Stepwise chromatin remodelling by a cascade of transcription initiation of non-coding RNAs

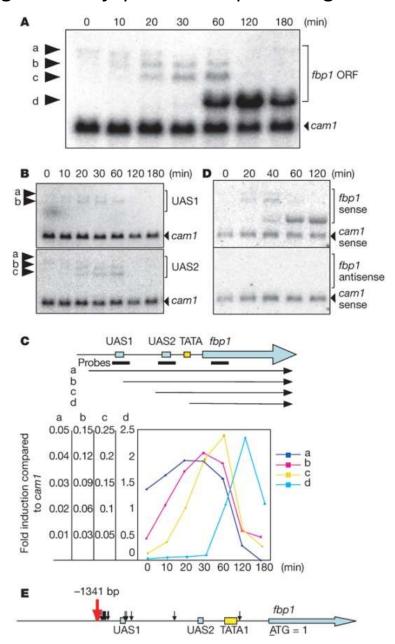
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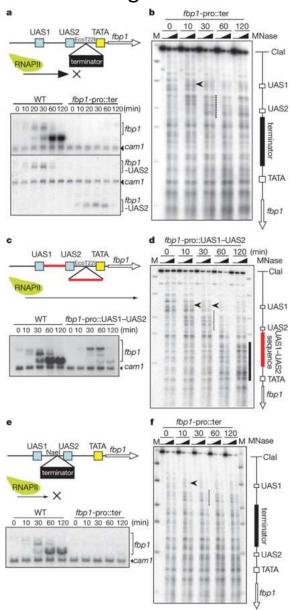
Recent transcriptome analyses using high-density tiling arrays $\frac{1}{2}$ - $\frac{1}{2}$ - $\frac{1}{2}$ and data from large-scale analyses of full-length complementary DNA libraries by the FANTOM3 consortium $\frac{4.5}{1}$ demonstrate that many transcripts are non-coding RNAs (ncRNAs). These transcriptome analyses indicate that many of the non-coding regions, previously thought to be functionally inert, are actually transcriptionally active regions with various features. Furthermore, most relatively large (~several kilobases) polyadenylated messenger RNA transcripts are transcribed from regions harbouring little coding potential. However, the function of such ncRNAs is mostly unknown and has been a matter of debate². Here we show that RNA polymerase II (RNAPII) transcription of ncRNAs is required for chromatin remodelling at the fission yeast Schizosaccharomyces pombe fbp1+ locus during transcriptional activation. The chromatin at $fbp1^+$ is progressively converted to an open configuration, as several species of ncRNAs are transcribed through fbp1+. This is coupled with the translocation of RNAPII through the region upstream of the eventual fbp1 + transcriptional start site. Insertion of a transcription terminator into this upstream region abolishes both the cascade of transcription of ncRNAs and the progressive chromatin alteration. Our results demonstrate that transcription through the promoter region is required to make DNA sequences accessible to transcriptional activators and to RNAPII.

Long and rare *fbp1*⁺ transcripts during transcriptional activation.

