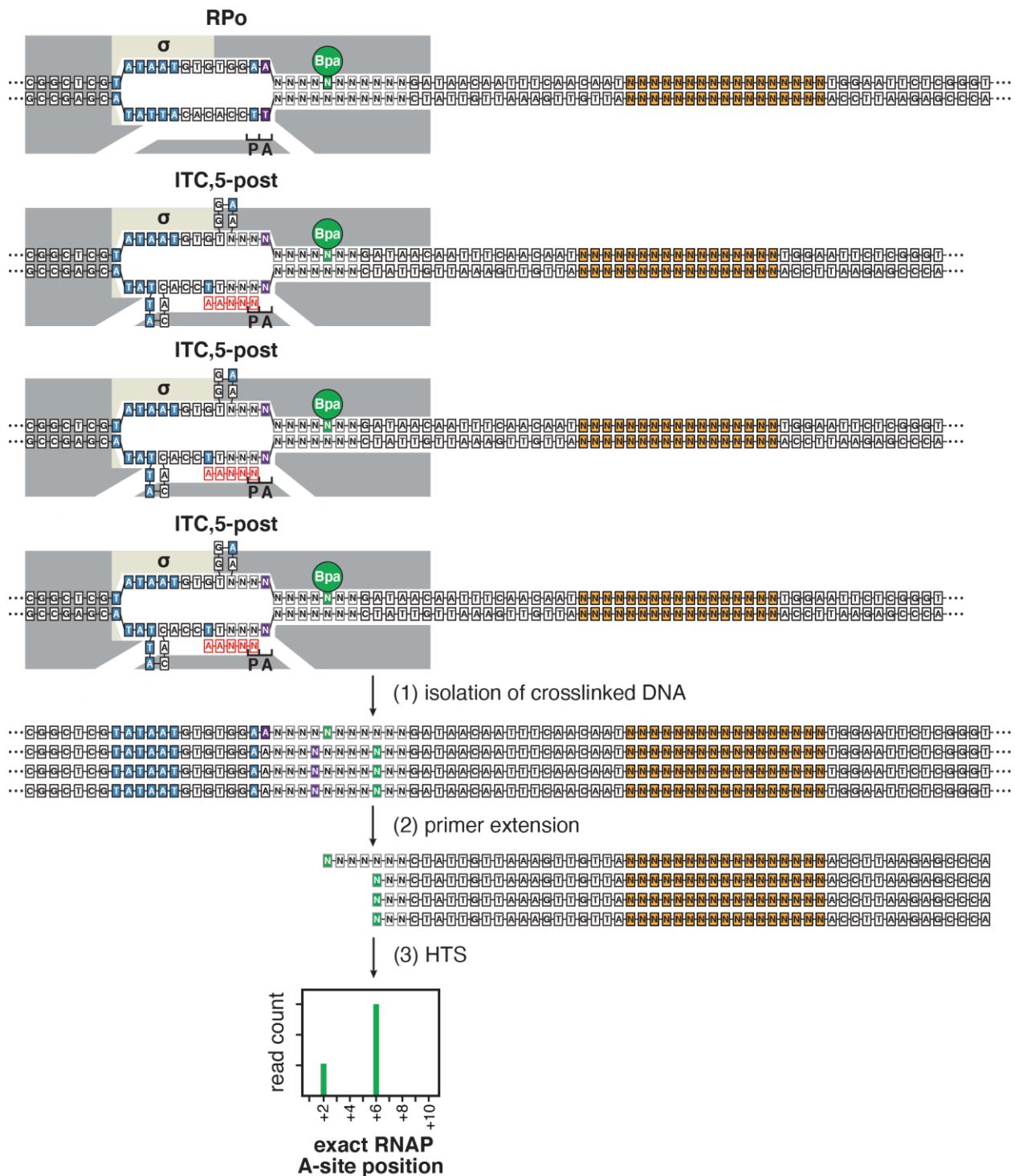


Figure S5. Identification of RNAP-active-center A-site positions in initial transcription by XACT-seq, related to Figure 6.

Identification of RNAP-active-center A-site positions for transcription complexes formed on *placCONS-N11* template sequences. Grey boxes, nucleotides of the randomized initial-transcribed region (+3 to +13); orange-filled boxes, nucleotides of the randomized barcode region (+32 to +48). Other colors and symbols as in Figure 4C.

