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## Functional elements in the non-coding genome: from populations to single cells

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Our genome is pervasively transcribed into RNAs, the majority of which are non-coding RNAs (ncRNAs) of unknown function. Many of these ncRNAs derive from gene distal DNA regions that regulate gene expression (cis-regulatory elements, CRE), known as enhancers. These enhancers harbor a large fraction of the genetic variants associated with diseases, which contribute to the disease predispositions through regulation of gene expression. Thus, mapping these non-coding transcription events can serve as a proxy to understand enhancer activities and their contributions to genetic predispositions. To build an accurate transcription map of our genome, we have developed molecular and bioinformatic methods to quantify transcription initiation events genome-wide, revealing the extensively intertwining transcription units, prompting us to reimagine the definition of a gene. Systematic knockdown of randomly selected ncRNAs revealed a significant fraction of them are potentially functional. To identify potentially