**Supplementary Information**

**Supplementary text.**

In general, single-round transcription assays allows us to identify abortive transcripts as a time-dependent increase in short transcripts up to 20 min. This is because abortive transcripts are very slowly and iteratively synthesized by the binary moribund complex. We compared the short transcript fraction at 20 min incubation with NTPs with that of 1.5 min incubation. The short transcripts increased time-dependently in 7 promoters but decreased in the remaining 2 promoters (nanA and pqiA) (Supplementary Figure S1A), consistent with the abortive/pausing-depleted classification (*X*≤0.5) of the 2 promoters. In the trpL promoter of the same *X*≤0.5 group, the short transcripts exceptionally increased over time. This inconsistency may be due to the different methods employed in the experiments in vivo and in vitro: we analyzed the nascent transcripts retained in the RNAP in vivo in our previous study [21] but here analyzed total transcripts in vitro because of the weak initiation from some promoters tested in vitro. Such an inconsistency may also be related to substantial anti-sense transcription observed in the experiment in vitro. In fact, the high level of anti-sense transcription was induced by GreAB in pykF promoter (Supplementary Figure S1B), which can explain why the short transcripts were increased by the Gre addition in this promoter while is classified as the abortive/pausing-enriched (*X*≥2) group.

**Supplementary Table S1.** DNA Sequences of the in vitro transcription templates.





**Supplementary Figure S1.** In vitro transcription from 9 different promoters that focus on short transcripts and antisense transcripts. (A) Time- and Gre-dependent changes in the fraction of short transcripts. (B) Antisense transcription that is stopped around TSS may affect initiation of sense transcription. See the legend of Figure 5B for details. (C) The condition of 1.5 min incubation with NTPs in the presence of Gre proteins provided the least abortive transcripts from the 9 promoters on average.



**Supplementary Figure S2.** Assignment of the imino proton signals. (A) The integrated signals of 14.2-13.0 ppm were assigned to *ITA* because of the tendency of negative correlation with GC content in the 9 promoter DNAs tested. (B) The remaining integrated signals of 13.0-11.6 ppm were assigned to *IGC* because of the tendency of positive correlation with the GC content as well as the larger intensities of the signals.