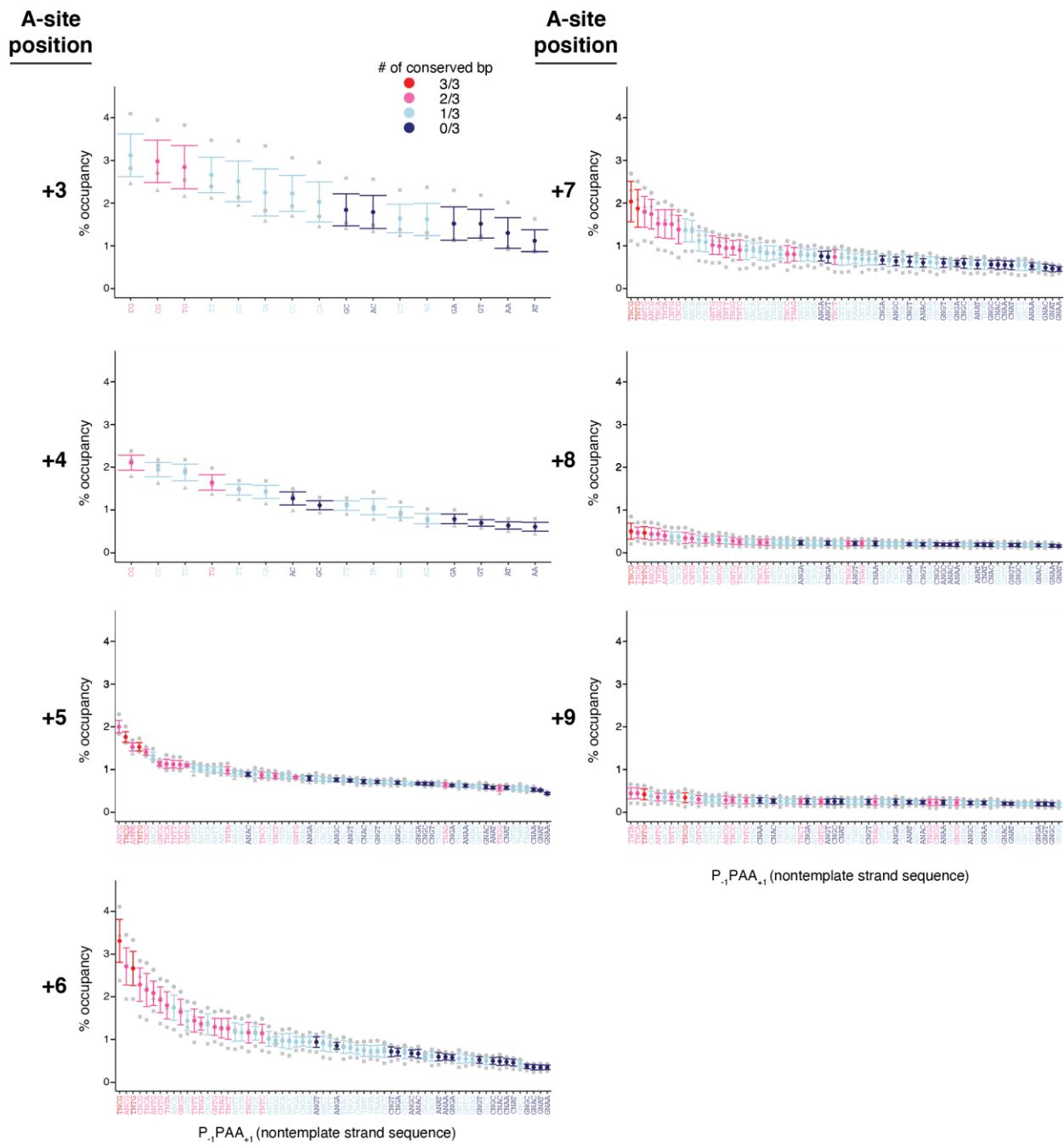


Figure S6. Promoter-sequence determinants for initial-transcription pausing in a library of 4^{11} (~4,000,000) promoters *in vivo*: additional data, related to Figure 6.

Percent occupancy at each dinucleotide sequence (for RNAP-active-center A-site positions +3 and +4) or at each tetranucleotide sequence (for RNAP-active-center A-site positions +5 to +9). Colors as in Figure 6B. Mean \pm SEM ($n = 3$).

