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The regulated retrotransposon transcriptome of mammalian cells

Geoffrey J Faulkner, Yasumasa Kimura, Carsten O Daub, Shivangi Wani, Charles Plessy, Katharine M Irvine, Kate Schroder, Nicole Cloonan, Anita L Steptoe, Timo Lassmann, Kazunori Waki, Nadine Hornig, Takahiro Arakawa, Hazuki Takahashi, Jun Kawai, Alistair R R Forrest, Harukazu Suzuki, Yoshihide Hayashizaki, David A Hume[7], Valerio Orlando, Sean M Grimmond & Piero Carninci

Abstract

Although repetitive elements pervade mammalian genomes, their overall contribution to transcriptional activity is poorly defined. Here, as part of the FANTOM4 project, we report that 6–30% of cap-selected mouse and human RNA transcripts initiate within repetitive elements. Analysis of approximately 250,000 retrotransposon-derived transcription start sites shows that the associated transcripts are generally tissue specific, coincide with gene-dense regions and form pronounced clusters when aligned to full-length retrotransposon sequences. Retrotransposons located immediately 5' of protein-coding loci frequently function as alternative promoters and/or express noncoding RNAs. More than a quarter of RefSeqs possess a retrotransposon in their 3' UTR, with strong evidence for the reduced expression of these transcripts relative to retrotransposon-free transcripts. Finally, a genome-wide screen identifies 23,000 candidate regulatory regions derived from retrotransposons, in addition to more than 2,000 examples of bidirectional transcription. We conclude that retrotransposon transcription has a key influence upon the transcriptional output of the mammalian genome.

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