

Insights: Publications

NET-prism enables RNA polymerase-dedicated transcriptional interrogation at nucleotide resolution

RNA Biology, Volume 16, No. 9, 1156-1165

May 14, 2019

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The advent of quantitative approaches that enable interrogation of transcription at single nucleotide resolution has allowed a novel understanding of transcriptional regulation previously undefined. However, little is known, at such high resolution, how transcription factors directly influence RNA Pol II pausing and directionality. To map the impact of transcription/elongation factors on transcription dynamics genome-wide at base pair resolution, we developed an adapted NET-seq protocol called NET-prism (Native Elongating Transcription by Polymerase-Regulated Immunoprecipitants in the Mammalian genome). Application of NET-prism on elongation factors (Spt6, Ssrp1), splicing factors (Sf1), and components of the pre-initiation complex (PIC) (TFIID, and Mediator) reveals their inherent command on transcription dynamics, with regards to directionality and pausing over promoters, splice sites, and enhancers/super-enhancers. NET-prism will be broadly applicable as it exposes transcription factor/Pol II dependent topographic specificity and thus, a new degree of regulatory complexity during gene expression.

Related People



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