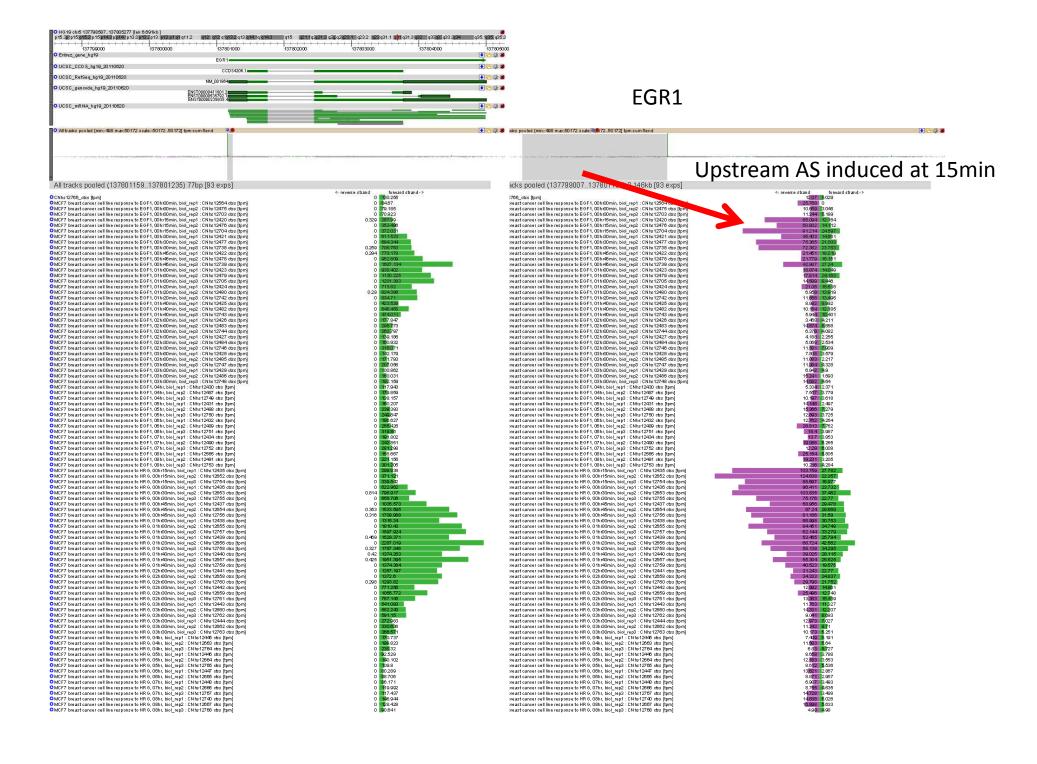


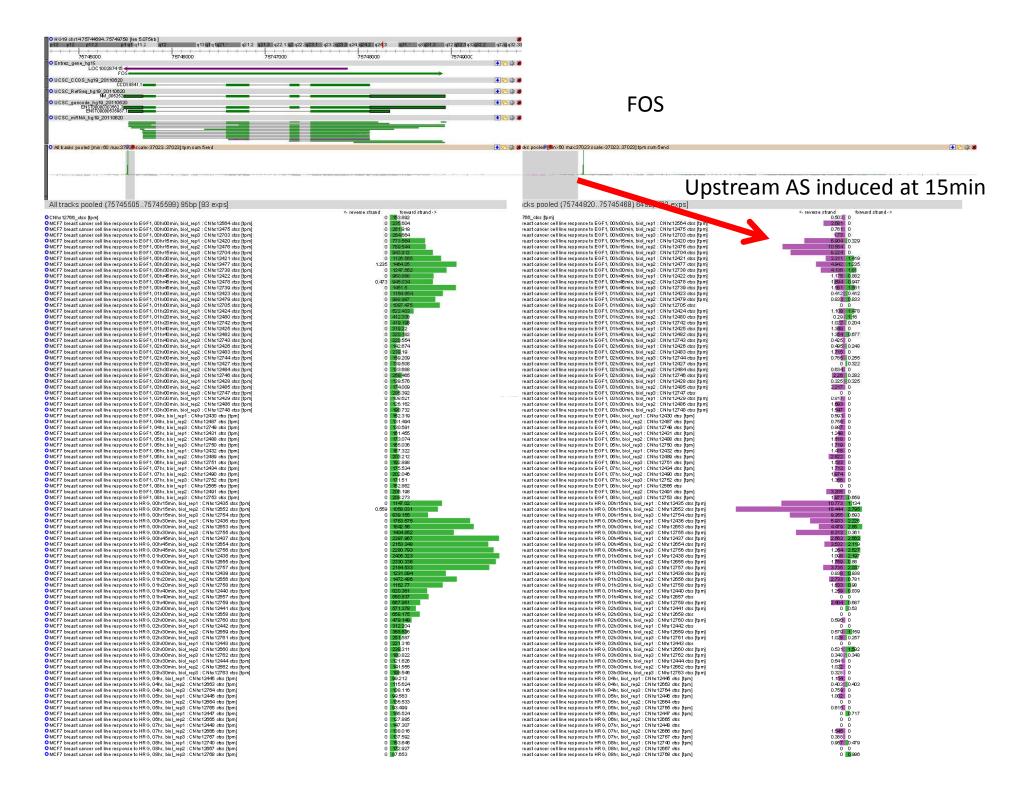


RNAPII passage along the $fbp1^+$ promoter is required for chromatin remodelling.









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