

Tiny RNAs associated with transcription start sites in animals

Ryan J Taft¹, Evgeny A Glazov², Nicole Cloonan¹, Cas Simons¹, Stuart Stephen¹, Geoffrey J Faulkner¹, Timo Lassmann³, Alistair R R Forrest^{3,4}, Sean M Grimmond¹, Kate Schroder¹, Katharine Irvine¹, Takahiro Arakawa³, Mari Nakamura³, Atsutaka Kubosaki³, Kengo Hayashida³, Chika Kawazu³, Mitsuyoshi Murata³, Hiromi Nishiyori³, Shiro Fukuda³, Jun Kawai³, Carsten O Daub³, David A Hume^{1,5}, Harukazu Suzuki³, Valerio Orlando^{6,7}, Piero Carninci³, Yoshihide Hayashizaki³ & John S Mattick¹

Abstract

It has been reported that relatively short RNAs of heterogeneous sizes are derived from sequences near the promoters of eukaryotic genes. In conjunction with the FANTOM4 project, we have identified tiny RNAs with a modal length of 18 nt that map within -60 to +120 nt of transcription start sites (TSSs) in human, chicken and *Drosophila*. These transcription initiation RNAs (tiRNAs) are derived from sequences on the same strand as the TSS and are preferentially associated with G+C-rich promoters. The 5' ends of tiRNAs show peak density 10–30 nt downstream of TSSs, indicating that they are processed. tiRNAs are generally, although not exclusively, associated with highly expressed transcripts and sites of RNA polymerase II binding. We suggest that tiRNAs may be a general feature of transcription in metazoa and possibly all eukaryotes.

<http://www.nature.com/ng/journal/v41/n5/full/ng.312.html>