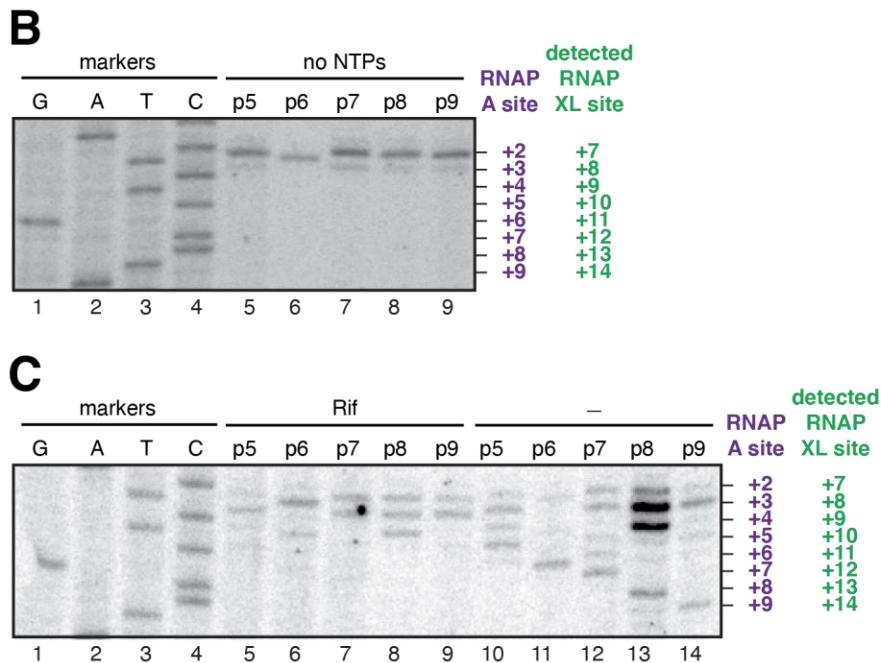


Figure S7. Promoter-sequence determinants for initial-transcription pausing in a library of 4^{11} (~4,000,000) promoters *in vivo*: additional data, related to Figure 6.

- (A) Representative sequences yielding high RNAP occupancy at RNAP-active-center A-site positions +5, +6, +7, +8, or +9, respectively. Colors as in Figure 5C.
- (B) RNAP-active-center A-site positions and crosslinking positions *in vivo* for the sequences of A with high RNAP occupancy at RNAP-active-center A-site positions +5, +6, +7, +8, or +9. Lanes 1-4 present sequence markers, lanes 5-9 present data for RNAP- β' R1148Bpa in the presence of the RNAP inhibitor rifampin, and lanes 10-14 present data for RNAP- β' R1148Bpa in the absence of rifampin.
- (C) RNAP-active-center A-site positions and crosslinking positions *in vitro* for the sequences of A with high RNAP occupancy at RNAP-active-center A-site positions +5, +6, +7, +8, +9. Lanes 1-4 present sequence markers, lanes 5-9 present data for RNAP- β' R1148Bpa in the absence of NTPs.

Table S1. *lacCONS-N11* template sequences containing pauses at positions +3 to +9 identified by XACT-seq, Related to Figure 6

A-site position	sequences with pausing	percentage of all sequences	above-background pausing defined by comparison of XACT-seq +/- rifampin	
			sequences with pausing	percentage of all sequences
+3	60,983	7.5	60,983	7.5
+4	21,572	2.7	21,572	2.7
+5	14,475	1.8	11,451	1.4
+6	24,635	3.0	20,165	2.5
+7	12,228	1.5	10,772	1.3
+8	596	.07	543	.06
+9	304	.04	299	.04
+3 to +9	119,662	14.7	113,692	14.0

Table S2. Oligonucleotides, Related to STAR Methods

s1219	tataatgcctgaccggcggttcagagttcacagtccgac gatc	oligo for amplifying and cloning <i>placCONS</i> libraries
s1220	aattaagccgctggggcccttggcacccgagaattcc	oligo for amplifying and cloning <i>placCONS</i> libraries
RP1	aatgatacggcgaccaccgagatctacacgttcagag ttctacagtccga	Illumina PCR primer (HPLC purified)
RPI1	caagcagaagacggcatacgagatcgatgtgactg gagttccttggcacccgagaattcca	Illumina indexing PCR primer 1 (HPLC purified)
s128a	ccttggcacccgagaattcc	used for primer extension on library templates
s1248	/5'Phos/nnnnnnnnnngatcgteggactgttagaa ctctgaac/3ddC/	3' adapter with 10N at 5' end (HPLC purified)