

DNase Hypersensitivity Analysis for Identification and Localization of Non-Coding Functional Elements

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Abstract

Identification and Characterization of non-coding functional elements also referred to as cis-regulatory sequences in the human genome remains a challenge for the post-genomic era. These elements are thought to coincide with DNase hypersensitive sites and form the major gene regulatory networks. Human genome contains a significant amount of regulatory DNA, the identification of which is proving somewhat recalcitrant to both in silico and functional methods. In this study, we used Quantitative PCR as a high throughput method for mapping these sites in the KIBRA gene. Robust primary and statistical analysis was performed to delineate the functional elements corresponding to spectrum of cis-regulatory activities including enhancers, promoters, locus control regions and insulators as well as novel elements.